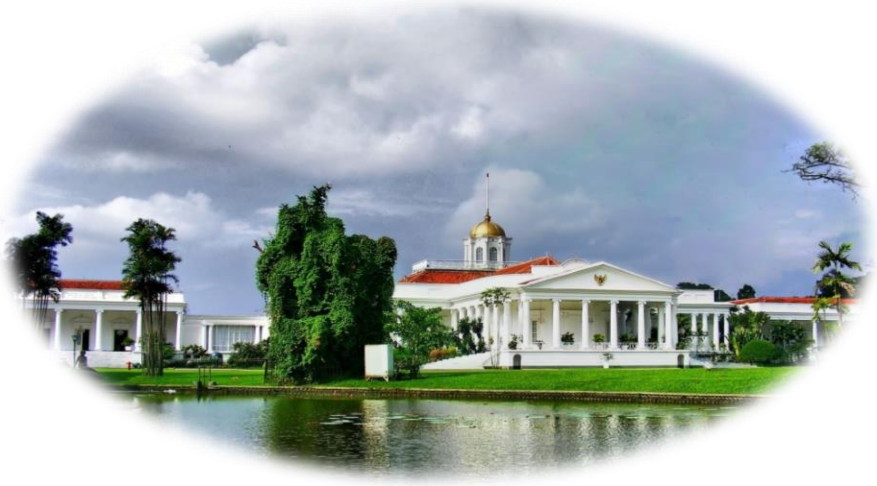
SABRAO 13th Congress and International Conference

Welcome to Bogor



IPB International Convention Center, 14-16 September 2015

SABRAO 13th Congress and International Conference

Welcoming Address from the President of SABRAO

Dear colleagues;

I welcome you to the 13th SABRAO Congress on “Contribution of Breeding Research for Sustainable Agricultural Production under Changing Environment for Food Security in Asia and Ocenia” organized by Society for the Advancement of Breeding Research in Asia and Oceania (SABRAO). The SABRAO Congress is a great scientific platform for scholars to exchange new research face to face.

This Conference is committed to actively raising the issues regarding breeding researches for future. As scientists, we should be prepared for possible agricultural problems in the future and our mission is to provide practical and step by step solution. Our conference covers a wide range of issues this time: conventional and molecular breeding, tolerance to biotic and abiotic stresses, genomics.

There are altogether over 100 oral and poster presentations from 13 countries in this Congress. Among them, six are invited speakers who will introduce the advancement of breeding research in their fields. I thank all speakers who come from various countries to give presentations and to join discussion.

I would like to thank all the members of the organizing committee and other staff from Department of Agronomy and Horticulture, Bogor Agricultural University for their hard work making the 13th SABRAO Congress a successful event.

I hope it will be an informative and inspiring experience for you.

Professor Dr. Sang-Nag Ahn
President, SABRAO

Schedule of the Conference

IPB International Convention Center, 14-16 September 2015

SABRAO 13th Congress and International Conference

Day 1 14 September 2015			
Time	**Activity**	**Title/person**	**Venue**
08.00-09.00	Registration		
09.00-09.15	Welcoming Address	President of the Society for the Advancement of Breeding Research in Asia and Oceania Prof Sang-Nag Ahn (Chungnam National University, South Korea)	Ballroom
09.15–09.30	Opening Ceremony	Rector of Bogor Agricultural University (Prof Herry Suhardiyanto)	Ballroom
09.30-10.00	Keynote Speech	NGS approach for understanding evolution and molecular breeding of resource crops Prof Tae-Jin Yang (Seoul National University, South Korea)	Ballroom
10.00 – 10.30	Coffee Break		
I. Plenary Sessions			
10.00-10.20	Invited Speaker	The role of breeding research in achieving food security: an Indonesian Experience Dr Satoto (Indonesian Center for Rice Research)	Ballroom
10.20-10.40	Invited Speaker	Genetic research for improvement of quality of crops for food, feed and bio-industry Prof Ian Godwin (University of Queensland)	
10.40-11.00	Discussion	Moderator	
11.00-11.30	Poster Session		
11.30-13.00	Lunch break and Poster viewing		
13.00-15.00	**Parallel Session I**		Meeting rooms

Day 1 14 September 2015

Time	Activity	Title/person	Venue
15.00–15.30	Poster Session and Coffee Break		
15.30-16.30	**Parallel Session II***		Meeting rooms
19.00–21.00	**Welcoming Dinner**		**Ballroom**

Day 2, 15 September 2015

Time	Activity	Topic & Person	Venue
08.30 -09.00	Poster Session and Coffee Break		
Plenary Session			
09.00 -09.30	Invited Speaker	Understanding Crop Stress Tolerance Mechanism to Improve Genetic Research Prof Tetsuo Takano (The University of Tokyo)	Ballrroom
09.30 -10.00	Invited Speaker	Breeding to support sustainable oil palm production Dr Dwi Asmono (PT Sampurna Agro. Tbk)	
10.00 -10.30	Invited Speaker	Preparing Future Breeders to Meet the Challange of Changing Environment. Prof Sobir (Bogor Agricultural University)	
10.30 -11.00	Discussion	Moderator	
11.00 -12.00	Poster Session		
11.00 -13.00	Lunch Break		
13.00 -15.00	**Parallel Session III**		
15.00 -15.30	Poster Session and Coffee Break		
15.30 -17.00	**Parallel Session IV**		

Day 3, 16 September 2015

Time	Activity	Topic & Person	Venue
07.00 -16.00	Excursion	Mekar Sari Fruit Garden and Research Center	

PARALLEL ORAL PRESENTATION
14 September 2015
Functional Genomic and Molecular -based Breeding
Venue : Ball Room 1

Time	Presentation	
	Parallel Session 1	
13.00 – 13.30	**Primary** Functional Genomic and Molecular-based Breeding Paper Prof Sudarsono (Bogor Agricultural University)	
13.30 – 13.45	**Discussion**	
13.45 – 14.00	Next-Gen-Based DNA Marker Development of Several Importance Crop and Animal Species. I Made Tasma, Habib Rijzaani, Dani Satyawan, Puji Lestari, Ida Rosdianti, Reflinur, Kristianto Nugroho, Rerenstradika Tizar, Razak Purba, Ellina Mansyah, Agus Sutanto, Rinda Kirana, Kusmana, Anneke Anggraeni, Marcia Pabendon, Rubiyo.	O-34
14.00 – 14.15	Global Alternative Splicing Profile of Mungbean (*Vigna radiata*) and Adzuki Bean (*Vigna angularis*) and Its Implications in Breeding and Genetic Studies. Dani Satyawan, Su Yeon Ha, Eun Soo Lee, Suk-Ha Lee	O-14
14.15 – 14.30	Mapping Major QTLs for Resistance to Cercospora Leaf Spot Disease in Yardlong Bean. Prakit Somta′, Usa Duangsong, Anochar Kaewwongwal, Sompong Chankaew, Peerasak Srinives	O-49

14.30 – 14.45	**Discussion**	
14.45 – 15.30	**Coffee Break and Poster Session**	
15.30 – 15.45	Development of Genome-Wide and Gene-Specific Markers for Assisting *Phalaenopsis* sp. Breeding in Indonesia. Sudarsono, Dewi Sukma, Aline S. Handini, Juanita Elina Asrina, Mega Dewi Indica	O-63
15.45 – 16.00	Marker Assisted Pyramiding of Drought Yield QTLs into a Quality Malaysian Rice Cultivar, Mas Wangi. Noraziyah Abd Aziz Shamsudin, Mallikarjuna M. Swamy,WickneswariRatnam, Ma. Teressa Sta. Cruz , Arvind Kumar	O-46
16.00 – 16.15	**Discussion**	

PARALLEL ORAL PRESENTATION
14 September 2015

Genetic diversity and sustainable use of genetic resources

Venue : Meeting Room A

Time	Presentation	
	Parallel Session 1	
13.00 – 13.30	**Primary Paper** Sustainable Use and Conservation of Indonesian Horticulture Germplasm. Dr Darda Efendi (Bogor Agricultural University)	
13.30 – 13.45	**Discussion**	
13.45 – 14.00	An Efforts of Mutation Breeding on Wild Raspberry (*Rubus*spp.) in Cibodas Botanical Garden. Muhammad Imam Surya, Lily Ismaini, Destri, Suluh Normasiwi	O-42
14.00 – 14.15	Exploration and Collection Sumatran Manggo Adaptable to High Rain Fall Sesion. Fitmawati, Nery Sofianti	O-28
14.15 – 14.30	Exploration and Collection of Saccharum Germplasm in Papua and Its Significance. Bambang Heliyanto, Abdurrahman	O-13
14.30 – 14.45	**Discussion**	
14.45 – 15.30	**Coffee Break and Poster Session**	
15.30 – 15.45	Reprobing the Misconception for the Reproduction System of Bali Salak Cultivars. G.G. Hambali, A Natawijaya	O-12
15.45 – 16.00	Genetic Diversity Analysis of Wheat Germplasm Collection of Indonesian Cereals Research Institute using SSR Markers. Reflinur, Aviv Andriani, Marcia B. Pabendon	O-53
16.00 – 16.15	Genetic diversity in Indonesian Waxy Corn inbred lines Using SSR markers. Sigit Budi Santoso, M. Yasin H.G, Marcia B. Pabendon	O-61
16.15 – 16.30	**Discussion**	

PARALLEL ORAL PRESENTATION
14 September 2015
Genetic improvement for adaptation to biotic and abiotic stress
Venue : Meeting Room B

Time	Presentation	
	Parallel Session 1	
13.00 – 13.30	**Primary** The use of anther culture to accelerate breeding program for abiotic stress tolerance in rice Prof Bambang S. Purwoko (Bogor Agricultural University)	
13.30 – 13.45	**Discussion**	
13.45 – 14.00	Plant Mutation Breeding using Gamma Greenhouse for the Improvement of Agronomic Traits with regards to Climate Change in Rice. Abdul Rahim Harun, Rusli Ibrahim, Khairuddin Abdul Rahim, Sobri Hussein, Shyful Azizi Abd Rahman, Shakinah Salleh, Faiz Ahmad	O-02
14.00 – 14.15	Heat Stress Tolerance in Seeds of Japonica Rice Cultivar under Treatment of Hot Water Disinfection Method. Permana, H; Kashiwagi, M; Murata, K; Nakaoka, K; Yamada,T; Kanekatsu	O-30
14.15 – 14.30	Performance of F_1 Genotypes and Their Parents Under High Temperature Conditions. Desta Wirnas, Rizky Paramita Sasti, Trikoesoemaningtyas, Hajrial Aswiwdinnoor, Surjono Hadi Sutjahjo, Siti Marwiyah	O-18
14.30 – 14.45	Evaluation of Brown Planthopper Resistant Related Traits, Aromatic, and Early Maturity by Molecular and Phenotypic Markers on Rice Genotypes Derived From a Pyrimiding. Riski Gusri Utami, Nono Carsono	O-57
14.45 – 15.00	**Discussion**	
15.00 – 15.30	**Coffee Break and Poster Session**	

15.30 – 15.45	Selection characters in early generation for adaptation of rice to high temperature strees. Victor Manotar Pademan Manalu, Desta Wirnas, S. Sudarsono, Hajrial Aswidinnoor, Surjono Hadi Sutjahjo, Siti Marwiyah	O-66
15.45 – 16.00	Search for Tomato Hybrids Suited for High Temperature Stress Condition. Kartikeya Srivastava, Sunil Kumar, H. R. Bhandari, A. Vaishampayan	O-36
16.00 – 16.15	Line x Tester Analysis to Study Combining Ability and Genetic Parameters of Hybrid Rice Drought Tolerance Traits at Germination Stage. Yuni Widyastuti, Bambang S. Purwoko, Iswari S. Dewi	O-72
16.15 – 16.30	**Discussion**	

PARALLEL ORAL PRESENTATION
14 September 2015
Genetic improvement for productivity and quality
Venue : Meeting Room C

Time	Presentation	
	Parallel Session 1	
13.00 – 13.15	Genotypes X Environments Interaction of Rice Genotypes at Altitude Difference. Trias Sitaresmi, Cucu Gunarsih, Nafisah, Buang Abdullah, Aan A. Daradjat	O-65
13.15 - 13.30	Genotype x Environment Interaction and Stability for Yield and Its Components in Hybrids Rice Adapted to Different Environment in Indonesia. Satoto, Y. Widyastuti, I.A. Rumanti, B.P. Wibowo	O-58
13.30 – 13.45	Analysis of Genotype × Environment Interaction using Stability Estimates in Maize (*Zea mays* L.). A. Aly , M.A. Al-Ashry, T. Bayoum, Manal Hefny, S. Okasha	O-01
13.45 – 14.00	**Discussion**	
14.00 – 14.15	Challenges Facing the Genetic Improvement of Underutilised Crops: Progress in Bambara Groundnut. Aryo B. Feldman	O-10
14.15 – 14.30	Bambara Groundnut Breeding for High Yielding and Early Maturity. Darmawan Saptadi, Niken Kendarini, Noer Rahmi Ardiarini, Kuswanto	O-16
14.30 – 14.45	Efficiency Single Seed Descent Method on Purify Morphological Characters of Bambara Groundnut (*Vigna subterranea* L. Verdcourt). Kuswanto, Niken Kendarini, Ainin Arif	O-37
14.45 – 15.00	**Discussion**	
15.00 – 15.30	**Coffee Break and Poster Presentation**	

15.30 – 15.45	Transgressive Segregation Selection in Peanut: Detection of F2 Transgressive Segregant Plants of Some Crosses. Yudiwanti Wahyu, Willy Bayuardi, Heni Purnamawati, Siti Nurhidayah, Andi Sauleka, Ika Inayah	O-71
15.45 – 16.00	Analysis on the Genetic Parameter and Combining Ability of Agronomic and Quality Traits of Hybrid Sorghum. Erin Puspita Rini, Trikoesoemanintyas, Desta Wirnas	O-24
16.00 – 16.15	Selection of Wheat Lines (Oasis x HP1744) in Two Tropical Agroecosystems. Yushi Mardiana, Yudiwanti Wahyu, Trikoesoemaningtyas, Amin Nur	O-73
16.15 – 16.30	**Discussion**	

PARALLEL ORAL PRESENTATION
14 September 2015

Genetic improvement for productivity and quality

(Parallel II)
Venue : Meeting Room D

Time	Presentation	
	Parallel Session 1	
	Others (Information technology, forest and tree breeding, animal breeding)	
13.00 – 13.15	Growth Rate of F-1 and F-2 Anglo Nubian x Etawah Grade Kids. Lisa Praharani.	O-39
13.15 – 13.30	CTAB's Modification : High-Quality Plant DNA Extraction for PCR with Heat Shock Treatment. Eka Jan Virgin Haquarsum, Surjono H Sutjahjo, Yudiansyah	O-22
13.30 – 13.45	The Response of Three New Varieties of Red Pepper to Biofertilizer Treatments. Neni Rostini, Farida Damayanti, Ade Ismail, Sudarjat, Reginawanti Hindersah, Arviandra, Geusan, Rio Fernando	O-45
13.45 – 14.00	Flowering Biology and Pollination of Dragon Fruits (*Hylocereus spp. and Selenicereus megalanthus*). Dea Nadila, Endah Retno Palupi, Winarso Drajad Widodo.	O-74
14.00 – 14.15	Characterization of Programmed Cell Death in Hybrid Tobacco Cells Expressing Hybrid Lethality. Naoya Ueno, Saori Nihei, Naoto Miyakawa, Motoki Kanekatsu, Wataru Marubashi, Wouter G. van Doorn, Tetsuya Yamada	O-43
14.15 – 14.30	**Discussion**	
14.30 – 15.30	**Coffee Break and Poster Session**	

	Genetic improvement for productivity and quality	
15.30 – 15.45	Level Difference of Natural Cross-Pollination on Three Genotypes of Chili Pepper (*Capsicum annuum* L.). Arya Widura Ritonga, Muhamad Syukur, Rahmi Yunianti, Sobir	O-09
15.45 – 16.00	Participatory Selection of Sweet Potato Based on Farmers Preferences in Banjar City, West Java, Indonesia. Haris Maulana, M. Divo Nugroho, Lucyana Trimo, Agung Karuniawan	O-31
16.00 – 16.15	Pedigree Selection for High Yielding Chili (*Capsicum annuum* L.). Respatijarti, Izmi Yulianah, Darmawan Saptadi	O-55
16.15 – 16.30	**Discussion**	

PARALLEL ORAL PRESENTATION

15 September 2015

Functional Genomic and molecular -based breeding

Venue : Ball Room 1

Time	**Presentation**	
	Parallel Session III	
13.00 – 13.15	Isolation of APETALA1 Homologous from Mangosteen(*Garcinia mangostana* L.). Darda Efendi, Roedhy Poerwanto, Tetty Chaidamsari, Herti Sugiarti, Warid Ali Qosim	O-15
13.00 – 13.15	Simple Sequence Repeat (SSR) Marker Development From Walnut (*Juglans regia*. L). Adi Surya Ikhsan, Hayat Topçu, Mehmet Sütyemez, Salih Kafkas	O-03
13.30 – 13.45	Comparative Sequence Analysis of Mungbean DNA Mismatch Repair Genes. Andari Risliawati, Tae-Young Lee, Dani Satyawan, Suk-Ha Lee	O-07
13.45 – 14.00	**Discussion**	
14.00 – 14.15	Chromosomal Location of QTL for Leaf Area and Leaf Area Duration Associated with QTL for Leaf Carbon Isotope Discrimination in Sunflower (*Helianthus annuus* L.). Afifuddin Latif Adiredjo	O-05
14.15 – 14.30	SNAP Markers as Indicators for Identification and Pigment Content Characterization Associated With Flower Color in *Phalaenopsis*. Dewi Sukma, Aline Sisi Handini, Sudarsono	O-19
14.30 – 14.45	Isolating Compound Microsatellite Markers and Its Application on Amorphophallus variabilis Populations in Darmaga Conservation Forest, Bogor, Indonesia. Edi Santosa, Chunlan Lian, Nobuo Sugiyama	O-78
14.45 – 15.00	**Discussion**	
15.00 – 15.30	**Coffee Break and Poster Session**	

	Parallel Session IV	
15.30 – 15.45	Utilization of 384-SNP Genotyping Technology for Seed Purity Test of New Rice Varieties Inpari HDB and Inpari Blast. D.W. Utami, I. Rosdianti, I.S. Dewi, D. Ambarwati, A. Sisharmini, A. Apriana, S.Yuriyah, I. Ridwan dan I. Hanarida	O-20
15.45 – 16.00	Genomic Prediction for Carotenoids in Maize. Willy B. Suwarno, Kevin V. Pixley, Natalia Palacios-Rojas, Shawn M. Kaeppler, Raman Babu	O-67
16.00 – 16.15	In Vitro Chromosome Mutation Induction in Dendrobium lasianthera (J.J. Smith) using Colchisine. Ni Made Armini Wiendi , Yogo Ardi Nugroho	O-82
16.15 – 16.30	**Discussion**	

PARALLEL ORAL PRESENTATION

15 September 2015

Genetic diversity and sustainable use of genetic resources

Venue : Meeting Room A

Time	**Presentation**	
	Parallel Session III	
13.00 – 13.15	Two different types of mangosteen (Garcinia mangostana L) from swampy area of Tembilahan-Indonesia and their level to gamboge disorder. Ellina Mansyah	O-23
13.00 – 13.15	Ploidy Level of Plans Derivedcallus Induced by Gamma Radiation and Ethyl Methane Sulphonate Affects Diversityof Leaves Number and Plant Height of Steviarebaudiana Bertoni. Suseno Amin	O-75
13.30 – 13.45	A preliminary study of Garcinia malaccensis collection in Taman Buah Mekarsari, Cileungsi, Bogor, Indonesia. G.G. Hambali, A. Natawijaya	O-29
13.45 – 14.00	**Discussion**	
14.00 – 14.15	Characterization Genetic Variability of Landrace Tomato Genotypes from Induced Mutation Process. Galuh Kusuma Wardani, Anggi Nindita, Surjono Hadi Sutjahjo	O-77
14.15 – 14.30	Mutagenic Effectiveness and Efficiency of Gamma Irradiation Techniques in 3 Wheat Lines. Wijaya Murti Indriatama, Trikoesoemaningtyas, Syarifah Iis Aisyah, Soeranto Human	O-80
14.30 – 14.45	A Decade of Durian Breeding at ITFRI. Panca Jarot Santoso, Ni Luh Putu Indriyan, Mizu Istianto	O-48
14.45 – 15.00	**Discussion**	
15.00 – 15.30	**Coffee Break and Poster Session**	

	Parallel Session IV	
15.30 – 15.45	Analysis of Genetic Diversity and Heterosis Potential of Recombinant Maize Inbred Lines Based on SSRs Marker (Simple Sequence Repeats). Mejaya, M.J., Sri Sunarti, dan M.B. Pabendon	O-62
15.45 – 16.00	Morphological Variability of Indonesian Rice Germplasm and the Associated SNP Markers. Puji Lestari, Dwinita Wikan Utami, Ida Rosdianti.	O-50
16.00 – 16.15	**Discussion**	

PARALLEL ORAL PRESENTATION
15 September 2015
Genetic improvement for adaptation to biotic and abiotic stress

Venue : Meeting Room B

Time	**Presentation**	
	Parallel Session 1	
13.00 – 13.15	Enhancing for Broad-Spectrum Resistance to Leaf and Neck Blast in *Japonica* Rice Using Weedy Rice (*Oryza sativa* L.). Young-Chan Cho, Man-Ki Baek, Jung-Pil Suh, Hyun-Su Park, Jong-Min Jeong, Jaw-Hwan Roh, Sung-Hoon Lee, Kshirod K. Jena, Bo-Kyeong Kim	O-69
13.15 – 13.00	Determination of NaCl Level for Screening of Rice Salinity Tolerance in the Green House. Heni Safitri, Bambang S. Purwoko, Iswari S. Dewi, Sintho W. Ardie	O-32
13.30 – 13.45	A Novel Phenotyping Technique for Reproductive-Stage Salinity Tolerance in Rice. Naireen A. Vispo, Cecilia Diana O. Calapit-Palao, Iris Dawn Pangaan, Rakesh. K. Singh	O-51
13.45 – 14.00	**Discussion**	
14.00 – 14.15	Antixenosis and Antibiosis Resistance of Chili Pepper Lines to Melon Aphid (Hemiptera: Aphididae). Ady Daryanto, Muhamad Syukur, Awang Maharijaya, Purnama Hidayat	O-04
14.15 – 14.30	Developing Bruchid Resistant Mungbean Varieties. R. M. Nair, M-R Yan, R. Srinivasan, R. Schafleitner	O-52
14.30 – 14.45	Generation Mean Analysis of Leaf Bronzing of Rice Seedling Using Digital Imaging Methods under High Levels of Iron. Yudhistira Nugraha, Sintho Wahyuning Ardie, Munif Ghulammahdi, Suwarno, Hajrial Aswidinnoor	O-70
14.45 - 15.00	**Discussion**	
15.00 – 15.30	**Coffee Break and Poster Session**	

15.30 – 15.45	Screening of 14 Potato Genotypes for Their Adaptation to Tropical Medium Altitude Conditions. Awang Maharijaya, G.A. Wattimena, Muhammad Syukur, Sobir, Muhamad Khudori, Sulaeman Taufik, Agus Purwito	O-11
15.45 – 16.00	Reaction to BPH resistance genes at seedling stageofrice. Kim Woo-Jae, Hyun-Su Park, Hyun-Soon Kim, Kyung-Ho Kang, Ji-Ung Jeong, Jae-BeomChun,Jae-Kwon Ko, Seong-Woo Cho, Bo-Kyeong Kim	O-68
16.00 – 16.15	Selection of Resistance for 24 Family F5 Chili (*Capsicum annuum*) to Bacterial Wilt (*Ralstonia Solanacearum*). Izmi Yulianah, Respatijarti, Darmawan Saptadi	O-76
16.15 – 16.30	Resistance of Banana Variants cv. Ampyang (*Musa acuminata*, AAA, subgroup non-Cavendish) to *Fusarium* Wilt. Reni Indrayanti Sukardiono, Asep Setiawan, Sudarsono	O-54
16.30 – 16.45	Assessment of Indonesian Rice Varieties for Tolerance to Aluminum Toxicity using Magnavaca Solution and 384 SNP array. Nurul Hidayatun, Joko Prasetiyono, Tobias Kretzschmar, Genaleen M Q Diaz, Sigrid Heuer, Abdelbagi M. Ismail	O-47
16.45 – 17.00	**Discussion**	

PARALLEL ORAL PRESENTATION

15 September 2015

Genetic improvement for productivity and quality

Venue : Meeting Room C

Time	Presentation	
	Parallel Session III	
13.00 – 13.15	Upland Rice Breeding Lines Adaptable to High Elevation Areas and Selected through Participatory Approaches. Aris Hairmansis, Supartopo, Yullianida, Warsono, Digna Manzanilla, Cassiana Vera Cruz, Ali Jamil, Suwarno.	O-08
13.00 – 13.15	Pedigree Selection of Red Rice (*Oryza sativa* L.) Offspring to New Plant Idiotype. Etti Swasti, Andrianto, Nurwanita Ekasari Putri, Aswaldi Anwar.	O-26
13.30 – 13.45	Effect of Mesocotyl Elongation on Seedling Emergence under Deep-Seeding Condition in Rice. Hyun-Sook Lee, Ju-Won Kang, Tadashi Sato, Sang-Nag Ahn.	O-33
13.45 – 14.00	**Discussion**	
14.00 – 14.15	Combining Ability for Yield and Agronomic Traits in Hybrid Rice Derived from WA, Gambiaca, and Kalinga Cytoplasmic Male Sterile System. Indrastuti A. Rumanti, Bambang S. Purwoko, Iswari S. Dewi, Yuni Widyastuti.	O-35
14.15 – 14.30	Evaluation and Selection of Double-haploid Lines for Enhancement of High-yielding Rice in Africa through KAFACI Program of Korea. Kang Kyung-Ho, Kyung-Rae Cho, Geun-Pyo Lee, Woo-Jae Kim, Jong-Min Jeong, Ji-Ung Jeung, Jae-beom Jeon, Bo-Kyeong Kim.	O-38
14.30 – 14.45	Combining Ability through Line × Tester Analysis and Heritability Studies in Upland Cotton. Naqib Ullah Khan	O-44
14.45 – 15.00	**Discussion**	
15.00 – 15.30	**Coffee Break and Poster Session**	

	Parallel Session IV	
15.30 – 15.45	Crossbreeding of *cry1Ac/bar* Transgenic Progeny with a Non-transgenic Elite Cultivar for Minimizing the Underlying Grain Cost of *Bt* Transgenic Rice. Mi-Ok Woo, Eunbyeol Koh, Hee-Jong Koh, Seok-Cheol Suh.	O-40
15.45 – 16.00	Conventional Rice Breeding for Meeting the Future Demands with Special Reference to Genetic Yield Enhancement and Stability. S.R. Das, B.C.Y. Collard, E. Septiningsih, U.S. Singh	O-59
16.00 – 16.15	Genetic x Environment Interaction of 180 New Superior Sweet Potato Clones on Low Land and Dry Land in Sumedang, West Java. Agung Karuniawan, Hanny Hidayati Nafi'ah, Fitratul H. Rusli, Debby Ustari, Wolfgang Grueneberg	O-06
16.15 – 16.30	Genetic Variability Orange Fleshed Sweet Potato as Industrial Raw Materials. Debby Ustari, Fitratul, Hanny, Agung Karuniawan	O-17
16.30 – 16.45	**Discussion**	

PARALLEL ORAL PRESENTATION

15 September 2015

Genetic improvement for productivity and quality

Parallel 2

Venue : Meeting Room D

Time	Presentation	
	Parallel Session III	
13.00 – 13.15	Genetic Variability and Selection of Coconut (*Cocos nucifera*) Genotypes for High Coconut Milk Yield in Malaysian Agricultural and Research Development Institute (MARDI). G.K. Sentoor, I.Khairol, M.Y.Rafii, D.Thiyagu.	O-60
13.00 – 13.15	Breeding Tomato (*Lycopersicon esculentum* Mill.) for Lowland Area Using Half Diallel Crossing. Estriana Riti, Muhamad Syukur	O-25
13.30 – 13.45	Estimation of Combining Ability and Heterosis for Yield Component of Local Tomatoes in Half Diallel. Gumelar RMR, Sutjahjo SH, Wirnas D, Herison C, Sulastri I, Nindita A, Marwiyah S	O-56
13.45 – 14.00	**Discussion**	
14.00 – 14.15	Characteristic Stability Analysis of Eggplant (*Solanum melongena* L.) Genotypes using Parametric and Nonparametric Approaches. Faradila Danasworo Putri, Sobir, Muhamad Syukur, Awang Maharijaya	O-27
14.15 – 14.30	Physiochemical Properties of Flours and Starches of Cassava Accessions from Western Ceram, Indonesia. Febby J. Polnaya, Helen Hetharie, Gelora H. Augustyn, Simon H.T. Raharjo	O-81
14.30 – 14.45	Genetic Control of Soybean Seed Storability Under Room Temperature Conditions. Eny Widajati, Desta Wirnas, Kade Ari Oktaviani	O-79
14.45 – 15.00	**Discussion**	
15.00 – 15.30	**Coffee Break and Poster Session**	

	Parallel Session IV	
15.30 – 15.45	Current Status on Oil Palm Breeding in Indonesia. Edy Suprianto, Yurna Yenni, Sri Wening, Abdul Razak Purba	O-21
15.45 – 16.00	Genetic Performance of Vegetative Traits of MPOB Oil Palm Interspecific Hybrids in Inland and Coastal Soils. Mohd Din Amiruddin, Rajanaidu, N., Kushairi, A, Marhalil, M.	O-41
16.00 – 16.15	The Use of Embryo Culture in Rice Amylose Breeding. Taryono, Didi Hardjanto, Nasrullah.	O-64
16.15 – 16.30	**Discussion**	

Poster Presentation

N0	Name	Title
P-01	Abebe Megersa Diriba, Dongryung Lee, Jeonghwan Seo, Backki Kim, Zhuo Jin and Hee-Jong Koh	Fine Mapping of Panicle Tip Mutant *pnt* in rice (*Oryza sativa* L.)
P-02	Apri Sulistyo, Sumartini	Heritability of Rust Disease Resistance in F_3-F_4 Soybean Populations Using Variance Component Analysis and Parent-Offspring Regression Method
P-03	Dewi Indriyani Roslim, Nur Octavia, Herman	Analysis of Partial DNA Sequences of *Linamarase* Gene on Roti and Menggalo Cassavas (*Manihot esculenta* Crantz.)
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N0	Name	Title

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N0	Name	Title

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P-34	Yunandra	Inheritance Yield Component Character of Pepper (*Capsicum annuum* L.) Curly and Big Chili Pepper Crosses
P-35	Hapsoh, Gusmawartati and Di Ajeng Prameswari[2]	Isolation and Identification of Peat Soils Phosphate Solvent Bacteria in Giam Siak Kecil Biosphere Conservation-Bukit Batu, Bengkalis, Riau

N0	Name	Title

P-36	Maria Afnita Lelang, Yudiwanti Wahyu, Heni Purnamawati	Stability Analysis on Leaf Spot Resistance of Peanut (*Arachis hypogaea* L.) Promising Lines Developed by BAU
P-37	Junghoon Lee, Nur Kholilatul Izzah, Beom-Soon Choi, Ho Jun Joh, Sang-Choon Lee, Sampath Perumal, Joodeok Seo, Kyounggu Ahn, Eun Ju Jo, Gyung Ja Choi, Ill-Sup Nou, Yeisoo Yu, Tae-JinYang	Identification of clubroot resistance QTLs and revision of reference genome assembly in cabbage using a new genotyping-by-sequencing map
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P-39	Simon HT Raharjo, Helen Hetharie, Meitty L. Hehanussa, Jeter D. Siwalette, Edyzon Jambormias	Diversity of Minor Food Legumes in Maluku Tenggara Barat District, Maluku Province, Indonesia
P-40	Ery Leonardo, Trikoesoemaningtyas, Desta Wirnas	Estimation of Genetics Variance and Selection Sorghum (*Sorgum bicolor* (L.) Moench) of Threee F2 Populations

Abstracts of Plenary Presentation

SABRAO 13th Congress and International Conference
“IPB International Convention Center, 14-16 September 2015”

Genetics and Biotech for Improving Crop Product Quality: Food, Feed and the Bio-Economy

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Abstract

In a world of rapidly growing human population, the demands on the agricultural systems for improved productivity are enormous. Increasing societal affluence has also led to increases in demand for animal protein (meat, eggs and dairy), and a requirement for improved nutritional quality of food and feed. Plant breeding and biotechnology have a key role to play in delivering not just more crop product, but higher quality crop product with a more sustainable ecological footprint. Using cereals (predominantly rice and sorghum) as a case study, I will discuss some of the advances which have been made in improving crop quality for specific end-uses. Using NextGen genomics technologies, we have found key signatures of directional and balancing selection in major starch biosynthesis genes. Association studies have identified a number of genes that have significant implications for human food uses, in particular the GBSS (waxy) and pullulanase debranching enzymes, which confer enhanced digestibility in monogastric animals and humans. Pullullanase allelic variants encoding two amino acid substitutions have higher enzyme activity which significantly alters starch branching patterns and molecule size in both amylose and amylopectin. We have also expressed some of the key genes ectopically using transgenic approaches. This has led to altered grain size, digestibility and end-use processing qualities. There are also implications for the growth of plant biomass, where the rates of transient starch turnover have been affected by various starch biosynthesis pathway genes.

The Role of Breeding Research in Achieving Rice Self-Sufficiency: An Indonesian Experience

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ABSTRACT

The 2015-2019 strategic plan of the Indonesian government targets the achievement of sustainable rice self-sufficiency from 2015. High yielding rice varieties has important roles in achieving a sustainable rice production. It is estimated about 90% of total areas for the national rice production in Indonesia are currently cultivated by improved rice varieties. Different strategies have been made to continuously increase rice production through breeding programs. Improvement in yield potential has been made through development of hybrid rice and new plant type of rice. A numberof hybrid rice and the new plant type of rice varieties have been commercially released having high yield potential. To increase rice harvest areas, the national rice production has been directed to unfavorable rice environments including swampy and upland rice areas which largely available outside Java island. Cultivation of rice in such marginal areas needs adaptable rice varieties to different problemsoils such as acidity, iron toxicity and nutrient deficiencies. Breeding to improve rice varieties for unfavorable rice environments has shown significant progress supporting the sustainability of national rice production. New rice varieties for swampy and upland rice areas have been developed through national and international collaborative research network. Furthermore, the negative impact of climate change on the rice production such as drought, flash flood and soil salinity have been anticipated through the development of tolerant rice varieties to these problems. More importantly, climate change has increased variability in pest and disease races. Therefore, high priorities have also been given to the improvement of rice resistance to different biotic stressessuch as brown plant hopper, blast, bacterial leaf blight and rice tungro virus diseases,to minimize yield losses caused by pest and diseases. This paper will discuss the role of breeding research in supporting rice self-sufficiency program in Indonesia. Current progress of the rice breeding programs in the country and future strategies to accelerate the impact of the research will be also discussed.

Key words: food self-sufficiency, rice, breeding, yield potential, climate change

Abstracts of Oral Presentation

SABRAO 13th Congress and International Conference
"International Convention Center, 14-16 September 2015"

Functional Genomic and Molecular Based Breeding

Simple Sequence Repeat (SSR) Marker Development from Walnut (*Juglans regia*. L)

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ABSTRACT

Walnut (*Juglans regia*.L) has been cultivated for its nut. Walnut contains essential nutrition for human such as fat, protein, vitamins and minerals. Therefore, it becomes one of the most economically crops. Comparing with the other plants, there are only few literatures about SSR marker development in walnut. For this reason, 270 SSR primer pairs originally from bacterial artificial chromosomes end sequences (BESs) of *J. regia* were randomly designed, 255 successfully amplified and 159 polymorphic loci were identified by characterizing 8 walnut cultivar. A total of 572 alleles generated varied from 2 to 9 with an average of 3.6. The polymorphic information content values varied from 0.11 to 0.81 with an average of 0.47. This study will be useful for genetic study in genetic studies in *J. regia* and also related species.

Keywords: SSR development, walnut, J. regia, BES-SSR

Chromosomal Location of QTL for Leaf Area and Leaf Area Duration Associated with QTL for Leaf Carbon Isotope Discrimination in Sunflower (*Helianthus annuus* L.)

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ABSTRACT

The present study was carried out to identify the quantitative trait loci (QTL) controlling leaf area (LA) and leaf area duration (LAD) and to analyze their relationships with QTL for leaf carbon isotope discrimination (CID). The traits were scored in a population of recombinant inbred lines (RILs) from a cross between XRQ and PSC8.The experiment was designed as a randomized block with 150 genotypes (148RILs and two parents) and two replicates. Each replicate consisted of two treatments, well-watered (ww) and water-stressed (ws). A total of 39 QTL was found for the traits investigated. Several QTL were detected to be associated with QTL for CID which was previously found. We identified common chromosomal location controlling LA and LAD corresponding to linkage group 06 (LG06). Our results indicated that identification of QTL for LA and LAD can be used to identify chromosomal location for a physiological complex trait like CID. The association between LA, LAD and CID in the genomic regions is relevant to marker-assisted selection (MAS) method in plant breeding.

Key word : QTL, Leaf Area, CID, sunflower

Comparative Sequence Analysis of Mungbean DNA Mismatch Repair Genes

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ABSTRACT

Mungbean is a high-protein grain legume that grown widely in southern Asia. It is also a promising drought-tolerant crop due to its adaptation to dry environment. However, world mungbean production has been stagnant and its breeding progress is hampered by low genetic diversity. Some efforts have been done such as germplasm exploration and induced-mutation. However, both of them have not given satisfactory result due to strong activity of *MSH* genes which has been reported to preserve genomic integrity in other species. To test this hypothesis, mungbean *MSH* genes were sequenced and compared to 78 *MSH* protein sequences from eudicots clade. We identified the location of mungbean *MSH* paralogs that involved in DNA mismatch repair, i.e. *MSH1* and *MSH3* in chromosome 8, *MSH2* in chromosome 7, *MSH6* in chromosome 3, and *MSH7* in chromosome 1. All five conserved domains present in mungbean *MSH2*, *MSH3*, and *MSH6*, whereas *MSH1* lost three domains and *MSH7* lost one domain, which could affect the protein function. Amino acid residue variations among *MSH* genes orthologs were identified within N-terminal and C-terminal of *MSH* genes. Single nucleotide polymorphisms (SNPs) at neighbored-motifs were also identified among 12 mungbean germplasm from 8 countries, and their effects on gene function are being investigated. This identification will facilitate the design of SNP markers to screen appropriate germplasm carrying favorable allele. Our result will also assist *MSH* gene manipulation via TALEN or CRISPR to produce altered gene function that may improve mungbean response toward induced-mutation.

Keywords: mungbean, MSH, domain, motifs, SNPs, alignment

Global Alternative Splicing Profile of Mungbean (*Vigna radiata*) and Adzuki Bean (*Vigna angularis*) and Its Implications in Breeding and Genetic Studies

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ABSTRACT

Alternative splicing (AS) is a ubiquitous phenomenon in eukaryotes, where transcribed mRNA from a gene could be processed in various ways to produce diverse mature mRNA. Consequently, AS could generateadditional proteins and phenotypesfrom the same gene, which could confound genetic mapping of phenotypes and functional studies of coding regions in the genome. To assess the extent of AS in mungbean and adzuki bean, global transcript splicing profile was examined in RNA-Seq data from root, leaf, flower, and pod tissues. Approximately 36% of mungbean genes and 32% of adzuki bean genes are subjected to AS. However, several observations indicated that stochastic splicing is the source of numerous AS isoforms in mungbean. For example, 36% of AS isoforms may not even exist as a single complete RNA in an average cell, making them unlikely to have any function. Moreover, around 24.4% of AS isoform is present at less than 1/10th of the default transcript. The proportion of missense splicing, which has a higher possibility to generate non-functional transcripts, is close to the expected frequency of random splicing (67%). However, alternative donor and acceptor AS types have more tendencies to occur at multiples of codon length. Genes with high exon number and expression level, which should have the most AS if splicing is stochastic, were found to have less AS, suggesting the presence of negative selection for accumulation of non-functional AS that could be detrimental to the cell's survival. The number of conserved AS among both species is only found in 349 genes (1.5%), even though 1503 genes (6.7%) share conserved intron sequences.These observations suggest that cataloguing global AS events will mostly yield non-functional isoforms. Despitethe fact that functional AS isoforms have been characterized in several species, the contribution of AS to functional protein diversity is probably relatively minor.

Keywords: Alternative splicing, Mungbean, Adzuki bean, stochastic process

Isolation of APETALA1 Homologous from Mangosteen (*Garcinia mangostana* L.)

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ABSTRACT

Mangosteen, "The Queen of Tropical Fruits", is one of the best Indonesian fruit in term of export value. Most of the fruits were harvested from traditional orchard since there is very few of new orchard has been established, because very long juvenile phase and low flowering and fruit-set of mangosteen. Conventional breeding was not appropriate way for mangosteen crop improvement, since mangosteen produce only apomictic seed. The best alternative is to use molecular and biotechnology approach to overcome the problems. The flowering process is controlled by many genes, including the *Apetala1*. Our group has been succeed to isolate a 483 and 538 bp of *Apetala1* gene sequence using two pairs of primers from *Arabidopsis thaliana* MgsAP1-F: 5'-TGTGATGCTGAAGTTGCTGTT-3'; MgsAP1-R: 5'-TTAAGCAAGG-AGGTGGCTGT-3', and from *Vitis vinifera* MgsAP2-F: 5'- TGCTGAGGTCGCTTTGATTG-3'; MgsAP2-R: 5'-TTCCTCCTCATCTCTGGTGCTT– 3'. NCBI Blast has shown that the sequences have very high homogogy with *Apetala1* from *A. thaliana, Brassica oleraceae, Citrus cinensis, Malus x domestica, Prunus persica, Salix discolor, Vitis vinifera,* and several other plants.

***Key words:* MgsAP1-F, MgsAP1-R, queen, tropical, fruits, primers, Vitis**

SNAP Markers as Indicators for Identification and Pigment Content Characterization Associated With Flower Color in *Phalaenopsis*

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ABSTRACT

Phalaenopsis breeding has generated wide flower color variations, however, it needs at least three years before one can do phenotype evaluation. Molecular markers associated with flower color is beneficial for prediction of flower color at early stages. Chalchone synthase (CHS) is key enzyme in flavonoid biosynthetic pathway affecting anthocyanin biosynthesis. The objectives of this research are to characterize morphology and pigment content of different *Phalaenopsis* flower, to develop SNAP markers based on CHS gene and evaluate their use for flower color prediction. A number of *Phalaenopsis* genotypes having different flower color characters were used. The color of flower were visually observed, carotenoid and anthocyanin content of flower were analysed by spectrophotometry. The CHS genomic fragments were amplified using PCR, sequenced, and analyzed for the presence of single nucleotide polymorphism (SNP). The SNAP markers were developed based on identified SNP of CHS fragment. Results of analysis indicated that pink to purple flowered *Phalaenopsis* contain high anthocyanin and no carotene while white, yellow to brown flowered one contained high carotene and wide values of anthocyanin to carotene ratios. Two out of three SNAP marker developed in this study are polymorphic but their usefulness as indirect indicator for certain flower color requires further studies. More SNAP marker based on a number of genes associated with flavonoid or carotenoid biosynthetic pathways are still being developed.

Keywords : *Flower pigments, Anthocyanin, Carotene, chalchone synthase (CHS), Sequence variabilities, Gene specific markers*

Utilization of 384-SNP Genotyping Technology for Seed Purity Test of New Rice Varieties Inpari HDB and Inpari Blas

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ABSTRACT

The seed purity of a variety is needed for producing the good seed quality of commercial variety. Inpari Blas and Inpari HDB are two new Indonesian rice varieties released in 2014 which are resistant to main rice diseases such as Blast, Bacterial Leaf Blight and Tungro. The objectives of this research were to identify genotype profiles of those new rice varieties by using 384 SNP markers and to establish the basis for assessing and monitoring seed purity for these varieties. The study revealed 41 polymorphic markers between Inpari Blas and Inpari HDB which were mapped in chromosomes 2-5, 7-9, 11 and 12. Three pure homozygous lines from both Inpari Blas (i.e. line number 16, 21 and 22) and Inpari HDB (i.e. line number 10, 15 and 18) were detected by inter-varietal genotyping. The seed from those selected lines can be used further as breeder seed for Inpari Blas and Inpari HDB, respectively. The total of 41 SNPs were detected by intra-varietal genotyping method as the unique markers for Inpari Blas and Inpari HDB varieties. Those unique markers could be used for ID variety development to prove assessing and monitoring of seed purity for these varieties. Significant results from inter-varietal polymorphisms indicated that the inter-varietal genotyping method could be used for selecting homozygous lines in order to detect genotype purity of Inpari Blas and Inpari HDB varieties. In general, the 384 SNPchips platform could be used further for other varietal seed purity detection.

Key Words : Inpari Blas and Inpari HDB, Genotyping, Single Nucleotide Polymorphism (SNP), seed purity.

Next-Gen-Based DNA Marker Development of Several Importance Crop and Animal Species

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ABSTRACT

Next generation sequencing (NGS) platform revolutionized plant and animal genomic studies including high density DNA marker technology to expedite breeding program. NGS-based DNA variation discovery is facilitated by the availability of genome reference maps of important crop and animal species to map genetic variations contained by a genetic resource collection of a crop and animal species using a cheaper whole-genome re-sequencing technology. The re-sequencing projects result millions of single nucleotide polymorphisms (SNPs), insertions and deletions (INDELs), and other type of DNA variations. The DNA variants can be used to expedite breeding programs. Many commercial SNP chips containing hundreds to hundred thousands of SNP markers are currently available to assist breeding programs of the important crop and animal species. For DNA marker discovery purposes including SNP chip development, the Indonesian Agency for Agricultural Research and Development (IAARD) have re-sequenced representative whole genomes of several important crop and animal species since 2010. The crops and animal under studies included soybean, maize, oil palm, cacao, chili pepper, potato, banana, and cattle. Millions of SNPs and INDELs have been discovered from each of the species. In this report we present several results of the next-gen-derived DNA marker discovery of the crop and animal species under study.

Keywords: NGS, DNA marker, SNP discovery, high throughput SNP genotyping, breeding

Marker Assisted Pyramiding of Drought Yield QTLs into a Quality Malaysian Rice Cultivar, Mas Wangi

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ABSTRACT

Drought has affected the yield stability of rice especially in rainfed areas of many Asian countries. Drought yield QTLs or simply *qDTYs* with high and consistent effect has been identified at International Rice Research Institute (IRRI). With the objective of improving grain yield of Malaysia high quality rice cultivar under reproductive stage drought stress (RS), three *qDTYs*, viz. $qDTY_{2.2}$, $qDTY_{3.1}$ and $qDTY_{12.1}$ were pyramided into Mas Wangi by marker assisted breeding (MAB). Foreground and recombinant selection using *qDTYs* specific and flanking markers was performed in every generation. BC_1F_3 and BC_1F_5 Mas Wangi pyramided lines (PLs) with different combinations of the three *qDTYs* were evaluated under both RS and non-stress (NS) conditions during dry season (DS) of 2013 and 2014. PLs with *qDTY/s* were found superior than their recipient parent under severe RS as well as in NS condition. Mas Wangi produced 55 to 579 kg ha^{-1} and 4044 to 5104 kg ha^{-1} of yield under RS and NS conditions, however, its selected PLs gave a yield advantage of up to 3473 kg ha^{-1} under RS with acceptable yield potential under NS. Generally, PLs with single *qDTY* (either $qDTY_{2.2}$ or $qDTY_{12.1}$) seems to be superior that other *qDTY* combinations under RS. Furthermore, under NS, PLs with two *qDTYs* combination ($qDTY_{2.2} + qDTY_{12.1}$) performed better than PLs with other *qDTY* combinations indicating the presence of positive interaction between $qDTY_{2.2}$ and $qDTY_{12.1.}$ Drought tolerant Mas Wangi PLs were successfully developed. Differential yield advantages of different combinations of the *qDTYs* indicate a differential synergistic relationship among *qDTY*. The study proved marker assisted QTL pyramiding to be an effective strategy to transfer several *qDTYs* from donor parents to mega-varieties.

Keywords:* *drought, marker assisted breeding, drought yield QTLs, QTLs pyramiding, recombinant selection, background selection

Mapping Major QTLs for Resistance to Cercospora Leaf Spot Disease in Yardlong Bean

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ABSTRACT

Yardlong bean *Vigna unguiculata* ssp. *sesquipedalis* (L.) Verdc.) is the most important vegetable legume crop of Thailand. It is widely grown in all parts of the country year-round. Pods of yardlong bean are consumed as fresh and processed forms. One of the important problems in yardlong bean production is Cercospora leaf spot (CLS) disease caused by fungi *Cercospora canescens* Ellis & Matin and *Pseudocercospora cruenta* (Sacc.) Deighton. The disease can cause yield loss up to 30-40%. Although the disease can be controlled by chemical control, it increases production cost and causes health problems of farmers and consumers. Thus, increasing resistance to CLS disease is one of the major goals in yardlong bean breeding programs. The objectives of this study were to locate major gene(s) controlling CLS resistance for marker-assisted selection (MAS) in yardlong bean. Yardlong bean (susceptible to CLS) and cowpea (*Vigna unguiculata* ssp. *unguiculata* (L.) Walps; resistant to CLS) were used to develop an F_2 population of 189 individuals. The F_2 and $F_{2:3}$ progenies were evaluated for the resistance under the field condition. Segregation analysis revealed that CLS disease caused by *C. canescens* and by *P. cruenta* is a quantitative trait and possibly controlled by oligogenes. Bulk-segregant analysis showed that SSR marker CEDG070 is associated with the CLS disease. Inclusive composite interval mapping demonstrated that CLS caused by *C. canescens* and by *P. cruenta* is controlled by different major QTLs that tightly linked to each others.

Development of Genome-Wide and Gene-Specific Markers for Assisting *Phalaenopsis* sp. Breeding in Indonesia

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ABSTRACT

Phalaenopsis sp. is one of the orchid species having high commercial value. A number of contrains exist in breeding and cultivar development of this species, such as long juvenile period before they flower and the soft rot disease infestation. Since this orchids are valued for their flowers, availability of tool to predict flowers characters at the seedling stage of newly develop *Phalaenopsis* hybrids will be beneficial. Similarly, tool to predict resistance response without actually inoculate the evaluated *Phalaenopsis* accessions are very valuable. The general objective of this presentation are to outline the potential use of co-dominantly inherited molecular markers to support *Phalaenopsis* breeding program in Indonesia. The specific objectives are to develop and validate the effectiveness of genome-wide and gene specific markers for studying genetic diversity and identifying specific markers associated with flower or soft rot disease resistance characters in *Phalaenopsis*. The specific primers to obtain genome-wide and co-dominant SSR markers are identified based on the *Phalaenopsis* genome sequences available in the NCBI DNA Database. Genomic DNA fragments of genes associated with flower color (PAL, F3H, F3’H, F3’5’H, DFR, and PSY) or that of disease resistance (RGA and DGA genes) are PCR amplified using gene specific primers. After sequencing of the PCR amplified DNA fragments, sequence variabilities of the identified genes are evaluated. The specific primers are designed based on the identified SNP sites existed in the target genes and used to generate gene-specific and co-dominant SNAP markers. The identified primers are validated using a number of *Phalaenopsis* species and hybrids to determine informativeness of the generated SSR and SNAP markers. The polymorphic SSR and SNAP markers identified in the process will be used for further analysis to support *Phalaenopsis* breeding for unique flower characters and soft rot disease resistance. Implementation progress of these strategies are outlined in the presentation.

Keywords: ***flower characters, molecular characterization, ssr marker, snap marker, disease resistance***

Genomic Prediction for Carotenoids in Maize

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ABSTRACT

Provitamin A biofortification of important staple food crops such as maize is potential to overcome the widespread vitamin A deficiency problem. With the increasing accessibility of high volume-low cost genotyping platforms, genomic selection can be of potential use in the breeding programs. The objectives of this study were to estimate the prediction ability of a relatively small data set of SNP markers on predicting carotenoid concentrations. A set of 380 lines in CIMMYT carotenoid association mapping panel was phenotyped for carotenoid concentrations in four environments and genotyped using the GBS and 55K platforms. A subset of 10,000 random SNPs were taken for the genomic prediction exercises, which used the Genomic Best Linear Unbiased Prediction (GBLUP) method with five-fold cross validations and five iterations. The results showed that the prediction accuracy (i.e., correlation among observed and predicted values) for four carotenoid traits were promising (0.49 for zeaxanthin, 0.55 for β-cryptoxanthin, 0.60 for β-carotene, and 0.57 for total provitamin-A concentrations). These results may improve with a larger genotypic data set, and suggest that genomic prediction can be a valuable tool to increase the efficiency of maize provitamin A biofortification breeding programs.

Keywords: biofortification, carotenoids, genomic prediction, maize

Isolating Compound Microsatellite Markers and Its Application on *Amorphophallus variabilis* Populations in Darmaga Conservation Forest, Bogor, Indonesia

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ABSTRACT

Amorphophallus variabilis Blume locally called *cumpleng*, member of Araceae, is a fleshy perennial tuber crop endemic in Java island, Indonesia. White tuber of the plant was used as food in Java during famine time before 1960s. Due to rapid ecological changing and land fragmentation in Java, populations of *A. variabilis* now under threaten. We isolated microsatellite markers in order to develop breeding and conservation strategies in *A. variabilis* population. Twenty-two primers were designed and twelve primers pairs produced polymorphic microsatellite loci from *A. variabilis*. These loci provided microsatellite markers with high polymorphism ranging from 5 to 22 alleles per locus. The observed and expected heterozygosities ranged from 0.191 to 0.851 and 0.380 to 0.943, respectively. This high allelic diversity indicates that these markers are suitable for the study on population genetic structure in the present study. Cross-amplification on related and non related species was performed. Populations of *A. variabilis* from Darmaga Conservation Forest showed high allelic richness, high diversity within and among populations. Genetic distance among populations increased, by increasing geographic distance. This present study implies that in order to develop better breeding and *in situ* conservation programs, it is important to study larger population of *A. variabilis* order to understand the population genetic structure.

Keywords: Amorphophallus variabilis, Araceae, iles-iles, Java, root crop

In Vitro Chromosome Mutation Induction in Dendrobium lasianthera (J.J. Smith) using Colchisine

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ABSTRACT

The development of genetic diversity in orchid breeding as cut flower in Indonesia are still limited. *Dendrobium lasianthera* (J.J. Smith) is one of the best parent as character source for cut flower. Chromosome mutation induction using colchicine are expected to increase the ploidy for genetic diversity of *Dendrobium lasianthera* (J.J. Smith), as a first step in plant breeding. In this research aims are to observe the effect of colchicine consentration and submersion duration to the explant growth and ploidy level of *Dendrobium lasianthera* (J.J Smith). The experiment design used a completely randomized design (CRD) with two factor, colchicine consentration and submersion duration. The results showed that colchicine consentration 0.025% in 1 hour submersion give the highest number for plb, leave, shoot, and root. The highest callogenesis percentage obtained from treatment without colchicine with 1 hour submertion. Colchine treatment give diversity to chloroplast, stomata, stomata size, and ploidy level. We were obtained the highest number of chloroplast from 0.025% colchicine with 24 hours submersion. The highest stomata density was obtained from submersion duration for 1 and 24 hours without colchicine. The highest diameter of stomata obtained from 0.025% colchicine in 1 hour and 24 hours submertion . The highest rate of polyploid cell we obtained from 0.050% colchicine. The highest chromosome number was obtained from 0.075% colchicine consentration for 48 hours submersion. LD_{50} vallue for colchicine consentration are 0.136%, while for submersion duration are 70.32 hours.

Key words: Colchicine, Dendrobium lasianthera (J.J. Smith), LD_{50}, ploidy, stomata

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Primary Paper

Sustainable Use and Conservation of Indonesian Horticulture Germplasm

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Abstract

Officially there are 323 species of horticulture crops in Indonesia based on Minister of Agriculture decree no: 511/kpts/PD.310/9/2006, consist of 60 spp of fruit crops, 80 spp vegetable crops, 66 spp medicinal crops, and 117 spp ornamental crops. Each species then consist of several varieties, and than there are also many other horticulture crops grown in farm other than the official crops that make so many horticulture germplasm need to be considered for their use and conservation. Indigeneous and underutilized crops are also need to be consider and reintroduce as some of them can become eonomiclly important in the future. These plant genetic resources are the fuel for breeding, which in the search for higher yield and quality, or adapted genotypes in order to meet the needs of consumers. However, a limited number of species or varieties that we use for our livelihood presents a huge concern about genetic vurnerability of Indonesian horticulture germplasm since economiclly improtant crops becoming more uniform. Sustainable use of the germplasm and their conservation have to be strengthening, including exploration of new germplasm before disappearing from nature, in situ conservation, ex situ concervation such as seed storage, field genebanks, and *in vitro* storage. In Indonesia, conservation of horticulture germplasms have been done in several research centers under Department of Agriculture and research centers belong to Universities. Center for Research and Development of Horticulture, Department of Agriculture has an Infomation System on Horticulture Germplasm that has database on some vegetables, tropical fruits, ornamental plants, and citrus and subtropical fruits.

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Reprobing the Misconception for the Reproduction System of Bali Salak Cultivars

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ABSTRACT

Despite the current notion of some salak researchers that Bali salak cultivars are andromonoecious i.e. having male and hermaphrodite flowers in the same inflorescence, as far as the authors' knowledge nobody has ever proved that the seemingly normal pollen grains produced by both flowers are functional for fecundation. In Yatazawa R&D Gardens, up to now Gula Pasir and Pada as two of the most important Bali salak cultivars in the Gardens' breeding programme are practically only usable as female plants in the many crosses with males of other salak plants. When the flowers are left alone, all the so-called andromonoecious Bali salaks occacionally produce seeds with twin embryos or poorly-developed seeds with no embryos, this aberrant condition has never been found in cultivars other than Bali salaks. And hence, along with the occurence of sterile or abnormally-developed anthers in the flowers and also the absence of pollen providing male plants, they represent a reflection of the apomictic nature of these cultivars. Muani, the fruitless non apomictic Bali salak cultivar, is considered a normal female salak plant which is only capable of setting fruit if pollinated. In conclusion Bali salak cultivars are still considered dioecious and despite having no male plants can still exist with the apomictic reproduction.

Keywords : Bali salak cultivars, no functional pollen, apomictic, twin embryos, embryoless seeds.

Exploration and Collection of Saccharum Germplasm in Papua and Its Significance

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ABSTRACT

Papua is believed to be part of the center of origin for sugarcane. To widen the genetic base of sugarcane, incountry germplasm collecting mission was mobilized to Boven Digoel , Jayapura and Okaba Regencies, Papua in 2013. The collector team, lead by ISFCRI's scientist, and supported by local staffs of BPTP and Estate Crop offices, had successfully collected a total of 99 accessions consisted of 83 accessions of *Saccharum oficinarum*; 3accessions of *S. edule*; 4 accessions of *S. spontaneum* sp, 3 accessions of Erianthus and the rest 2 accessions of *Saccharum sp*. Variability were seen in term of stalk and leaves color, stem wax , eye shape and brix vaule. These wide morphological variability and expected genetic potential related to biotic and abiotic stresses poses by the wild relative would be of immense use for the future national sugarcane breeding program aiming at developing HYV sugarcane varieties suitable for marginal land.

Keywords: exploration, germplasm, Sacharum officinarum, S. edule, S. spontaneum, Erianthus, Papua, variability

Two Different Types of Mangosteen *(Garcinia mangostana L)* from Swampy Area of Tembilahan-Indonesia and Their Level To Gamboge Disorder

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ABSTRACT

Twenty one mangosteen *(Garcinia mangostana* L.) accessions which were collected from the swampy area of Riau province - Indonesia, were evaluated using morphological characters, RAPD (Randomly Amplified Polymorphysm DNA) and ISSR (Inter Simple Sequence Repeat) markers. The objectives of this study were to identify the diversity of mangosteen that were cultivated in Tembilahan, analyse their genetic relationships, and to know their levels to gamboge disorder. The RAPD and ISSR analysis generated 108 scorable DNA fragments of which 49 (43,8 %) polymorphic and 59 (56,2 %) monomorphic bands. These markers range in size between 250 and 2400 bp. Cluster analysis separated the accessions into two different types with similarity coefficient ranging from 0.84 to 0.99. RAPD markers are more reliable than ISSR to detect differences between the two types. Both types different morphologycally and in their response to gamboge disorder. The first group called as Tembilahan on non gamboge disorder type and the second as non-Tembilahan or gamboge disorder type. The unique markers were found in non-Tembilahan type and absent in Tembilahan type. This results have important implications for developing new variety of mangosteen.

***Keywords**: gamboge disorder, Garcinia mangostana .L, ISSR , RAPD, swampy area ,*

Exploration and Collection Sumatran Manggo Adaptable to High Rain Fall Sesion

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ABSTRACT

One of the problems in the development of mango plantion an industrial scale in Sumatra island is the rendering of the cultivars that are grown with climate and soil type on Sumatra. During this time, the use of mango cultivars as a source of seed originating from the other island is not showing the fruits of the harvest. To improve the results of mango plantations in Sumatra for the foreseeable future, the need for exploration and collection of germplasm resources resistant to the high rainfall. The uniqueness of the Sumatran mangoes is able to grow and adapt to environments that have high rainfall as well as the diverse habitat types and their interaction with genetic factors will generate the wealth of rich mango and different with other areas in Indonesia. The exploration and collection of germplasm mangifera in Sumatra has been done to get the mango that is resistant to precipitation and soil moisture content is high. The results of exploration in Sumatra mango retrieved 10 species of mangoes grow and adapt to the environment have in Sumatra are namely Mangifera foetida, M.ordorata, M.indica, M. zyelanica, M. kemanga, M. laurina, M. sumaterana, M.torquenda, M. quadrifida, Mangifera sp1. In getting some cultivars of Mangifera ordorata which are adapted to the nature of Sumatra developed well and comes from the western part of Sumatra's East Coast

Keyword : ***exploration, collection, sumatran manggos, high rainfall.***

A Preliminary Study of *Garcinia malaccensis* Collection in Taman Buah Mekarsari, Cileungsi, Bogor, Indonesia

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ABSTRACT

The synchronous first time flowering in 2014 of most *Garcinia malaccensis* plants (2n=2x=48) in Taman Buah Mekarsari reveals a considerable variation in the flower and fruit characters of the female plants of this dioecious species. The variability of this progenitor species of mangosteen is apparently reflected partially in the establishment of primary variation in mangosteen (2n=4x=96). Further variation which develops later in the apomictic mangosteen is considered as secondary variation due to mutation. A detection of four plants of fruit-bearing triploid mangosteen (2n=3x=72) in the mangosteen collection of Taman Buah Mekarsari suggests that mangosteen is actually a higher ploidy form of apomictic female *Garcinia malaccensis* plants. And hence in mangosteen reproduction, the male plants which have never been proven to exist are unneccesary. The ongoing deforestation in the native area of *Garcinia malaccensis* i.e. in the Malay Peninsula, Sumatra, and Borneo, where different types of mangosteen originated, renders an imminent *Garcinia malaccensis* salvaging programme necessary.

Keywords : mangosteen, chromosome number, ploidy level, place of origin, apomictic, taman buah mekarsari

An Efforts of Mutation Breeding on Wild Raspberry (*Rubus* spp.) in Cibodas Botanical Garden

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ABSTRACT

Recently, Cibodas Botanical Garden (CBG) has a domestication programme of wild raspberries (*Rubus* spp.) from Indonesia mountain forest. One of the activities in the domestication programme is fruit breeding. In order to improve the quality of wild raspberry, two mutagens i.e. chemical (oryzalin) and physical (gamma rays) mutagens were used in the breeding programme. Moreover, seed and germinated seed of wild raspberries from collection of CBG were used in the programme of mutation breeding. The results show that each species of wild raspberries has different response on the mutagen.

Keywords: Rubus, mutation breeding, chemical and physical mutagens

A Decade of Durian Breeding at ITFRI

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ABSTRACT

To support the increment of durian quality and production, Indonesian Tropical Fruit Research Institute has been conducting a series of breeding activities since 2006. The research were starting with consumer preference survey to establish durian ‘idiotype’ as a quality formula as a guidance to the goal of breeding program, then subsequently continued with activities to attain it, *viz*. exploration of superior indigeneous durian meets the idiotype components, phylogeny and diversity analysis of durian germplasm, screening of disease resistant cultivars, inter- and intra-species crossing, and establishment of SSR markers for involving MAS approaches. Based on the consumer preference survey, it could be formulated the idiotype of Indonesian durian and discussed in this manuscript. Exploration found various indigenous durian germplasm which meet the superior characteristic such as edible portion more than 35%, bright yellow aril, thick aril, wrinkle seed, etc. Molecular phylogeny and diversity analysis found a scientific evident that Kalimantan is the center of durian origin, also verified several speciation of debated cultivars and new emerging durian variation. The result could be used to determine parent trees and method approaches for durian breeding. Based on detached leaf bioassay it could be screened 22 cultivars resistant to *Pythiaceae*. Incomplete reciprocal inter- and intra-crossing among 35 parent trees produced 4234 F1 progenies, which achieved through 39 crossing combination. Isolation of simple sequence repeat from durian genomic library found 354 recombinants which consisted of motifs could be used as genetic markers. Through bulked psudo-segregant analysis it was found two SSR markers were associated to *Pythiaceae* resistance trait. The achievements are just the starting phase as a foundation for further durian breeding in Indonesia, more efforts yet still to be done to gain the goal to get ideal durian.

Keywords: durian, breeding, exploration, selection, diversity, phylogeny, inter-and intra-species crossing, resistance to Phytiaceae, MAS, SSR, BSA

Morphological Variability of Indonesian Rice Germplasm and the Associated SNP Markers

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ABSTRACT

Diverse rice germplasm in Indonesia is a valuable genetic material for development of improved varieties. Morphological and molecular characterization of rice accessions with varied genetic background is highly considerable to be carried out to their utilization and to genetic variability incorporation into rice breeding program. In this study, the diversity within 60 rice accessions comprising indica, japonica and tropical japonica cultivars was analyzed for 19 morphological traits and 384-SNPs-plex with GoldenGate assay. Combined analysis of the qualitative and quantitative traits using XLSTAT and Flapjack revealed variability of rice accessions germplasm. Correlation matrix estimated with the Pearson showed significant correlation between few qualitative traits with quantitative variables ($P \leq 0.5$). Principal component analysis (PCA) clustered the germplasm into two main groups (indica/japonica and indica/tropical-japonica). PCA axes 1 and 2 and morphological traits with eigen values at arbitrary above 0.2, explained 24.60% of total variation in the rice germplasm. Seven traits (leaf color, leaf sheats colour, ligule colour, diameter of basal internode, culm colour, ligule length, and flag leaf angle) could be the most important traits for further characterization and conservation studies in rice germplasm. Based on total morphological traits and 384 SNPs, three major clades were generated and differentiated most accessions into indica/japonica/tropical japonica belonged to the two main clades according to their individual genetic background. Association analysis demonstrated that 154 SNPs across rice chromosomes were associated with 14 morphological traits related to leaf, stem and panicles. Approximately 17, 9, 5 and 8 SNPs were significantly associated with quantitative traits namely panicle length, diameter of basal internode, leaf width and ligule length, respectively; and 115 SNPs were found to have significant association with qualitative traits. These alleles could provide breeders to effectively identify, track and incorporate regions of chromosomes governing the desired morphological traits to improve rice varieties in Indonesia.

Keywords: morphological trait, principal component analysis, rice, SNP

Genetic Diversity Analysis of Wheat Germplasm Collection of Indonesian Cereals Research Institute using SSR Markers

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ABSTRACT

Wheat (*Triticum aestivum L.*) is one of the world's most important cereal crops. A set of wheat accession introduced from abroad has been collected in Indonesian Cereals Research Institute (ICERI), called as ICERI wheat accessions. This study aimed to evaluate the genetic diversity of ICERI wheat accessions using SSR markers. A total of 59 wheat accessions were analyzed using 49 SSR markers. Genotype data were subjected to NTSYS-pc and PowerMarker software to analyze genetic diversity among accessions and to calculate the summary statistics of SSR markers, respectively. The results showed that 43 out of 49 primers were polymorphic and those were further used in performing cluster analysis of ICERI wheat accessions. The ICERI wheat accession clustered into four major groups at genetic similarity coefficient of 71% in which 10, 23, 5, and 21 ICERI wheat accessions were clustered in group I, group II, group III, and group IV, respectively. The genetic distance of the ICERI wheat accessions ranged from 0.11 (SO3 and SO8) to 0.62 (GDM16 and GDM1) with the average of 0.39. Of these, eight combinations showed a high level of genetic distance values (>55%), indicating their potential for broadening the genetic basis of wheat in future. A total of 162 alleles were detected from the ICERI wheat accession with major alleles frequency found on Xbarc1142 (0.93). Twenty one out of 43 polymorphic SSR markers (44.5%) showed high discriminating power as represented by polymorphic information content (PIC) value higher than 0.5. An average of the PIC value was 0.47, ranged from 0.118 (xbarc112) to 0.762 (xbarc1142). These findings would be useful for wheat breeding program, especially in development of wheat breeding strategy in order to obtain improved wheat varieties adaptive to warm tropical climate of Indonesia.

Keywords: wheat, SSR markers, genetic diversity

Genetic Diversity in Indonesian Waxy Corn Inbred Lines Using SSR Markers

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ABSTRACT

Waxy corn is special type of corn that contain high amount of amylopectin with its distinct sticky characteristic compare to normal corn. Waxy corn has been long use as a food source and traditional snack especially in South Sulawesi. The objectives of this study was to determine the genetic diversity of waxy corn lines derived from Indonesian germplasm via SSR marker characterization, and to investigate relationship between inbred lines based on clustered heterotic group to be use as breeding material. Genetic materials were 30 lines of waxy corn with various kernel types, 23 white, 6 sweet-white, and 1 yellow, were analyzed with 27 SSR molecular marker and cluster analysis. Total amount of alleles was 75 with average allele per locus was 3.0. The mean value for polymorphic information content (PIC) was 0.40, with value ranged from 0.04 – 0.7, and the value of lines heterozygosity varied from 7.41 – 18.42 %. Based on genetic similarity value at 0.57, 30 inbred lines were clustered into 6 groups, and the highest amounts of lines (13) were in group 2, whereas group 4 and 6 only contain 1 inbred line. Lines with similar type of kernel color and pedigree related seems to be genetically close and clustered together, also lines with sweet-white kernel 5 were in the same group. Furthermore, SSR marker was able to differentiate yellow line waxy corn form other lines, and it was only belong to group 6. The results showed that there was considerable genetic diversity among 30 lines that can be used as potential source of parent to develop high yielding waxy corn variety.

Keywords: waxy corn, genetic diversity, SSR marker

Analysis of Genetic Diversity and Heterosis Potential of Recombinant Maize Inbred Lines Based on SSRS Marker (Simple Sequence Repeats)

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ABSTRACT

Analysis of genetic diversity and heterosis potential of recombinant maize inbred lines based on SSRs marker (Simple Sequence Repeats). Increasing demand of maize encourages breeders to develop high yielding hybrid variety with tolerance to biotic and abiotic stresses. Inbred development in large scale and originated from different population with various characters is routinely conducted and improved as genetic material for development of novel variety. Information on genetic diversity and relation among elite inbreds will help reduces genetic vulnerability and broaden genetic basic in the development of novel variety. This research analyzed 27 elite maize inbred lines using 34 SSRs markers. The aim was to study genetic diversity of the lines extracted from five populations and to figure out heterotic potency based on the estimation of genetic distance and heterotic group on the basis of SSRs. The result showed that genetic diversity of the population was relatively broad with high value of genetic diversity of 0.54, while number of average alleles per locus was 4.4 and polymorphism level of 0.50. There were 103 heterotic potencies identified based on heterotic group and estimation of genetic distance. However information on silking and anthesis time is required in order to enhance the efficiency of crossing in the field.

Keywords: genetic diversity, elite maize line, heterotic

Ploidy Level of Plans Derived Callus Induced by Gamma Radiation and Ethyl Methane Sulphonate Affects Diversity of Leaves Number and Plant Height of *Stevia rebaudiana* Bertoni

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ABSTRACT

Leaves of *Stevia rebaudiana* Bertoni have been popularly used as an alternative sweetener due to their sweetening potency, 200-300 times sweeter than sucrose with little caloric value. With poor success rate of Conventional Breeding, mutation breeding can be used to improve stevia. This study aimed to obtain information on the phenotype performance and high glycoside content of some individual stevia plants derived callus induced by gamma radiation and ethyl methane sulfonate. Callus was induced from Stevia leaves of Bogor, Garut, and Tawamangu accessions. The study was conducted at Tissue Culture Laboratory and experiment field of Agriculture Faculty, University of Padjadjaran. A Randomized Complete Block Design was used in this experiment with genotypes as treatment consisting of 80 mutation induced plant and 4 controls. The result showed that mutation induced plants were significantly different in plant height and number of leaves at 20 days after planting. Stevia T3, 5B has the highest number of leaves and Stevia G7, 5A and B5C has the highest height. Further data analysis will be in more detail discussed in this paper.

Keywords: stevia, in vitro, mutation, gamma radiation, ethyl methane sulfonate

Characterization Genetic Variability of Landrace Tomato Genotypes from Induced Mutation Process

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ABSTRACT

Tomato is one of the most important vegetables in Indonesia with increasing demand by increasing its population. The objective of this research was to obtain information of tomato genotype performance and morphological variability from induced mutation process. Genetic material of tomato genotype was obtained by germplasm exploration from different region in Indonesia. Local genotype was mutated by gamma rays at level 990 gray. The experiment research was conducted in September 2014 to January 2015 at Leuwikopo Experimental Field, Department of Agronomy and Horticulture, Faculty of Agriculture, Bogor Agricultural University. The characterization was conducted through variability comparison between tomato genotypes without irradiation (M0) and with irradiation (M1). The result of this research elucidated that there are variability in the performance of mutant tomato M1 generation i.e : plant height (cm), stem diameter (cm), flowering age (DAP), harvesting age (DAP), weight of fruit (g), average fruit weight (g), length of pedicel (cm), fruit length (cm), fruit diameter (cm) , fruit softness (mm $g^{-1}5s^{-1}$), and total dissolved solids (ºbrix). The variability in the genotype still occurs seen from the variability performance of qualitative character. The genetic similarity was analyzed by clustering analysis. Clustering analysis from dissimilarity distance resulted that the genotype M0 and M1 is not different at the level of 0.77, indicated that the dissimilarity is low (23%). Dissimilarity coefficient elucidated that M1 and M0 is divided into two cluster. Value of heritability was varied between genotype and character. Clustering analysis for group of genotype M1 resulted different at level 0.5, indicated that the similarity is high (50%). Broad senseof heritability value if more than 50% was stated as high criteria, medium at 20% - 50%, and low if less than 20%.

Keywords:* *characterization, gamma rays irradiation, genotype, Lycopersicon esculentum

Mutagenic Effectiveness and Efficiency of Gamma Irradiation Techniques in 3 Wheat Lines

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ABSTRACT

The adoption of mutagen application techniques depended on its mutagenic effectiveness and efficiency identification to increase spectrum of beneficial mutation. Mutagenic effectiveness means the rate of mutations as related to dose while efficiency refers to the mutation rate in relation to biological damage such as seedling injury, pollen sterility and lethality. This study revealed to analyze the mutagenic effectiveness and efficiency of 3 gamma irradiation techniques by using biological damages like lethality and seedling injury observed in M1 generation in relation with the frequency and spectrum of mutations in M2 generation. Three introduced wheat breeding lines (F-44, Kiran-95 & WL-711) were treated by 3 gamma irradiation techniques (acute, fractionated and intermittent), evaluated the combination of treatments on germination rate and reduction of seedling height at M1 generation, observed its mutation spectrum and frequencies to determine the mutagenic effectiveness and efficiency on M2 generation. Three types of chlorophyll mutants (xantha, chlorina and viridis) were screened in M2 progeny. There are 6 types of spike mutation were found in this research (speltoid, compactoid, super numerary spikelet, club ear, lax ear and awnless). The acute irradiation technique has the highest of mutagenic effectiveness and efficiency at 250 Gy dose of gamma irradiation application than the others.

Key word: spectrum and frequency of mutation, chlorophyll mutation, spike mutation

Genetic Improvement for Adaptation to Biotic and Abiotic Stress

Plant Mutation Breeding using Gamma Greenhouse for the Improvement of Agronomic Traits with regards to Climate Change in Rice

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ABSTRACT

Radiation Induced Mutation has been widely used in crop improvement around the world. Mutation variety database of International Atomic Energy Agency (IAEA) has recorded more than 3800 mutant variety has been registered and some of them has been commercially cultivated in the respected countries. Gamma radiation has been widely used as a mutagen for mutation breeding program. In Malaysia, a chronic irradiation facility so called Gamma Green House was build in 2005 and fully operated in 2009 for plant breeding purposes. Mutation breeding objective is now more focusing in improving the crop trait to face future uncertainty climate in the country. The climate change will cause many disasters around the world such as draught and flooding which lead to the devastating destructive of the crop cultivation. The Change in climate also creates new pest and microbe which evolved and will make the existing genotype/cultivar prone to diseases and pest. In realizing these future shortcoming with regards to climate change objectives of mutation breeding will focus on mitigating the problem that will face in the future due to unfavorable climate. At present, Malaysian Nuclear Agency has embarked rice mutation breeding project for sustainable agriculture under Nuclear Forum Cooperation in Asia (FNCA). Besides that, the project supported with technical assistant by International Atomic Energy Agency (IAEA) has also been carried out based on the objective to produce a potential cultivar in mitigating the climate change occurs in Malaysia.

***Keywords:* rice, mutation breeding, Gamma radiation,climate change**

Antixenosis and Antibiosis Resistance of Chili Pepper Lines to Melon Aphid (Hemiptera: Aphididae)

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ABSTRACT

The melon aphid or cotton aphid, Aphis gossypii, is one of the major pest of low land chili pepper and vector of 50 plant viruses. Large aphid colonies will cause significant yield loss. Up to now, chemical based crop protection is seen as the major way to combat aphid. However, melon aphid has been resistant to the insecticide and insecticides also damage beneficial insects, predators, parasitoids, and pollinators. Host-plant resistance is one of the best management strategy against *A. gossypii*. There are three types of resistance: antixenosis, antibiosis, or tolerance and there were no reports about chili pepper line resistance to aphid in Indonesia. The objective of this research were screening and identifying antixenosis (choice test) and also antibiosis (no-choice test) of melon aphids in several chili pepper lines. The seedling were hand-infested with 2 wingless aphids for antixenosis experiment and evaluated 12 d after infestation. Detached leaf used for antibiosis assessment. Antixenosis experiment showed the IPB C20 was the lowest line infested by aphid per leaf, total aphid per plant, and winged aphid per plant. For antibiosis experiment showed significant differences in the longevity time and reproduction time, number of aphid progeny per day, and fecundity of the melon aphid among genotypes. The genotype IPB C20 showed shorter longevity days and reproduction time, lower aphid progeny per day and fecundity compared to IPB C313. Any positive correlation of leaf length and leaf position (middle leaf) for total aphids per plant. Resistance of antixenosis and antibiosis provides breeding lines for breeders and additional option for pest management through host-plant resistance.

Keyword: Capsicum annuum, choice test, cotton aphid, host-plant resistance, no-choice test

Screening of 14 Potato Genotypes for Their Adaptation to Tropical Medium Altitude Conditions

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ABSTRACT

Potato is one of the most important crops in the world, including some tropical countries. The limitation of land availability for potato production in highland areas of some tropical countries had steered the recent development of production technology of some important vegetables normally growing in highland area, including potatoes, to lower altitude areas. To increase the effectiveness of the program tolerant varieties to those particular conditions are needed. Our study aimed at screening of potato genotypes for their adaptation to low-medium altitude condition (300-700 above sea level).We evaluate and compare the growth and production of 14 potato genotypes collected from several sources including potato wild relatives growing at 1500 versus 550 above sea level. We also evaluate the ability of genotypes to produce tuber in an *in vitro* setup. Our results showed that several genotypes of potato produced tuber at medium altitude and high temperature at *in vitro* laboratory condition. We identified one genotype, derived from single seed descent of CIP394614 (*Solanum tuberosum*), were superior for its ability to produce tuber at those particular area. Thus, it might be very suitable to be used in breeding program to develop tolerant varieties of potato to low-medium highland.

Keywords:* *crop wild relatives, climate change, high-temperature, in vitro, Solanum tuberosum, tolerant varieties

Performance of F_1 Genotypes And Their Parents Under High Temperature Conditions

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ABSTRACT

The experiment was conducted at the greenhouse of Bogor Agricultural Universsity. The purpose of research was to obtain information on variability of F_1 rice genotypes and parents under high temperature in the tropical conditions. The design used was a completely randomized design with three replications. Genetic materials used were parents, namely: Mekongga, Situ Patenggang, IPB 6R, Marinah, IR64, IPB 4S and 9 F_1 genotypes. Traits observed were plant height 110 HSS, leaf greenness 110 HSS, the total number of tillers, number of productive tillers, time of heading, time of flowering, time of harvesting, length of panicle, number of grain, number of filled grain, number of total grain, percent of unfilled grain, weight of filled grain, and weight of 1000 grain. Genotyping results showed a significant effect on plant height 110 HSS, leaf greenness 110 HSS, the total number of tillers, number of productive tillers, time of harvesting, length of penicle, number of grain, number of filled grain, number of total grain, percent of unfilled grain, weight of filled grain, and weight of 1000 grain. Results showed that there was different mean of plant height 110 HSS, leaf greenness 110 HSS, the total number of tillers, number of productive tillers, time of harvesting, length of penicle, number of unfilled grain, number of filled grain, number of total grain, percent of unfilled grain, weight of filled grain, and weight of 1000 grain among genotypes evaluated. IPB 6R, Marinah, dan IPB 4S were good combiner for the characters observed under high temperature conditions.

Keywords: F_1, rice, abiotic stress, heat stress

Heat Stress Tolerance in Seeds of Japonica Rice Cultivar under Treatment of Hot Water Disinfection Method

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ABSTRACT

Seed disinfection is very important part of rice cultivation process to prevent seed-borne rice plant diseases. Hot water disinfection method disinfects rice seeds at 60ºC water for 10 minutes without expensive agricultural chemicals. In Japan, this method has been gaining considerable amount of attention as a clean farming technique because it does not produce hazardous waste. However, disinfection condition at 60ºC for 10 minutes is not always completely effective to control some diseases, while using higher temperature could decrease the seeds germinability. In this study, the seeds of various cultivars were treated with hot water at 69ºC for 10 minutes to examine their tolerability against heat stress. It was found that *Indica* rice cultivars were more sensitive to heat stress compared to *Japonica* and the germination rate of Koshihikari, a *Japonica* cultivar, was more than 70%. In addition, the de-hulled seeds of Koshihikari were also tolerant under treatment at 65ºC for 10 minutes. Using Chromosome Segment Substitution Lines (CSSLs) derived from some crosses of Koshihikari as genetic background and Habataki (*Indica*) as a donor, chromosome fragment containing the genes responsible for heat-stress tolerance in Koshihikari was investigated. Most of the Koshihikari-Habataki Substitution Lines (KHSL) seeds showed more than 90% germination rates under treatment at low temperature (64ºC) for 10 minutes. However, the germinability of KHSL26 seeds which have a fragment of Habataki chromosome 10 was reduced by this treatment. These results indicate that the gene(s) responsible for the heat-stress tolerance in the seeds of Koshihikari might be located on chromosome 10.

Keywords: hot water disinfection method, Chromosome Segment Substitution Lines, rice seeds

Determination of NaCl Level for Screening of Rice Salinity Tolerance in the Green House

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ABSTRACT

Salt accumulation in irrigated soil is one of the main factors that decrease rice productivity. A greenhouse experiment was conducted at Cimanggu Experiment Station, Bogor, Indonesia during May to September 2014 in a complete randomized block design with three replications. Four salt tolerant and two salt sensitive genotypes of rice were used in this experiment. The treatment in this studi was application of five levels of NaCl (0, 20, 40, 60 and 80 mM, respectively). These NaCl treatments were applied at 21 days seedling stage until harvest time. The aim of this study was to determine the NaCl level that can be used for screening of rice salinity tolerance in the greenhouse through observation on agronomic characters. The result of this study showed that increased in NaCl levels in soil significanly decreased plant height, number of panicles, panicle length, number of grains per panicle, number of filled grains per panicle, and grain yield. The addition of 40 mM NaCl can distinguish tolerant and sensitive genotipes. The grain yield of sensitive genotypes decreased 90-100%, while the tolerant ones showed < 70% in grain yield decreasing. Therefore, this level can be used for determining rice salinity tolerance in green house.

Keywords: NaCl levels, salinity tolerance, agronomic characters, green house

Search for Tomato Hybrids Suited for High Temperature Stress Condition

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ABSTRACT

Thirty hybrid combinations generated from crossing ten elite lines with three testers in line x tester (LxT) fashion were evaluated for yield and yield contributing traits in two different conditions namely (i) normal temperature regime (*rabi* season) and (ii) high temperature regime (summer season) in the year 2010-11 and 2011-12 along with parents at Banaras Hindu University, India. The data across two years were pooled for both the temperature regimes for statistical analysis. Heterobeltiosis (heterosis over better parent) and standard heterosis (over commercial check) were estimated for yield and yield traits and crosses were grouped into heterotic groups. The mean of all the traits in high temperature regime was found to reduce when compared to the normal temperature regime. The fruit yield/plant (kg) was in the range of 253.31(Sun Cherry x Super bug) to 1538.61(NDTVR-60x FLA7171) in high temperature regime and 1046 (Sun Cherry x FLA7171) to 3009.34 (Selection-7x FLA7171) in normal temperature regime. The percentage reduction in fruit yield /plant was in the range of 36.10 to 84.76. The cross NDTVR-60 x FLA-7171 recorded minimum reduction percentage (36.1) followed by the cross PS-1 x FLA-7171 (36.91). These two hybrid combinations can be further tested for areas experiencing high temperature during the crop period and utilized in tomato breeding under changing environment conditions with special reference to temperature.

Key words: Tomato, high temperature stress, heterosis, fruit yield, hybrids

Assessment of Indonesian Rice Varieties for Tolerance to Aluminum Toxicity using Magnavaca Solution and 384 SNP array

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ABSTRACT

The study was subjected to assess the tolerance of Indonesian rice varieties to Aluminum (Al) toxicity. Forty-eight rice varieties consisting of Indonesian local and some international varieties were screened in Magnavaca nutrient solution treated with and without Al (650 µM of). The level of Al tolerance was determined based on the inhibition of the root growth. The most tolerant and most sensitif varieties were then genotyped with 384-plex SNPs using GoldenGate VeraCode oligo pool assay and grouped with Power Marker analysis tool. Phenotypic sreening showed the root growth inhibition due to Al stress. The root growth in the most sensitive varieties were more severely decreased and inhibited, compared to the tolerant varieties.The SNP characters grouped the varieties set into two major clades. The first clade preferentailly consisted of tropical japonica which were tolerant to Al. The second group consisted 3 sub-clades, of which one of grouped only the most susceptible varieties being as indica type. This indicate that, probably, tropical japonica rice is suitable source of Al tolerance for rice breeding program to develop rice tolerant to Al toxicity.

Key words: aluminum tolerance, magnava, rice, total root length, SNP

A Novel Phenotyping Technique for Reproductive-Stage Salinity Tolerance in Rice

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ABSTRACT

Rice responds differentially at different stages of development. The seedling and reproductive stages are the most sensitive growth stages with very weak association, suggesting that they are regulated by different processes and sets of genes/QTLs. There are numerous reports on seedling-stage salinity tolerance in rice but, hardly any studies exist on reproductive-stage salinity tolerance mainly because of the lack of reliable reproductive-stage-specific phenotyping techniques and incomplete knowledge of the stage-specific mechanisms of salinity tolerance. There are two major challenges for salinity screening exclusively for the reproductive stage. First, how to stress plants at the reproductive stage without stressing them at the seedling or late vegetative stage. Second, how to impose the stress on different genotypes or mapping populations at equivalent growth stages of development (for 10-20 critical days) because of the variability in the progression of growth rate through developmental stages. We standardise a methodology that allows salt translocation to the reproductive organs such as the flag leaf (the largest source for the sink) and panicle as quickly as possible just at the initiation of booting when the genotypes are at the same stage of tissue/organ development rather depending on age of the plant. Extra leaves were clipped, leaving only a minimum number of leaves needed by the rice plant that will not significantly affect grain yield and yield components. Salt stress equivalent to EC 10 dSm^{-1} was imposed on rice plants with trimmed leaves starting from boot leaf emergence up to 20 days in an experiment. Stage-specific effect of salt stress was verified by observing salt-sensitive and salt-tolerant genotypes. Leaf cutting before the booting stage efficiently directed the salt to reproductive organs and helped in discriminating genotypes based on their tolerance as evidenced by the lower pollen viability and higher accumulation of toxic ions. Details will be presented.

Developing Bruchid Resistant Mungbean Varieties

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ABSTRACT

Bean weevils or bruchids (*Callosobruchus chinensis* L. and *C. maculatus*F.) damage mungbean [*Vigna radiata* (L.) R.Wilczek var. *radiata*] seed and are one of the major biotic stressors affecting the crop.Although infestation starts in the field, most damage occurs during storage,leading to weight loss in beans, low germination, and beans unfit for human consumption or sowing. All the available varieties of mungbean are susceptible to bruchids. AVRDC – The World Vegetable Center identified two mungbean accessions (V02802 and V02709) and one black gram (*V. mungo* (L.) Hepper) accession,V02164, with resistance to bruchids. Populations were established from crosses between bruchid resistant V02802, V02709 and V02164 with bruchid sensitive cultivar 'NM94.' $F_3$to F_7families of these populations were generated and submitted to bruchid resistance testing. Populations V02802 × 'NM94' and V02709 × 'NM94' showed segregation for resistance; a few F_3 families were 100% resistant against the pest. Resistance testing of 'NM94'×V02164 F_3 families is ongoing. Currently, 144 F_7 families are available for cross V02802 × 'NM94' and 149F_6 families of cross V02709 × 'NM94.'After repeated exposure of these populations to bruchids, we identified 57 F_7 lines derived from V02802 with resistance. Bruchid resistance has been tentatively mapped in V02802 ×'NM94' to four loci on chromosomes 2, 3, 4 and 5. The resistance locus on chromosome 5 overlaps with previously mapped bruchid resistance loci from *V. radiata* ssp. *sublobata*. Validated molecular markers associated with bruchid resistance in V02802 will be recommended for use in marker assisted selection.

Keywords:mungbean, bruchids, resistance breeding, molecular markers

Resistance of Banana Variants cv. Ampyang (*Musa acuminata*, AAA, subgroup non-Cavendish) to *Fusarium* Wilt

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ABSTRACT

Fusarium wilt caused by *Fusarium oxysporum* Schlecht f.sp. *cubense* (EF Smith) Snyd & Hans (*Foc*) is one of the most important disease infecting root of banana and *plantain* (*Musa* spp.). Chemical control of this disease is economically impractical, and to widen banana genetic diversity is also a difficult task because most of edible banana are either triploid, male sterility and partenocarp. The objectives of this research were (1) to increase phenotypic diversity of banana cv. Ampyang through induced mutation; (2) to obtain banana cv. Ampyang resistant to *Fusarium* wilt through *in vitro* and *in vivo* selection. Explants of *in vitro* grown shoots were exposed to different doses of gamma irradiation at 0-50 Gy to determine their radiosensitivity. The CurveExpert ver. 1.4 analysis results indicated that lethal doses of irradiation reducing 20% to 50% of shoot growth (LD_{20-50}) were 51.07-64.54 Gy. In this approach, plantlets variant regenerated from induced mutation followed by *in vitro* proliferation for 10 months then were selected in culture filtrate (CF) of *Foc*. This study showed that *Foc* of Banyuwangi isolate were virulent to banana cv. Ampyang, and culture filtrate of *Foc* concentration 40-60% (v/v) was an effective concentration to obtain banana shoots insensitive to CF of *Foc*. However the highest plantlet growth inhibition were observed at addition 60% of *Foc* CF into selective media, and 2 months after shoots were on regeneration media found that 1695 plantlet (57.7%) were insensitif to CF *Foc*. *In vitro* regeneration of insensitive shoots variant and aclimatization process of plantlets found that 118 plantlet (23.7%) were survived and identified as banana clones resistance to culture fíltrate of *Foc*. Evaluation resistances of those plantlets in a green house showed that inoculation methods by dipping banana roots for 2 hours into *Foc* conidial suspensión 2.5 x 10^7 conidial mL^{-1} is the most effective methods to identifying banana cv. Ampyang resistant to *Fusarium* wilt. Induced mutation followed by *in vitro* and *in vivo* selection procedures found that 48 clones (40.7%) indicated resistant to *Fusarium* wilt, most of them originated from gamma irradiated explants of 30 and 50 Gy.

Keywords: Fusarium oxysporum Schlecht f.sp. cubense (Foc), induced mutation, in vitro selection, cultura fíltrate, Foc conidial suspensión

Evaluation of Brown Planthopper Resistant Related Traits, Aromatic, and Early Maturity by Molecular and Phenotypic Markers on Rice Genotypes Derived From a Pyrimiding

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ABSTRACT

Rice that resistant to brown planthopper, aromatic, and early maturity is important breeding objectives. The aim of this experiment was to obtain genotypes with such traits assessed by molecular and phenotypic markers analysis. This study was conducted from May to September 2014 at Plant Breeding Laboratory and Greenhouse Faculty of Agriculture, Universitas Padjadjaran. Descriptive analysis was applied by using molecular marker i.e., SSR markers RM586, RM589, RM8213 (markers for brown planthopper resistant gene), Bradbury's marker (marker for aromatic), SSR markers RM7601 and RM19414 (markers of early maturity). Phenotypic evaluation was performed for brown planthopper resistant traits such as chlorophyll content, stomatal conductance, and density of trichomes, while sensory test and heading date were performed for aromatic and early maturity characters, respectively. Based on this study it was observed that 7 genotypes (#2, #3, #4, #5, #6, #10, #11) were related to brown planthopper resistant-related traits, aromatic, and early maturity characters based on the analysis of molecular marker. Whereas, genotypes #1, #2, #4, #6 and #11were similar with their parents based on phenotypic analysis. Pyramiding program based on molecular and phenotypic markers is enabling to combine three characters in one rice genotype.

Keywords: aromatic, brown planthopper, early maturity, molecular marker, pyramiding, rice.

Selection Characters in Early Generation for Adaptation of Rice to High Temperature Strees

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ABSTRACT

This research aimed to obtain information about gene action and inheritance in rice related to heat stress tolerance based on agronomy characters. The experiment for study inheritance in rice was carried out in a green house of University Farm, Bogor Agricultural University in September 2014 to Januari 2015. The minimum temperature in this research was 24°C and the maximum was 42.09 ° C. About 210 F2 population from parental cross IPB 4S x Situ Patenggang, 20 individuals of IPB 4S, and 20 indiviudals of Situ Patenggang were used as genetic materials. Based on filled grain number and seed weight, the inheritance of heat stress tolerance character in rice showed that the mean phenotypic value of F2 population from the cross IPB 4S x Situ Patenggang was higher than the mean value of two parent. The transgressive segregants were also observed. The performance of rice agronomic characters for yield components (filled grain number and seed weight) in heat stress condition was controlled by dominance gene and additive. The other performance of rice agronomic characters was controlled by epistasis duplicate, epistasis additive and epistasis complementer. The estimation of broad-sense heritability for agronomic characters was moderate to high, and the estimation of genetic variability coefficient was small to high.

Keywords:* *dominance, additive, gene action, genetic variabilitiy coefficient, heat stress, heritability, mean value, yield components.

Reaction to BPH Resistance Genes at Seedling Stage of Rice

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ABSTRACT

This experiments were carried out to know the reaction to Brown Planthopper(BPH) resistance genes at seedling stage using Biotype 1 for develoment of resistant cultivars. BPH for experiment was used for more than 10 generations bred BPH of Biotype 1, it gave Nampyeong(no resistance gene) to feed. Seedlings resistant reaction to BPH was investigated after inoculation with 10 BPH at 3-4 leaf stage. Varieties with Bph1, *Bph3* and *Bph18* genes showed a very strong resistance reaction, *Bph2, Bph6, bph7* and *Bph9* genes exhibited moderate resistance. *bph5* and *bph8* gene retention variaties and Nampyeongbyeo showed a very weak sensitivity in response to BPH. Antixenosis of BPH was investigated 3 times every 24 hours. After 72 hours, Nampyeongbyeo, *bph5* and *bph8* gene, *Bph6, bph7* and *Bph9* gene and *Bph1, bph2, Bph3* and *Bph18* gene were showed a feed-preference over 50%, below 40%, below 30% and below 20%, respectively. Results of Antixenosis and seedling resistance reaction to BPH were grouped into similar by specific resistance genes. 10 days after inoculation, BPH survival rate of vareities with resistance genes were below 30%, whereas Nampyeongbyeo was more than 70%. The results showed that *Bph3* and *Bph18* genes are highly resistant reaction against BPH, these genes are very useful for improve the rice cultivars with various resistance genes

Keywords: BPH, Bph3, Bph18, Resistance gene, Biotype 1, antixenosis

Enhancing for Broad-Spectrum Resistance to Leaf and Neck Blast in *Japonica* Rice Using Weedy Rice (*Oryza sativa* L.)

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ABSTRACT

Rice blast caused by the fungal pathogen, *Magnaporthe grisea*, is a serious disease affecting yield loss and decreasing its quality in rice production. The resistance in most varieties has broken down within a few years after they were released to farmers because of the differentiation of new races of *M. grisea*. It is necessary to look for novel resistance gene(s) showing a broad-spectrum resistance to blast in diverse environmental conditions. A RIL population was developed from a cross between Ilpum (*japonica*) and Geumleungaengmi33 (weedy rice), and screened to blast nursery and isolates. We identified a major QTL *qLB4.1* on chromosome 4 associated with the resistance to blast nursery and isolates. This QTL explained 45.3~53.1% and 26.1~28.6% of total phenotypic variation by the allele of GL33, respectively. The QTL *qLB4.1* was tightly linked to RM6352 and RM3643 of 52.6cM region. These markers were comprised into a BAC clone OSJNBb0012E08 consisting of 14 candidate ORFs. An ORF in Os04g32940 would be related to the putative candidate *R* gene to blast. A QTL-NIL SR30058(52)-1-1-1 from a backcross of Ilpum*4/GL33 was developed by marker-assisted backcross method. This line showed resistant reactions at blast nursery across regions and years, and also showed resistance to neck blast in hot-spot field. A QTL-NIL SR30058(52)-1-1-1 had durable resistance of lower 10% of diseased leaf areas in sequential planting method.

Keywords: weedy rice, blast, isolate, nursery, resistance, QTL

Generation Mean Analysis of Leaf Bronzing of Rice Seedling Using Digital Imaging Methods under High Levels of Iron

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ABSTRACT

The effectiveness of rice germ-plasms utilization in rice breeding program requires an understanding of their genetics mode. Determining the iron toxic tolerant rice usually uses visual scoring of leaf bronzing symptom (LBS). This method has an inherent weakness in its applicability on quantitative genetics analysis. Here, we studied estimating genetics effect using digital imaging method for tolerance to iron toxicity. The proportions of intensity of color red (R)/green (G) index were analyzed by Adobe Photoshop CS©. We identified various respond of 23 genotypes of rice seedling under 400 mg.L-1 Fe 2+ for 10 d using Yoshida nutrient solution. We found that R/G index was correlated with LBS, shoot dry weight, and iron shoot content. Based on this result the crosses were made between the iron-toxic tolerant varieties Mahsuri and Pokkali with Inpara5, an iron-toxic sensitive variety. The Seedlings of parents and their progeny generations were phenotyping in high iron nutrient solutions. Means of R/G index, shoot length, root length and fresh weight of P1, P2, F1, F2, BC1, and BC2 generations, in all crosses showed significant variation. The simple additive-dominance did not fit to the model indicating the presence of non-allelic gene interactions or epistasis in all observed traits. Five parameter models, additive x additive (i), additive x dominance (j) and dominance x dominance (l) epistasis, in addition to additive (d) and dominance (h) were fit for explanation the gene action of the observed traits in both populations. The type of gene actions were duplicate epistasis in both crosses, except for R/G in cross of Inpara5/Pokkali. R/G index showed strong correlation with LBS, shoot length, and root length in the F2 population. A preponderance of medium to narrow of narrow sense heritability indicated that selection for iron-toxic tolerance would be effective in late generations or recurrent selection.

Keywords: RGB model, epistasis, gene action, quantitative inheritance, heritability

Line x Tester Analysis to Study Combining Ability and Genetic Parameters of Hybrid Rice Drought Tolerance Traits at Germination Stage

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ABSTRACT

The hybrid rice breeding for tolerance to drought is one of the important ways to reduce yield loss due to drought stress. Therefore, an experiment was conducted to estimate the combining ability and determine the genetic mechanism of drought tolerance during the germination stage. The genetic materials were thirty hybrid rice combinations from six CMS and five Restorer lines. The germinating seed of parents and F1 were subjected to drought stress in 25% PEG 6000 for 7 days. The germination traits i.e. germination percentage, relative length of radicule, plumule and seedling, relative dry weight of plumule and radicule, relative ratio length of radicule/seedling, and relative ratio dry weight radicule/plumule were measured. General and special combining ability of germination traits and genetic parameters were analyzed using line x tester analysis. Among 30 hybrid combinations, the GCA was significantly different among eight drought resistance traits. The SCA of these traits was significantly different except the SCA of germination percentage. The genotypes PK 90 and PK 12 (Restorer lines) had higher tolerance potential to drought stress and could be alternative parents for hybrid rice tolerant to drought.

Keywords: line x tester, combining ability, genetic analysis, hybrid rice, drought, germination

Selection of Resistance for 24 Family F5 Chili (*Capsicum annuum*) to Bacterial Wilt (*Ralstonia Solanacearum*)

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ABSTRACT

Bacterial wilt caused by *Ralstonia solanacearum* (EF Smith) is an important disease in chili. The use of resistant varieties is the most effective and efficient way to control this desease. Resistant varieties can be obtained through the selection of families derived from hybridization. Two sets of crosses have been carried out, ie between resistant parent (PBC 473 and Jatilaba) with high yielding variety TW2. This study aims to get the families from F5 population which are resistant to bacterial wilt disease. The research was conducted in Gesingan, Pujon, Malang with an altitude of 1100 m above sea level, February to August 2015. 24 families F5 and 3 parent genotypes grown and disease resistance variables observed. Observations at the variable incubation period of bacterial wilt disease ranged from 49 to 105 dap. While the incidence of disease between 3.45 to 45.28% categorized as moderate susceptible to resistant. Of the families that were tested, 11 families classified as resistant, 11 families classified as moderate resistant, and 2 families as moderate susceptible.

***Keyword: Selection, chili, resistance, bacterial wilt, the incidence disease*.**

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Analysis of Genotype × Environment Interaction using Stability Estimates in Maize (*Zea mays* L.)

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ABSTRACT

The present investigation was aimed to evaluate the relative performance and stability of six maize inbred lines and their one way crosses, with respect to different quantitative traits under twelve different environments. GxE interactions (linear) component of variation of stability were significant for the studied traits, revealing the differential response of the genotypes to studied environments. Gx E was also significant when tested against pooled deviation in most traits, suggesting that the linear regression and the deviation from linearity were important for describing stability for theses traits. A simultaneous consideration of used stability parameters, provide evidence that, P_5, P_1xP_3, P_1xP_5, P_3xP_5 and P_4xP_6 were ranked as the most desired and high stable genotypes as they had high mean performance and good adaptability to wide range over environments, with "b" value approach near unity and the deviation from regression as minimum as possible. Positive significantly correlation was detected between bi and S^2di (yield plant^{-1}); bi and r2i (most studied traits); bi and αi (most studied traits); S^2di and r^2i (plant height, and yield plant^{-1}); r^2i and αi (most studied traits) as well as between αi and λi (ear length, 100-grain weight and yield plant^{-1}). This showed that ranking of genotypes for either statistic were generally the same, indicating the similarity of both parameters for measuring stability and one can be used as a good alternative for the other in a GxE interaction evaluation. The recorded lack of correlations between the other pairs of statistics for some studied traits, showing that each of bi, S^2di and r^2i was independent and suggest that has its own characteristic and using of any one depends upon its easy to be calculated, and of common use, since all of them to obtain reliable estimate for stability will be expected.

Keywords:* *genotype-environment (GxE) interaction, maize - phenotypic stability - Stability statistics

Selection Of 180 Sweet Potato Superior Clones In Wet Land And Dry Land

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ABSTRACT

Selection of sweet potato clones were done to obtain new superior clones which appropriate with the consumer preferences. Selection were done at two locations on wet land and dry land in experimental field, Ciparanje Universitas Padjadjaran. This research used augmented design and Principal Component Analysis (PCA) for analized the genetic diversity, for analyzed the interaction of genotype and environment used Ms.Excel 2007, and used LSI Test to find out the potential yield of 9 characters that observed. Based on PCA analysis, the genetic variability in two locations were extensive. G x E Analysis showed that reduced sugar levels, total number, economic weight, number of economi, tuber dimter were significantly different. Starch content, moisture content, total weights, tuber length, were not significantly different. 13 new superior genotypes of sweet potato with different color which had potential and superior character compared with the check. On dry land that presented there were 11 genotypes that had superior character from the checks. From both of the data, there was a genotype which has the superior character than the checks at two locations, it was 274 numbers (565). This study can be used as a basic consideration for the best location for breeding sweet potato.

Keywords: Augmented design, G X E, PCA, Sweet Potato, Variability

Upland Rice Breeding Lines Adaptable to High Elevation Areas and Selected through Participatory Approaches

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ABSTRACT

Upland rice in Indonesia is cultivated in about 1.15 million ha area comprising diverse geographical areas of low to high altitude. To this day, in the high altitude areas, farmers still cultivate traditional rice varieties mainly due to absence of improved varieties specifically released for the areas. A set of 12 upland rice lines selected from the previous trials were evaluated in replicated yield trials to assess their adaptability in two sites representing different altitudes. The first experiment was conducted in Cianjur district with an elevation of 1099 meters above sea level (masl). The second experiment was carried out in Wonosobo district with an elevation of 900 masl. Two check varieties were used in both experiments including a traditional rice variety Sigambiri Putih and improved variety Jatiluhur. To assess farmers' acceptance of the breeding lines, a participatory varietal selection was conducted in Wonosobo district involving 10 female and 10 male farmers. These trials demonstrated the differences in agronomic characteristics and yields among genotypes grown under two different altitudes. Most of the upland rice breeding lines performed well in 900 masl site only. In contrast, the traditional variety Sigambiri Putih consistently performed well in both altitudes. In 1099 masl site, the highest yielding genotype was Sigambiri Putih (4.45 t/ha). In 900 masl site, the line B11592F-MR-23-2-2 yielded 3.2 t/ha and was higher than check varieties Jatiluhur (2.75 t/ha) and Sigambiri Putih (3.09 t/ha). Participatory varietal selection in Wonosobo district revealed only four genotypes with positive preference scores including Jatiluhur, Sigambiri Putih, B13650E-TB-80-2 and B11592F-MR-23-2-2. The line B11592F-MR-23-2-2 which has high yield and obtained positive preference score has the potential for release as a new upland rice variety for high elevation areas of up to 900 masl.

Keywords: upland rice, high elevation, participatory varietal selection

Level Difference of Natural Cross-Pollination on Three Genotypes of Chili Pepper (*Capsicum annuum* L.)

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ABSTRACT

Inconsistency information of natural cross-pollination stimulated this research to update natural cross-pollination rates of chili pepper in Indonesia. This experiment was conducted from 2011 until 2012 at IPB experimental field using four genotypes of chili peppers, “IPB C2, IPB C5, IPB C120” (green – hypocotyl) and IPB C20 (purple – hypocotyl). The experiment utilized the dominance of purple hypocotyl color over green hypocotyl color to identify natural cross-pollination. The experimental field consisted of three block of trial in which each of blocks was planted by purple hypocotyl genotype in the central plot and green hypocotyl genotypes in the four plots surrounding the central plot. Seeds were harvested from each plant and were examined for natural cross-pollination in the next generation. In this experiment, the observations were consisted of percentages of natural cross-pollination, flower morphologies, and percentages of artificial cross-pollination. The result showed that there was the different of natural cross-pollination percentages on different genotypes of chili pepper but there wasn’t the different of natural cross-pollination based on spacing radius from pollen source. The result also showed that there were different flower morphologies and percentages of artificial cross-pollination on different genotypes of chili pepper. IPB C2 genotype had the highest stigma exertion length, percentages of natural (24.52%) and artificial cross-pollination (50.57 %). Based on the result, level of natural cross-pollination in chili pepper could be expected by stigma exertion length and the level success of artificial cross-pollination.

Keywords: artificial cross-pollination, purple hypocotyl, and stigma exertion.

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Challenges Facing the Genetic Improvement of Underutilised Crops: Progress in Bambara Groundnut

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ABSTRACT

Bambara groundnut (*Vigna subterranea* (L.) Verdc.) is a resilient legume that has significant local importance in Sub-Saharan Africa and parts of Southeast Asia. Underlying the biological challenges that face this exemplar of underutilised crops is a lack of:

A. Quantitative and comparative data on traits of farmer-defined importance.
B. Purified genetic lines, mixes and controlled crosses.
C. Knowledge of optimal field management and genotype-by-environment interactions.
D. Replicated and properly designed multi-location field trials leading to locally selected varieties.

BamYIELD and its predecessor programmes have worked on overcoming existing limitations, such as photoperiod sensitivity that can restrict fruiting between a relatively small range of photoperiods (i.e. at or near 12 hour day lengths), crossbred contrasting lines for mapping traits of importance, such as peduncle length and drought tolerance, and explored the socioeconomic issues surrounding crop production in Ghana, Nigeria and Indonesia. Progress has accelerated recently and near future plans include an international multi-location field trial system that will serve as a germplasm evaluation and trait selection programme to both increase advantageous characteristics like drought tolerance and reduce bottlenecks like the poor cookability. The programme links partners from Africa and Asia, including the Council for Scientific Research – Crop Research Institute, Ghana, and Bogor Agricultural University, Indonesia. A component of the field trials programme will be an association genetics panel, being developed with the International Institute for Tropical Institute, Nigeria, that will consist of 500 accessions from around the world to be developed by single genotype line selection for phenotyping and genotyping. In addition, nutritional profiling will take place on a range of genotypes in various agro-environments and value-added products are being developed. The overall framework and methodological toolkit being designed by BamYIELD will be applicable to many other underutilised crops.

Keywords: bambara groundnut, underutilized crops, multi-location field trials, drought tolerance, cookability

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Bambara Groundnut Breeding for High Yielding and Early Maturity

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ABSTRACT

Bambara groundnut (*Vigna subterranea* L.) is one potential alternative food sources in Indonesia. Efforts to improve production can be done by assembling new varieties that have high yield, tolerant to drought and early maturity. In Brawijaya University, bambara ground nut breeding efforts have been initiated since 2010 by performing a collection of several production centers as well as the evaluation of genetic diversity. Evaluation of genetic diversity has been conducted on 50 local strains. Observations were made on some morphological characters and yield such as: the type of growth, plant height, leaf number, internodes length, petiole length, peduncle length, flower stem length, banners length, number of flowers per peduncle, crown width, number of pods per plant, number of leaves, number of stems, number of nodes per plant, number of branches and the weight of fresh pods per plant. The results showed that a high diversity found either in a group collection (from the same origin) or between groups of collections. High diversity between populations could potentially be selected to obtain the desired genotype. The selection was done in 2015 and obtained eight lines are CCC 1.4.1, 3.1.2 GSG, GSG 2.5, 2.1.1 GSG, GSG 1.5, UB Cream, BBL 6.1.1, and 5.3.1 PWBG which were potential to be developed into new varieties. Work is underway to yield trials to these selected lines. New bambara varieties were expected to be released soon.

Keywords: bambara groundnut, genetic diversity, breeding, high yield, variety

Genetic Variability Orange Fleshed Sweet Potato as Industrial Raw Materials

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ABSTRACT

Identification of genetic variability used to see the diversity of Orange Fleshed Sweet Potato genotypes. This research used augmented design at two different locations on wet land and dry land in experimental field, Ciparanje Universitas Padjadjaran. Principal Component Analysis (PCA) for analized the genetic diversity (software *XLSTAT* 2015). Based on PCA analysis, the genetic variability in two locations were extensive with euclidean distance 0-8. Results of PCA analysis can be used as consideration in selecting material for breeding sweet potato.

Keywords: Augmented design, PCA, Sweet Potato, Variability

Current Status on Oil Palm Breeding in Indonesia

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ABSTRACT

Since it has been introduced in 1848 on the Bogor Botanical Garden, oil palm (*Elaeisguineensis*Jacq.) in Indonesia has grown tremendously and has brought the country to be the largest producer of palm oil in the world. Nowadays, oil palm area in Indonesia covers more than 10 million ha, and the Indonesian crude palm oil(CPO) production has reached 29 million tons. Breeding effort through the exploitation of heterosis effect from the crosses between dura (D) x pisifera (P) to produce DxP hybrid materials has undoubtedly contributed to the increasing of oil palm yield. TheDxP hybrid,tenera(T) type,is capable of producing oil about 25 – 30% higher than dura. By April 2015, it has been released forty six DxP hybrids varieties having potential oil yield 6 – 9 ton/ha/year developed by twelve breeding institutes in Indonesia. Breeding objectives currently have not only been focused on the increasing oil yield, but also on the secondary characters such as plant architecture for easiness on harvesting, the development of resistance variety as well as improving oil quality. Introduction of new oil palm genetic material from Cameroon and Angola has opened the opportunity for breeder to develop oil palm cultivars with novel traits. The integration of molecular markers to assist the selection offers a promising way to reduce the generation interval and the cost of oil palm breeding trials. This paper will elaborate current status on oil palm breeding in Indonesia including collection of existing genetic materials, breeding objectives, breeding strategies, breeding achievement, and the use of molecular markers in oil palm breeding as well as oil palm seed production system.

Keywords: oil palm, breeding, new genetic materials, novel traits, molecular markers

Analysis on the Genetic Parameter and Combining Ability of Agronomic and Quality Traits of Hybrid Sorghum

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ABSTRACT

Genetic parameter and combining ability of 14 sorghum hybrids developed by crossing 7 lines and 2 testers were analyzed by lines × testers analysis. Analysis of variance revealed significant differences among genotypes, parents and F_1. The presence of non-additive gene effect was realized by higher values of specific combining ability compared to general combining ability, ratio of variance of specific combining ability (SCA) to general combining ability (GCA) and average degree of non-aditive. The proportional contribution of testers was observed to be lower than that of lines × testers interaction resulted higher estimates of SCA variances. The estimates of GCA effect indicates male parent ‘Numbu’ and female parent ‘B-69’ were good general combiner for grain yield. Cross combination ‘B-69 × Numbu’ was found to be good specific combination for grain yield and need to be further development.

Keywords:* *additive, general combining ability, genetic parameter, non-additive, spesific combining ability

Breeding Tomato (*Lycopersicon esculentum* Mill.) for Lowland Area Using Half Diallel Crossing

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ABSTRACT

Tomato is highly cultivated in highland area, but the land conversion decreases the number of area alocated for vegetable cultivation including tomato. Therefor, tomato needs to be planted on area other than highland. In this case, lowland area can be an alternative. The chalenge is that lowland has high air temperature which is not suitable for most of tomato genotype. It causes the heat stress which decreases the yield. This research had propose to study the suitable genotype for lowland area which was determined by heterosis, heterobeltiosis, general combining ability (GCA) and specific combining ability (SCA) of six parental tomatoes (Lycopersicon esculentum Mill.) and fifteen hybrids of half diallel crossing. This research was conducted at lowland area which had 207 m altitude. The experimental was conducted by using randomized completed block design (RCBD) in three replications and one factor that was genotype. Plant material were six tomato inbreed lines, fifteen hybrids from hybridization half diallel crossing. The result showed that genotype T1xT13, T1xT64, T1xT73, T3xT64 had best heterosis and heterobeltiosis in many characters observed such as fruit width and fruit weight per plant. Genotype T73 had the best combining ability in characters plant height. Genotype T3xT73 had the best SCA in character plant height, day to harvest, and fruit long. It showed that those genotypes had good opportunities to be cultivated in lowland area or use as parental line for breeding programme.

Keyword : altitude, combining ability, heterosis, hybrid, tomato.

Pedigree Selection of Red Rice (*Oryza sativa* L.) Offspring to New Plant Idiotype

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ABSTRACT

The aim of this research was to know the genetic parameter of yield and yield component of trais and select the best family and genotypes within family that are new plant idiotype. This research was conduct at the UPT Farm Faculty of Agriculture, Andalas University from January to Juni 2014. Genetic material used was 3 F3 family and 2 parents, that are KF5, KF33 and KF 42 family, and the parent Karajut and Fatmawati. The red rice cultivar Karajut has smal seeds while the white rice variety Fatmawati has bigger seeds, higher productivity and mature earlier. The desired outcome from this cross is new plant type having high productivity, big seeds, a high number of grain per panicle and red grain color. The Head to Row method from the family was used. The result showed that the broad sense heritability of all characters was moderate to high, while Expected Genetic Gain was high for all character except time to harvest. Differenttial selection of the F3 population with 5% selection based on grain weight per plant, weight of 1000 grain and number of grains per panicle resulted in 20 selected plant. The seed of the selected plants was retained for the F4 generation.

Keywords : red rice, head to row, heritability, pedigree selection

Characteristic Stability Analysis of Eggplant (*Solanum melongena* L.) Genotypes using Parametric and Nonparametric Approaches

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ABSTRACT

Eggplant (*Solanum melongena* L.) is one of the important horticultural commodities in Indonesia that has a high productivity. Indonesia has an abundant eggplant germplasm collection in which some have a potential to become a superior variety. Stability analysis of prospective genotypes in different environments is needed to observe its general performance. This research aim to analyze eggplant genotypes performance and appearance in different locations based on altitude. Efforts to quantify the interaction between specific eggplant characteristics and environment can be done with both parametric and non-parametric approaches. A total of 25 eggplant genotypes were planted in three different locations in West Java, Indonesia during the time period of May 2014 – July 2015. This research was conducted using randomized complete block design in each location. Variables observed are fruit length, fruit diameter, fruit weight, plant height and stem diameter. Combined analysis of variance showed highly significant effect of location, genotypes and genotypes x location for all variables observed. Genotypes 2014-044, 2014-047, 2014-077, 2014-071 and Sriti were stable based on parametric analysis using Wricke (1962), Finlay & Wilkinson (1963), Eberhart & Russel (1966), Shukla (1972) and Francis & Kannenberg (1978) methods. Nonparametric analysis using Kang (1988) and Thennarasu (1955) methods showed that genotypes 2014-033, 2014-024, 2014-080, 2014-071 and THP were stable. Overall, genotype 2014-071 was the only genotype that was stable in both parametric and nonparametric analysis. This genotype performs well and has generally consistent appearance in all location.

Keywords: interaction, GxE, environment, multilocation, fruit, vegetable, performance

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Participatory Selection of Sweet Potato Based on Farmers Preferences in Banjar City, West Java, Indonesia

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ABSTRACT

Selection based on consumer preferences' aims to know the farmers' preferences and criteria in Banjar city against superior clones of sweet potato Universitas Padjadjaran. Clones were the result of plant breeding, which is one of the efforts in supporting the competitiveness of national food products. Research involved of farmers through participatory farmers' selection method to evaluate the quality of the preferred product, can be provided opportunities adoption of new varieties of sweet potato in the community. Field research used experimental design of augmenthed design with seven varieties. Evaluation of farmers' preference for clones test used questionnaires and the selection was done directly by farmers in field trials. Based on the results of the evaluation of farmers' preference in the region, there were a crop selection's criteria for sweet potato. On the type of growth character, 89.5% of respondents like the type of shrubs compared with the type of growth spread. For potato skins character , the percentage for the farmers who like light-yellow color is 36.8% as compared to the other skin color. For the shape parsnip Character, the percentage for potato farmers who like elongated oval shape is more than 68.4%. In addition, farmers also want plants with a high yield. The results of Farmers selection based on the type of growth, selected clones number 12. For the shape character, almost all of the clones had the desired criteria. Clone number 3, 6, 12,25, and 56 were selected, based on potato skin characters. While the potato flesh color preferred are clones number 2, 3, 12, 37, 55, and 56. The results of this study can be used as a reference in sweet potato breeding program further by looking at the criteria of farmers.

Keywords : sweet potato, participatory plant selection, augmenthed design, farmers preference

Effect of Mesocotyl Elongation on Seedling Emergence under Deep-Seeding Condition in Rice

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ABSTRACT

The direct-seeding cultivation by broadcasting or drilling seeds is becoming popular. However, poor emergence can lead to yield loss in direct-seeding cultivation by deep-sowing. Mesocotyl and coleoptile elongation are important for seedling emergence in direct-seeding cultivation. In this study, the quantitative trait loci (QTLs) for mesocotyl and coleoptile length at 5 cm burial depth were detected with a backcross inbred line population from a cross between Kasalath and Nipponbare. A total of 3 QTLs for mesocotyl length were identified on chromosomes 1, 3, and 6. At two QTL loci, *qMel-1* and *qMel-3*, the Kasalath alleles contributed to an increase in mesocotyl length, except qMel-6. Coleoptile length QTL, *qCol-3* and *qCol-5* were detected on chromosomes 3 and 5, and Nipponbare alleles contributed to an increase in coleoptile length. For evaluating the effect of QTLs for mesocotyl or coleoptile on seedling emergence at 5cm soil depth, 54 chromosome segment substitution lines (CSSLs) were used. A positive correlation between mesocotyl length and emergence was observed (r=0.77, P<0.0001), however the correlation between coleoptile and emergence was not significant. Among 54 CSSLs, 3 CSSLs were selected to confirm the effect of *qMel-1* and *qMel-3* on seedling emergence at various soil depths. Seedling emergence of Nipponbare, Kasalath, and 3 CSSLs rapidly decreased with sowing depth. However, Kasalath and CSSL-5, harboring the Kasalath allele across the *qMel-1* and *qMel-3* regions, showed faster emergence than other CSSLs and Nipponbare at 7cm and 10 cm soil depth. CSSL-5 showed the longest mesocotyl length among 3 CSSLs, but the coleoptile length of CSSL-5 was not different from the other 2 CSSLs at 7cm depth. The results indicated that the variation of mesocotyl elongation is responsible for seedling emergence. To our knowledge, this is the first report using CSSLs to test the effect of mesocotyl elongation on seedling emergence in rice.

Keywords: rice, direct-seeding, mesocotyl, coloptile, seedling emergence, QTLs

Combining Ability for Yield and Agronomic Traits in Hybrid Rice Derived from WA, Gambiaca, and Kalinga Cytoplasmic Male Sterile System

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ABSTRACT

Four CMS lines and 8 tester lines were crossed in 4 x 8 half diallel. Thirty-two hybrids and their parental lines were planted using randomized complete block design with 3 replications at Sukamandi during WS 2010/2011. These lines were used to estimate the heterosis values, general combining ability (GCA) of parents and specific combining ability (SCA) effect for grain yield and its components. The variances due to SCA were larger than GCA variances for plant height, panicle length, number of filled grain per panicle, unfilled grain per panicle, total grain per panicle, filled grain percentage per panicle, and grain yield. Those characters were controlled by non-additive genes. BI485A and BI599A lines were good general combiner for productive tiller per plant, filled grain per panicle, and filled grain percentage per panicle, while a good tester combiner were IR53942, CRS8, CRS9, SMD10 and SMD15. The high SCA for yield was shown by parental lines with low GCA. Therefore, the yield character was controlled by overdominant gene action, dominant x dominant or epistasis. Hybrid with high SCA were suitable for development of hybrid rice with high heterosis. The highest SCA for grain yield was achieved by BI855A/SMD11, a Gambiaca-derived and produced yield 9.88 t/ha. The hybrid has highest heterobeltiosis and standard heterosis value.

Key words: hybrid rice, lini x tester, combining ability, heterosis

Efficiency Singe Seed Discent Method on Purify Morphological Characters of Bambara Groundnut (*Vigna subterranea* L. Verdcourt)

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ABSTRACT

The most important issue in improving a genetic quality of bambara groundnut (*Vigna subterranea* L. Verdcourt) local lines in Indonesia was a variability within lines. The previous research informed that there was high variability on qualitative characters within and among lines. The breeding program of this bean will improve genetic quality, so it gotten expected lines that have uniformity of morphological characters, but always consistent to create many different lines. The research was conducted in Agricultural Research Station, Brawijaya University, in Malang, September 2013-September 2014. Singe seed descent (SSD) applied at this research to purify a genetic characters base on morphological ones. Purification consisted of seed selection, plant selection and yield selection. All of them held twice in laboratory and field. In the last field observation, gotten 20 genotypes derived from collected local lines. These genotypes were evaluated of uniformity and similarity within genotypes and variability among genotypes. Application of SSD method in twice, was not determine uniformity of morphological characters of bambara groundnut. The value of similarity coefficient of second SSD was higher than first SSD. But, there were only 5 genotypes, namely CCC 1.4.1, SS 2.2.2, GSG 1.5, BBL 10.1 and CCC 1.1.1 had a similarity coefficient more than 0.80. There were 15 genotypes had a similarity coefficient less than 0.80. It could be continued with the third SSD to get purified lines. Variability of qualitative morphological characters was medium until high on observed characters. Those indicate value in genetic variability. Genotype BBL 10.1 and GSG 1.5 had high similarity coefficient and yield components, so these were formulated as candidate of future potential varieties.

Keywords : bambara groundnut, uniformity, genetic variability, breeding, ssd

Evaluation and Selection of Double-haploid Lines for Enhancement of High-yielding Rice in Africa through KAFACI Program of Korea

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ABSTRACT

In Africa, rice is the fastest demanding staple food with the largest growth rate of consumption at 4.0% per annum. In order to raise rice production, Korea has launched the joint rice breeding project through Korea-Africa Food & Agriculture Cooperation Initiative (KAFACI) and Alliance for a Green Revolution in Africa (AGRA). That is aimed at developing high-yielding rice germplasm to contribute to national food security for African countries. As of 2014, the ten African member countries joined the rice breeding projects of KAFACI program. We adopted the breeding strategy of inter-varietal cross and anther culture to speed up the development of high-yielding breeding populations using Korean and African germplasm. Korean germplasm is evaluated for adaptability in Africa and African partners make crosses with local germplasm. Korea produce double-haploid lines from these crosses to be screened in Africa. The materials acquired have been tested in partner countries under both paddy and upland condition and have shown good performance such that, in Kenya for example, two lines have been selected and nominated for national performance trial. These varieties could soon be released and thus pave way for seed system establishment and thus production by farmers to meet food and nutritional security. Inter-varietal crosses and double-haploid technology could accelerate the development of high-yielding germplasm in Africa within short project period.

Key words: Double haploid, KAFACI, High yield, Rice germplasm

Crossbreeding of *cry1Ac/bar* Transgenic Progeny with a Non-transgenic Elite Cultivar for Minimizing the Underlying Grain Cost of *Bt* Transgenic Rice

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ABSTRACT

Most of the *Bt* transgenic rice events have underlying grain cost depending on insect pressure in the field. This study was conducted (1) to determine if the *cry1Ac/bar* genetically modified (GM) rice (designated Agb0101) based on a Korean *japonica* rice cultivar has underlying grain cost and (2) to develop *cry1Ac/bar* GM rice lines with similar yield performance as Korean elite cultivars using crossbreeding. A 3-year field experiment showed that Agb0101 had an underlying grain cost as much as 18% grain yield loss, mainly due to grain number per panicle and the *cry1Ac/bar* transgene was inherited as a single dominant gene. The BC_1F_4, or F_5 crossbred progeny derived from anther culture of Agb0101, showed phenotypic resemblance to non-transgenic Korean elite cultivars, resulting in a decrease in grain yield cost of Agb0101 from 27% to 10%. These results suggest that *Bt*-GM rice oriented cross-fertilization with a non-GM elite cultivar followed by two- or threefold selection is a feasible method to minimize or remove the underlying grain cost of the *Bt* transgenic insect-resistant rice line.

Keywords: cry1Ac, Bt transgenic rice, underlying grain cost, cross breeding

Genetic Performance of Vegetative Traits of MPOB Oil Palm Interspecific Hybrids in Inland and Coastal Soils

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ABSTRACT

Oil palm interspecific hybrids were created at the Malaysian Palm Oil Board (MPOB) as part of a progeny testing program based on the North Carolina mating design 1 (NCM 1) involving *Elaeis oleifera* palms as maternal parents and *Elaeis guineensis (pisifera)* palms as paternal parents. The progenies were planted on inland soils of Kluang, Johor and Ulu Paka, Trengganu and on coastal soil of Teluk Intan, Perak. Measurement of vegetative traits was done at the eighth year after field planting. Analysis of variance (ANOVA) showed significant differences between *pisiferas* for petiole cross-section (PCS) rachis length (RL), leaflet length (LL), leaflet width (LW), leaflet number (LN), height (HT) and leaf area (LA) at all the three sites. Small PCS, short RL and low HT are generally favoured by oil palm planters for ease of frond pruning, higher density planting and longer economic lifespan, respectively. The highest heritability due to *pisifera* parents, h^2_p were recorded in Teluk Intan for PCS, RL, LL, LW, LN, HT and LA. Families with the lowest PCS, RL and HT were recorded in Kluang. General combining ability (GCA) for lowest PCS, RL and HT were obtained from *pisiferas* in Kluang. This study showed the importance of using suitable *pisiferas* with good GCA as paternal parent when creating oil palm interspecific hybrids.

Keywords: oil palm, interspecific hybrids, Elaeis oleifera, Elaeis guineensis (pisifera), inland soil, coastal soil, vegetative traits, heritability, general combining ability

Combining Ability through Line × Tester Analysis and Heritability Studies in Upland Cotton

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ABSTRACT

Line × tester analysis and heritability studies were conducted in upland cotton during 2013-14. Five lines (CIM-446, CIM-473, CIM-506, CIM-554 and SLH-284) and three testers (CIM-496, CIM-499 and CIM-707) were crossed through L × T mating system to generate 15 F_1 hybrids. Genotypes revealed significant variations for all the traits. F_1 hybrids showed significant increase over parental means. Mean squares due to lines were significant for earliness, boll number and seed cotton yield per plant. For bolls per sympodia, boll number, yield and lint %, the testers showed significant variations. The L × T interaction mean squares were significant for all traits except lint %. The earliness, bolls per sympodia, boll weight, bolls and seed cotton yield per plant were controlled non-additively, while lint % was managed additively. In total sum of squares, the proportional contribution of L × T interaction was maximum followed by lines and testers. The lines (SLH-284, CIM-473) and pollinators (CIM-707, CIM-496) were leading general combiners. F_1 hybrids (CIM-473 × CIM-496, SLH-284 × CIM-707 and CIM-446 × CIM-496) which involve general combiners showed best performance for yield and lint traits. Heritability was moderate to high with appreciable genetic gain for majority traits. Except lint %, the correlation of yield was positive with other traits. However, bolls per sympodia and bolls per plant were the major contributors in managing the seed cotton yield. F_1 hybrids with high × high, high × low and low × high GCA parents performed better and could be improved through selection in early segregating generations.

Keywords: ***General and specific combining ability, additive and non-additive gene action, line x tester analysis, heritability, upland cotton***

Pedigree Selection for High Yielding Chili (*Capsicum annuum* L.)

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ABSTRACT

In the F_2 generation resulted from crossing between two chili parents (PBC TW2 x 473) high heritability values obtained on several agronomic characters. Pedigree selection in subsequent generations conducted to get high yielding chili. The purpose of this research is to get the families that have high yield as a candidate of new cultivars. On the selection of F_4 generation that was conducted in September 2014 - January 2015, 17 families are selected based on several characters, among others: the amount of good fruit, fruit total number, weight per fruit, good fruit weight, fruit weight in total which have low to moderate heritability. Selection at F_5 generation has been carried out in Pandesari, Pujon district, Malang in February 2015 - July 2015 and obtained eight selected lines. Results showed that the qualitative character has been uniform. Selected strains will be planted for the selection of the next generation.

Keywords: pedigree selection, chili, high yield cultivar, family

Estimation of Combining Ability and Heterosis for Yield Component of Local Tomatoes in Half Diallel

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ABSTRACT

Demand tomatoes in Indonesia continues to increase but can not be fulfilled from national production. Improvement of the quality and quantity of tomatoes should also continue to be made to meet consumer demand. Varieties based on local germplasm is one way to answer these problems. The aim of this research was to study general combining ability (GCA) and specific combining ability (SCA) of five tomato lokal genotype, heterosis and heterobeltiosis of F_1 populations from half dialel local tomatoes crosses. The experiment were conducted from July to December 2014 using a Randomized Complete Block Design with three replications at Leuwikopo University Farm, IPB. Genetic material consisted of 5 local tomato genotypes as parent and 10 F_1 from half dialel local tomatoes crosses. Genetic parameters observed were DGU, DGK, heterosis, and heterobeltiosis. Analysis of GCA and SCA were based on the Griffing's model of diallel design method II. Heterosis values were predicted based on the average values of their parents and heterobeltiosis were predicted based on the average values of the highest parents. Genotype Gondol had the highest GCA for fruit length and fruit width and Kuda 1 for yield and number of fruit for each plant. Crosses having positive SCA for all variable obsered were Aceh 5 x Lombok 4, Aceh 5 x Gondol, dan Lombok 4 x Gondol. Hibryd Lombok 4 x Gondol have positive heterosis for all variables observed. Hybrid Aceh 5 x Lombok 4, Aceh 5 x Gondol, dan Lombok 4 x Gondol have positif heterosis and heterobeltiosis value for yield for each plant.

Keywords: local genotype, heterobeltiosis, hybrid, genetic parameters, GCA, SCA

Genotype x Environment Interaction and Stability for Yield and Its Components in Hybrids Rice Adapted to Different Environment in Indonesia

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ABSTRACT

The phenotype of hybrid rice (Oryza sativa L.) is the observed expression of the genotype in response to the environment. Genotypes of differing genetic composition may respond differently when placed in various growing conditions. Genotype by environment (GE) interaction and stability of some traits in hybrid rice are very important for plant breeders to develop and evaluate the new varieties as well as for farmers to plant suitable varieties for commercial purpose. The aim of the research was to evaluate the effects of genotype, environment, and genotype x environment interaction on grain yield and its components and identify the stability of some promising hybrids rice at 16 locations during 2012. The experimental design used was randomized complete block design (RCBD) with three replications. Plant materials were seven hybrids (HIPA 18, HIPA 19, H 209, H 215, H 229, H 249, and H250) and two check varieties (HIPA 11 and Ciherang). Grain yield and yield components of nine genotypes were evaluated. The data were used to determine GE interaction variance components of the traits and yield stability. There was the significant effect of location on grain yield per plot. The genotypes differed significantly in all yield components and grain yield. Genotype x environment interaction significantly affected several crop performances such as flowering date, all yield components, and grain yield. Among the nine genotypes, HIPA 18 and HIPA 19 are classified as stable genotypes and could be grown in a wide area of Indonesia.

Keywords: hybrid rice, grain yield, GxE interaction, stability

Conventional Rice Breeding for Meeting the Future Demands with Special Reference to Genetic Yield Enhancement and Stability

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ABSTRACT

By the adoption of semi dwarf rice varieties, rice growing nations have made spectacular advance in rice production during last few decades, enabling to a period of self-sufficiency and surplus. National and International rice improvement programs have not made any significant increase in the genetic yield potential of varieties since the release of IR 8 and have only added values to the semi dwarf high yielding varieties by insulating them with resistance / tolerance to biotic and abiotic stresses. For example considerable progress in breeding new submergence tolerant rice varieties has been made during the last decade by the introgression of a major QTL SUB1 into many popular Asian mega-varieties by marker assisted backcrossing. Many of these SUB1 introgressed lines covered a sizeable area in flood prone environments of many Asian countries. Looking towards the future, there is a need to develop improved varieties for flood prone areas by enhancing submergence tolerance, improving tolerances to stagnant flooding and anaerobic germination, disease and insect resistances, agronomic traits, and combining multiple abiotic stresses together. However, none of the pyramided lines are superior to the recurrent mega varieties in respect of yield level under normal conditions. If this trend continues in coming years too then it may not be possible to sustain the self-sufficiency in rice. Therefore, there is a need to raise the genetic ceiling to yield by integrating both conventional and molecular approaches in rice. The following conventional research strategies are suggested to enhance the genetic yield potential of semi dwarf high yielding rice varieties by

- Exploiting the gene pool concept and use of weedy relatives
- Use of disruptive mating and innovative breeding and selection approaches
- Mutation breeding to generate mutations at multiple target loci
- Male sterile facilitated composite, recurrent selection and population improvement
- Scope for the development of heterogeneous population

Stay green trait with yield capacity and research on stay green traits in indica back ground has been proposed.

Keywords: gene pool, recurrent selection, heterogeneous population, stay green trait

Genetic Variability and Selection of Coconut (*cocos nucifera*) Genotypes for High Coconut Milk Yield in Malaysian Agricultural and Research Development Institute (MARDI)

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ABSTRACT

Coconut or scientifically known as Cocos nucifera is also known as tree of life as almost all the tree parts can be used for food and other non-food purposes. In this study, fruits of coconut genotypes were assessed morphologically of fruit characters, coconut milk yield, heritability and genetic advance to determine the desired high coconut milk yielding genotypes and the genetic inheritance of that trait. Twenty-six coconut genotypes fruits consist of tall, dwarf and hybrid types were evaluated for nine different traits of whole fruit weight (g), nut weight (g), husk weight (g), shell weight (g), water weight (g), split nut weight (g) and kernel weight (g). The coconut milk yield data were taken in weight (kg) and litres (l). All the trees were available in MARDI research stations and samplings were done in three intervals for data collections. The experimental design used was completely randomized design or CRD. The analysis of ANOVA showed the genotypes of coconut varieties in MARDI showed highly significant differences among the tested characters at the level of $P< 0.01$. The Bawang variety showed the highest weight of kernel (687.6 g), coconut milk weight per ten nuts (4.9 kg) and coconut milk volume per ten nuts (5.0 L). PCV values ranged from 16.0% to 48.7% and GCV values ranged from 21.5% to 51.4% in the studied characters. All the studied characters had high heritability values of 100% and high genetic advance (GA) values of above 58%. Thus the Bawang variety could be used as high coconut milk yielding inbred variety for farmers and as a pollen source to produce better hybrid nuts when cross pollinated with Malayan Yellow Dwarf in assisted breeding programs.

Keywords:* *coconut milk, coconut, coconut milk properties, Malayan tall, coconut hybrids, bawang variety

The Use of Embryo Culture in Rice Amylose Breeding

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ABSTRACT

Rice is the most important crop in developing world and staple food for over half world's population. Rice mainly consists of starch which comprises of two major chemical constituents i.e. amylose and amylopectin. The ratio of amylose and amylopectin governs the cooking characteristic of rice and because the measurement of amylose is longer established, therefore breeding of cooking quality can be done by managing the amylose content in the rice grain. Unfortunately, the amylose content in rice grain is determined destructively. This experiment tries to introduce embryo culture in combination with simple standard iodine colometric method to accelerate the rice amylose breeding. The experiment consists of two main stages i.e. development embryo rescue from excise grains, and amylose content analysis from the endosperm and its inheritance. To perform the experiment, two rice cultivars with contrasting amylose content i.e. Lusi - a low and IR-36 - high amylose content were exploited. The results showed that the excise embryo could grow well in half MS medium, whereas the endosperm could be used to analyze the amylose content. It was proved that Lusi has really low amylose content cultivar than IR-36. The average amylose content of F1 seed of Lusi x IR-36 tended near to average high amylose content of parent. The pattern of inheritance of amylose content followed Mendelian segregation and the segregation of amylose content of F2 selected seed in F3 progenies was dependent upon the amylose content of F2 selected seed. In general it can be concluded that embryo culture could be used to accelerate rice amylose breeding.

Keywords: embryo culture, amylose content, rice breeding

Genotypes X Environments Interaction of Rice Genotypes at Altitude Difference

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ABSTRACT

Rice variety having high yielding is demand by farmers at this time. Grain yield depends on genotypes, environments, and interaction of genotypes x environments. Varieties can obtain maximum yield if they grow in suitable environment. As well as grain yield, maturing character is also influenced by environment. The existence of G x E is often difficult for breeders to select superior genotypes. Efforts to quantify the interaction between the average results of genotype with environment can be done by AMMI stability analysis. This research aims to determine the adaptability and the yield stability of early maturing rice genotypes grown at different altitude. Sixteen rice genotypes were tested in 15 environment with low and medium altitude of wet and dry season of 2010 to 2012. The experiment was arranged by RCBD with three replications. Genotypes x environments is significant with probability < 0.00001. AMMI analysis showed the largest variation was contributed by environmental variation (55.42 %), followed by variation of genotypes x environments interactions (34.10 %), and genotype (10.48 %). Based on AMMI2 biplot, IR77298-12-7-17 and OM4495 lines are widely adapted genotypes in 15 locations. Otherwise B12515-9-SI-1-3-MR-3, B12344-3D-PN-35-4, Silugonggo, and INPARI 13 are specific adapted genotypes in Malang 2010 (medium altitude), Bali 2010 (low altitude), Bantul 2012, and Bandung 2012 (medium altitude).

Key words: rice genotypes, altitude difference, GEI, AMMI

Transgressive Segregation Selection in Peanut: Detection of F2 Transgressive Segregant Plants of Some Crosses

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ABSTRACT

Transgressive segregation selection supposed to be powerful tool to raise genetic improvement of self pollinated plants in shorter generations. Naturally being homozygous for all loci, the next promising lines had been provided in the individual of F2 generation on which all genotypes existed, and the candidate genotypes are those with more desired genes. It is important to detect transgressive segregation of F2 plants by space planted, followed by plant-to-row for F3 generation to detect transgressive segregants lines. The candidate transgressive segregants F3 lines are those with high mean and low variance. The promising F3 lines then verified in F4 generation. The F4 lines which maintain high mean and low variance performance will be the selected lines. This selection method may do primary yield test in F5 generation for self pollinated plant which produce many grain per plant such as rice or soybean. A series of experiments to detect F2 transgressive segregant plants of some crosses of peanut using IPB-GWS lines and national varieties had done during December 2013 – Februari 2015. The selection criteria was number of filled pod per plant. Besides detection transgressive segregant plants, genetic parameters were estimated, also number and gene action by kurtosis and skewness analyses. The results showed variability of transgressive segregant plant number for each cross. The influence of the gene action on the chance of improved lines which will be obtained was discussed.

Keywords: ***broad sense heritability, filled pod, gene action, gene number, genetic variability coefficient, kurtosis, skewness***

Selection of Wheat Lines (Oasis x HP1744) in Two Tropical Agroecosystems

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ABSTRACT

Wheat consumption in Indonesia is high, but it mainly supports by import. The environmental factor is the main constrain of wheat production in Indonesia. The purpose of this study was to select tolerant and or high yield wheat lines. The materials used were 48 wheat lines and 6 check varieties. The experiment was arranged in augmented design. Selection was conducted in Malino (± 1,600 m asl, 20 °C) and Cisarua (± 600 m asl, 24 °C) from April to September 2014. The results showed that at high altitude, the lines significantly had different to total number of tillers, grain filling rate, grain weight of main spike, and grain weight per plant, while at the medium altitude they significantly had different spike length, spikelet number, empty floret percentage, grain filling rate, grain number of main spike, grain weight of main spike, grain number per plant, and grain weight per plant. The character with highest heritability in both locations was grain weight of main spike (96.75 and 96.56). Line O/HP49-A1-2-9 had the lowest sensitivity index (0.51) and identified as tolerant to medium altitude.

Keywords: heat stress, morphological character, Triticum aestivum

Genetic Control to Soybean Seed Storability under Room Temperature Conditions

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ABSTRACT

The objective of the research was to obtain information on genetic control of seed soybean storability. The research was conducted at seed testing laboratorium of Dept. AGH (Bogor Agricultural University), Bogor, Indonesia. Genetic material used were 3 national varieties and 17 advanced breeding lines. The research was arranged in randomized completely block design with three replications. Black soybean seeds are stored in airtight plastic packaging at a temperature of 27-30 ° C and 57-60 % RH for a 14 weeks. The results showed that all characters observed was significantly affected by genotypes. Traits related to seed storability are affected by genetic factors. All traits observed showed a high heritability. There is possiblity to improve seed soybean storabilty by breeding program. Based on germination rate and vigor index, SSD-10, SSD-17, SSD-18, SSD-39, SSD-82, SSD-91 dan SC-39- are the best seed storaability.

Key words: soybean, seed storability, heritability

Physiochemical Properties of Flours and Starches of Cassava Accessions from Western Ceram, Indonesia

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ABSTRACT

Western Ceram in the Maluku Province, Indonesia, has great diversity of cassava. We have previously collected more than one hundred accessions from the area and identify several of those with promising agronomy characteristics. The research part reported here was aimed at characterizing physiochemical properties of flours and starches from the promising cassava clones. Flours and starches were produced or extracted from clones UP-uj-25, UP-uj-26, UP-uj-56, UP-uj-73, UP-uj 93, as well as var. Malang 6 and C4 as comparison. Physiochemical analyses of the flours and starches were conducted on the contents of carbohydrate, protein, fat, starch, ash, total sugar, HCN, as well as starch resistance, paste clarity, bubbling ability, solubility, viscosity, crystalinity and shape of granules; standard procedures for each analysis were employed. Flours and starches from the promising clones and comparison varieties showed variations in chemical and physical properties; however, in general they showed similarity crystalinity/crystal type (type C). This paper quantitatively presented and discus the results of the analyses.

Keywords: cassava, flour, starch, physiochemical properties

Others (Information Technology, Animal Breeding, Forest and Tree Breeding)

CTAB's Modification: High-Quality Plant DNA Extraction for PCR with Heat Shock Treatment

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ABSTRACT

DNA extraction is a critical base in PCR studies. This research aimed to get a extraction method that can increase the quality of DNA. This research used six local genotypes of tomato (Kudamati 1, STB GL, Lombok 4, Meranti 2, F1 Kudamati 1 x Lombok 4, dan F1 STB GL x Meranti 2). Samples was extracted use CTAB. Every samples was given heat shock treatment and without heat shock treatment. The results showed that heat shock treatment produce a high quality template DNA that can be saved in room temperature. RAPD's result showed that heat shock treatment give a better consistency of PCR compared without heat shock treatment.

Keywords: CTAB, tomato, heat shock, DNA extraction, room temperature, RAPD, consistency

Growth Rate of F-1 and F-2 Anglo Nubian X Etawah Grade Kids

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ABSTRACT

Crossbreeding between local dairy goats with exotic breeds aims to increase milk production. Body weight has positive correlation to milk yield in dairy goats. A study was done to evaluate growth rate of F1 and F2 of Anglo Nubian x Etawah Grade (ANxPE) crossbred kids. The study was conducted in the Experimental Unit of Dairy Goat at Livestock Research Institute using 60 kids. Data of birth weight (BW), weights at one month old (W-1), two months (W-2) and weaning weight (WW) were analyzed using a general linear model of SAS program. The results showed that BW, W-1 of F1 ANxPE kids were not different from F2 ANxPE ($P>0,05$), however W- 2 and WW was different significantly ($P<0,01$). The study concluded that W-2 and WW for F-1 were greater than those of BW and W-1 due to heterosis effects. This study is useful as early information for dairy goat breeding program.

Keywords: growth rate, Anglo Nubian, crossbreds, goats

Characterization of Programmed Cell Death in Hybrid Tobacco Cells Expressing Hybrid Lethality

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ABSTRACT

Hybrid lethality is an important problem for cross-breeding. However, its molecular mechanism is not clear sufficiently. Interspecific hybrids of *Nicotiana suaveolens* Lehm. x *N. tabacum* L. cv. Hicks-2 exhibit temperature-sensitive lethality. This lethality was induced by programmed cell death (PCD) in hybrid seedlings and suspension-cultured cells at 28°C, but not at 36°C. Recently plant PCD has been mainly classified into vacuolar cell death and necrotic cell death. Autophagy activation, vacuolar processingenzyme (VPE) activation, vacuolar membrane collapse, and actin disorganization were known as features of vacuolar cell death. In this study, we detected those features in hybrid tobacco cells (*N. tabacum* x *N. suaveolens*) expressing the lethality. Ion leakage and plasma membrane disruption were promoted inhybrid cells. Autophagic ultrastructures were also observed by transmission electron microscope. To confirm autophagy activation by gene expression, changes in transcript levels of nine*autophagy-related* (*ATG*) genes in hybrid cells was examined by quantitative PCR (qPCR). The levels in hybrid cells were mostly increased just before cell death at 28°C but not at 36°C. From these results, we suggested vacuolar cell death including autophagy conducted the lethality in hybrid tobacco cells.

Keywords: Hybrid lethality, programmed cell death, vacuolar cell death, autophagy

The Response of Three New Varieties of Red Pepper to Biofertilizer Treatments

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ABSTRACT

Red pepper is an important vegetable in Indonesia. UNPAD has two new varieties of red pepper and one potential genotype to be develop as a new variety. UNPAD has developed biofertilizer compound that has been produced by stakeholders. Research on three red pepper varieties needs to be done to obtain the optimum yield for each variety. The experiment was conducted in UNPAD screen house at Jatinangor, West Java from March – July 2015 and arranged in Split Plot Design with three varieties (UNPAD CB 2, UNPAD CK 3 and UNPAD CK 11) as the main plot and three fertilization treatments (20 kg ha^{-1} manure+ NPK 200 kg ha^{-1} without biofertilizer; manure 10 kg ha^{-1}+ NPK 100 kg ha^{-1} + biofertilizer 2 liters ha^{-1}; manure 20 kg ha^{-1} + NPK 200 kg ha^{-1} + biofertilizer 2 liters ha^{-1}) as sub plots, repeated three times. There was interaction between varieties and biofertilizer treatment on the character of fruit number per plant and dried yield percentage of red pepper. UNPAD variety of CK 3 had the best response in the character of fruit number per plant on the treatment of manure 20 kg ha^{-1} + NPK 200 kg ha^{-1} + biofertilizer 2 liters ha^{-1}. UNPAD variety of CK 11 had the best response in the character of dried yield percentage on manure 20 kg ha^{-1} + NPK 200 kg ha^{-1} + biofertilizer 2 liters ha^{-1}

Keywords : biofertilizer, new variety, red pepper

Flowering Biology and Pollination of Dragon Fruits (*Hylocereus spp.* and *Selenicereus megalanthus*)

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ABSTRACT

Dragon fruit has been cultivated and adapted well in various sites in Indonesia. As a result domesticly produced dragon fruit becomes available as oppose to the imported ones. The objectives of this reseach was to observe flowering biology of dragon fruit (*Hylocereus* spp. and *Selenicereus megalanthus*) and to investigate if pollination types affect fruit quality. This research covered observation on flowering biology of H. undatus, H. costaricensis and S. megalanthus. The experiment was arranged in randomized complete block design with type of pollination as the treatment, i.e open pollination of *H. undatus*; controlled self pollination of *H. undatus*; controlled cross pollination of *H. undatus* x *H. costaricensis*; open pollination of *H. costaricensis*, controlled self pollination of *H. costaricensis*; and controlled cross pollination of *H. costaricensis* x *H. undatus*. The treatments were repeated 4 times. The flower and fruit development was divided into three stages, i.e. from flower bud to blooming; from blooming to wilting and thereafter until fruit ripening. The first stage in *Hylocereus* spp. was about 19-21 days, while in *S. megalanthus* took 29-31 days. Based on pollen viability and stigma receptive period, the optimal pollination time was between 11.00 pm to 2.00 am for the three species. All type of pollination resulted in 100 % fruit set. However, fruit quality varies among type of pollination. Fruit weight and total soluble solid from cross pollination of *H. undatus* x *H. costaricensis* was the highest among types of pollination. Controlled pollination either self or cross of *H. costaricensis* produced bigger fruit than open pollination.

***Keywords:* cross pollination, flower bud, fruit quality, fruit ripening, fruit set, pollen viability, self pollination, stigma receptive period**

Abstracts of Poster Presentation

SABRAO 13th Congress and International Conference
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Genetic Analysis and Fine Mapping of Panicle Tip Mutant *pnt* in rice (*Oryza sativa* L.)

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ABSTRACT

In the rice inflorescence development, timing of inflorescent meristem abortion, conversion of the rachis branch meristem to the terminal spikelet meristem and shift to lateral meristem identity determine the overall architecture of the rice panicle (keda-Kawakatsu et al. 2009). Cheng et al. (2011) reported that quantitative trait loci (QTLs) have major effects on panicle apical abortion in rice. However, there have been very few reports about panicle tip mutants. Therefore, this research is conducted to fine map mutant gene and perform functional analysis of mutant gen. Hwacheongbyeo (japonica rice) seed was treated with ethyl methane sulfonate (EMS) for inducing mutation. Two F2 population (Japanica mutant crossed with wild type and Japanica mutant crossed with Milyang 23, Indica type) were established for Phenotyping and genomic analysis. STS markers in crop molecular Breeding laboratory. Additional STS markers for fine mapping were developed based on the Nipponbare genome sequence (http://rgp.dna.affrc.go.jp/blast/runblast.html). All F2 generations showed the segregation of normal plants and mutant following a ratio of 3:1 suggesting the mutant phenotype is caused by a single recessive gene. Initial BSA test made using STS markers confirmed the mutant gene is found in the long arm of chromosome 8. Panicle tip mutant gene, *pnt* has pleotropic effect which has been manifested in significant reduction of tiller development starting from late stage of vegetative growth and pronounced effect on possession of stay green nature of the rice during the vegetative stage of development. The only significant difference observed within panicle traits is the number of spikelet on primary branch and spikelet fertility. The first primary branch which contain aborted spikelet and elongated distance between spikelet is the most affected structure in the panicle.

Key Words: Rice, Spikelet, Rachis, STS markers, Panicle tip mutant, pleotropic

Heritability of Rust Disease Resistance in F_3-F_4 Soybean Populations Using Variance Component Analysis and Parent-Offspring Regression Method

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ABSTRACT

Rust disease is one of an important disease on soybean cultivation in Indonesia. Inheritance of resistance to rust disease can be known through the value of heritability. The aim of this study was to determine the heritability of resistance to leaf rust disease of soybean. This study was conducted at screen house of Indonesian Legumes and Tuber Crops Research Institute (ILETRI) in Malang, Indonesia from April to July 2015. Genetic material used is F_3 and F_4 soybean population from four crosses. The experimental design was randomized complete block design with four replications. The entire genetics material planted in polybag, five polybags for each crossing from the same populations, two plants each polybag. Three weeks after planting, all plants were inoculated with rust disease. Inoculation was done by spraying a suspension of spores (spore density of 10^4 spore ml^{-1}) to the leaves in the afternoon. Observations were carried out on the severity of the disease of each individual plant. Data were collected at one, two and three weeks after inoculation. The results showed that the heritability of disease severity using analysis of variance components on one, two and three weeks after inoculation was 22.28%, 17.99% and 13.56%, respectively. Meanwhile, the heritability of these characters using parent-offspring regression method was 36.2%, 27.2% and 29.5%, respectively. This result means that the heritability (narrow sense) of disease severity is narrow to moderate. In addition, the phenotype variability and genotype variability of this character was broad. This means that the selection using disease severity provide a chances of success.

Keywords: ***disease severity, Glycine max, heritability narrow sense, Phakopsora pachyrhizi, rust disease, selection, soybean population***

P-03

Analysis of Partial DNA Sequences of *Linamarase* Gene on Roti and Menggalo Cassavas (*Manihot esculenta* Crantz.)

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ABSTRACT

Linamarase gene involves in biosynthesis of the cyanide compound and suggested that the difference between bitter and sweet cassavas lies in DNA sequences of promoter and peptide signal of *linamarase* gene. The objective of this study was to analyze partial DNA sequences of *linamarase* gene which covered promoter and peptide signal regions on Roti as sweet cassava and Menggalo as bitter cassava. This research was conducted in March 2014 till January 2015 at Genetic Laboratory of Biologi Department, Faculty Mathematics and Natural Sciences, Riau University, Indonesia. Procedures included DNA extraction from fresh leaves of cassava plants (three plants for each cassava) using CTAB method, PCR (polymerase chain reaction), electrophoreses, sequencing, and data analysis using BLAST and MEGA version 6.0. This study obtained 527 bp DNA fragment of *linamarase* gene on both cassavas tested. The results showed that the amount of base A (31.16%) and T / U (29.72%) more than in C (18.29%) and G (20.83%). Highest number of transition substitution mutations was C to T / U (16.64%), and the highest transversion substitution mutations were C and T / U to A (11.39%). Promoter DNA sequences on Roti and Menggalo were the same, but petide signal DNA sequences between both cassava were different. Suggested that the differences of peptide signal DNA sequences may distinguish between bitter and sweet cassavas. This information is useful for cassava breeding thorugh genetic engineering technique.

Keywords: cassava, cyanide, linamarase gene, menggalo, PCR, peptide signal, promoter, roti

CESIM to fixed transgressive segregants of multiple traits in early generation of Mungbean (*Vigna radiata* L. Wilczek)

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ABSTRACT

Selection in early generation is one option for generating new varieties in conditions of rapid climate change. Fixation of transgressive segregation in the early generations is one solution. The use of selection index based on information from relatives with eigenanalysis and transgressive segregation analysis can fix the transgressive segregant families in early generations. Selection index can be used in multiple traits selection of BLUP breeding value under the assumption that this value is an empirical breeding value (EBV). Selection for EBV can maximize true breeding value (TBV). The objectives of this research were to generate a selection index of the EBV that can fix multiple traits of transgressive segregants, to estimate the selection response of multiple traits in early generation, and to verify the existence of multiple traits transgressive segregants of early generations in the next generation of mungbeans. The experiment design used a nested-augmented incomplete block design. There were 217 families of Generation F3 or about 4300 individual in base population. BLUP of quantitative traits were the phenotypic value recovery according transformed-generalized-linear mixed models. Analysis of covariance of the BLUP's produced EBV matrices. Selection index used EBV matrices (including dummy variables of transgressive segregant families) and economic vector in the combined-eigenvalue selection index method (CESIM). Simulation base of the economic value in CESIM equation is used to choice of best indeces (i.e. best R^2). Verification of transgressive segregant families used information of between- and within-family of mixed linear models and standard error of each family. The results showed that the best selection index equation is the index with $R^2 = 96.74\%$. This index produce selection response was 141.22, and component response of seed weight and simultaneous harvest index were 13-30 g and 0.35-0.80, respectively. Nine families were verified as the transgressive segregants family in early generation.

Keywords: selection, selection index, mixed linear models, BLUP, mungbean

Yield of Gamma Irradiation Generated Cassava (*Manihot esculenta* Crant) Mutants at the M_1V_3 Generation

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ABSTRACT

Cassava (*Manihot esculenta* Crantz) is an important carbohydrate source for food, feed and industries. Cassava breeding program is mainly targeted to improve the tuber yield. Induced mutation using Gamma irradiation is one of strategies to produce high yielding cassava varieties. The objective of this research was to analyze the yield and yield component of gamma irradiated cassava mutants at the M_1V_3 generation. There were 121 cassava mutant lines and five cassava background genotypes (Jame jame, Ratim, UJ-5, Malang 4, and Adira 4) used in this study. The results showed that the genotypes were highly varied in the tubers weight, number of tubers and number of economic tubers. Number of tuber and number of economic tuber were the yield components which showed high correlation with the tubers weight. This study identified 25 high yielding cassava mutant lines (i.e. tuber weight > 10 kg).

Keywords: characterization, cassava mutant, economic tuber, induced mutation, local genotype, yield

Genetic Diversity Analysis of Mungbean (*Vigna radiata* L.) from Riau Province based on Morphology and Agronomy Characters

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ABSTRACT

Mungbean (*Vigna radiata* L.) were an important crop because it has economic value, agronomy and nutrition. The genetic diversity information is needed to create new varieties as expected. The aim of this research was to collect and analyze genetic diversity of mungbean from Riau Province based on morphology and agronomy characters. The mungbean seeds collected from Riau were then grown at the Biology experimental farm, Riau University. The morphological characters observed were seed germination, plant habits, twining plant habit, colour tip of the stem, leaf characters, flower characters, plant height, number of productive branches, stem diameter, pod characters seed characters. Data were analyzed using SPSS, NTSYS and Heritability. The results showed that the genetic diversity of mungbeans from Riau Province was quite high (53%). The farthest distance was the Inhil genotypes with 11 other genotypes (Bengkalis I, Rohul II, Bengkalis II, Rohil, Kampar, Merpati, Vima, Rohul I, Pelalawan, Inhu and Siak), and the nearest distance was the Rohil and Kampar genotypes with genetic diversity level approximately 5%. Bengkalis I with Rohul and Inhil with Pelalawan can be parental in mungbean breeding program.

Keywords: Agronomi, morphology, mungbean, genetic diversity, Riau, Vigna radiata

P-07

Pyramiding of Four Bacterial Blight Resistance Genes into *japonica* Rice using Phenotypic and Marker-assisted Selection

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ABSTRACT

This study was conducted to develop four bacterial blight resistance genes, *Xa1*, *Xa3*, *xa5*, and *Xa21*, pyramided *japonica* rice for enhancing the resistance against *Xanthomonas oryzae* pv. *oryzae*. Ilmibyeo *japonica* high grain quality cultivar carrying *Xa1*(Chr.4) and HR27814-B-47-1 three genes, *Xa3*, *Xa21* (Chr.11), and *xa5* (Chr.5), pyramided elite *japonica* line were used to develop the segregation population. In an F_2 population consists of 199 plants, four plants having homozygous alleles for *Xa1*, *Xa3*, and *xa5* and homo- or heterozygous for *Xa21* were selected by gene specific DNA markers and double checked by bio-assay against K1 and K3a races. Using 47 panicles from the selected plants, anther culture was conducted and eight doubled haploid (DH) plants were developed. Among eight DH plants, seven were confirmed to have four resistance genes, *Xa1*+*Xa3*+*xa5*+*Xa21*. DH lines carrying four genes showed highly resistance reaction and broad-spectrum resistance against 16 Korean bacterial blight isolates. Along with anther culture, the pedigree method was conducted to develop the fixed lines carrying four genes through phenotypic and maker-assisted selection. Consequently, we developed seven DH lines and ten F_6 generation lines carrying four resistance genes and are conducting the evaluation for resistance against bacterial blight and yield trial to register as variety.

Keywords:* *Rice, Bacterial blight, Resistance gene, Pyramiding, Phenotypic selection, Marker-asissisted selection

Analysis of Regulatory Genes for Anthocyanin Biosynthesis Pathway and Cold/Freezing Tolerance in *Brassica rapa*

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ABSTRACT

Anthocyanins are responsible for vivid colors of flowers, fruits and vegetative tissues of Chinese cabbage and biosynthesis of it is primarily controlled by several structural and regulatory genes. This study identified 19 transcription factors of *Brassica rapa* and investigated their regulatory function in anthocyanin biosynthesis pathway genes and cold and/or freezing tolerance in *B. rapa*. Expression analysis these genes in the pigmented and non-pigmented portion of leaves of different lines of *B. rapa* revealed that BrMYB2-2 and BrTT8 showed responses contrasting with anthocyanin accumulation and cold stress. Sequences of these genes were analyzed and compared with similar gene sequences from other species and a high degree of homology with their respective functions was found. Co-regulated *cis* -elements were found in promoters of *BrPAL1*, *BrCHS*, *BrF3H1*, *BrF3'H1*, *BrFLS*, *BrBAN*, *BrDFR8*, *BrANS1*, and BrMYB2-2 and BrTT8 had binding sites of the promoters of those structural genes. Thus, the above results suggest the association of BrMYB2-2 and BrTT8 with regulation of anthocyanin biosynthesis pathway genes and cold and freezing stress tolerance and might be useful resources for development cold resistant *Brassica* crops with desirable colors as well.

Keywords: regulatory genes, anthocyanin, cold and freezing stress, Brassica rapa

P-09

Agronomic and Genetic Analysis on A Rice Mutant Line Exhibitng Reduced Amylose Content

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ABSTRACT

Changes in food preferences and dietary habits of Korean prone to decrease consumption of the traditional energy source, rice. There have been several efforts to facilitate rice consumption in Korea through various processed foods, and rice cultivars with various amylose contents would be demanded. Through previous studies, we found a dull mutant (amylose = 9.5 %) derived from chemical treatment (Sodium azide) on the 'Namil', a Korean japonica cultivar (amylose = 20 %). To address the genetic factor underlying the dull mutant, a total of 94 F_2 mapping population was constructed from a cross between the dull mutant and Milyang23 (Tong-il type). Association analysis between the genotypes of 57 SSR markers and amylose content of each F_2 individual suggested that the dull phenotype was contributed by a major recessive locus on sub-terminal region of the rice chromosome 6. Increasing marker density on the chromosomal region narrowed the putative locus down between 110.6 – 119.5 Mbp tagged by RM7555, by which 80.9 % of total variation of amylose content within 94 F_2 individuals. The dull mutant, therefore, would be useful genetic donor for developing promising breeding lines.

Keywords: Rice; Mutation; Sodium azide; Starch; Amylose content; SSR

P-10

QTL Detection Related to Cold Tolerance at the Flowering Stage in Rice

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ABSTRACT

The cold injury is the critical stress to limit rice growth and yield in rice cultivation area in temperate region. Low temperature can inhibit normal rice growth from seed germination to seed maturity. In particular, flowering stage which occurs fertilization between egg cell and pollen is very sensitive to cold stress, therefore the cold stress at the flowering stage decreases the seed fertility and lead final yield loss. This study identified two QTLs associated with cold tolerance during flowering stage. A 139 recombinant inbred lines derived from a cross between ‘Milyang23’ (Tong-il, cold susceptible) and ‘Gihobyeo’(Japonica, cold tolerance) were exposed to air and water of 17℃ at the same time for 14 days at flowering stage. The spikelet fertility was used as evaluation criteria of the cold tolerance. Illumina Bead Xpress 384-plex SNP and 671 SSR markers were used for genotyping and composite interval mapping (CIM) was employed for QTL analysis. Two QTLs for cold tolerance at flowering stage were detected *qFG3* on chromosome 3 and *qFG7* on chromosome 7, respectively. These two QTLs could explain 10.5% in *qFG3* and 11.8% in *qFG7* of the phenotypic variance for spikelet fertility. These QTL alleles, *qFG3* and *qFG7* were derived from cold susceptible parent ‘Milyang23’, and are different to QTL alleles from cold tolerant parent ‘Gihobyeo’ at booting stage. The QTLs detected in this study would be used to further improvement of cold tolerance in rice, and can also be used in marker-assisted selection.

Keywords: cold tolerance, QTL, rice, flowering stage

P-11

Enhancement of Seed Longevity in *Japonica* Rice Cultivars Using Weed Rice

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ABSTRACT

Seed germination is a main factor in rice cultivation. For *japonica* strains unlike *indica* lines, fast loss of germination ability during storage leads to risk of seeding and deterioration in the quality. To resolve these problems, germplasms screening for longevity was conducted using six days of compulsory aging stress of high temperature (50℃) and humidity (~95% RH). ‘Dharial’, a weedy rice collected in Bangladesh, was chosen as a source of seed longevity for long term storage. The strong germination trait originated from ‘Dharial’ was incorporated into Korean elite *japonica* cultivars, ‘Ilmi’ and ‘Gopum’, through backcross method. The germination ratio was evaluated after two years of room temperature storage conditions. A high germination ratio of 80.5% in donor plant of ‘Dharial’ and 77.3% in an introgression line were observed based on the two years of storage while the recurrent *japonica* cultivars, ‘Ilmi’ and ‘Gopum’, were failed in germination. As a result, we investigated the changes of quality affected by germination ability during storage. A gentle slope of palatability which is one of the measurement items for indirect selection indicator of high eating quality in *japonica* varieties was studied in a high germination ratio introgression line during storage. The introgression line could be useful to increase longevity and quality of *japonica* rice seed if molecular breeding strategy such as QTLs analysis is combined.

Keywords : rice, longevity, germination, storage

QTL Analysis for Drought Tolerance using Introgression Lines Carrying *O. glaberrima* Chromosome Segments in Milyang 23

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ABSTRACT

Drought stress is one of the major stress affecting growth and productivity in rice. Drought tolerance is a complex trait governed by quantitative trait loci (QTLs) making it difficult to understand mechanisms underlying in it. We generated a set of 55 introgression lines via backcross using Milyang23, the Korean Tongil-type rice variety as the recurrent parent and *O. glaberrima* (IRGC Acc. No. 103544) as a donor parent. 141 SSR markers were used to genotype 55 introgression lines. The 55 introgression lines with Milyang23 were evaluated for physiological traits such as fresh shoot weight (FSW), fresh root weight (FRW) and dry shoot weight (DSW) under the control and 20% PEG-treated condition. Three lines (IL9, IL12, and IL55) showing significant difference with Milyang23 were selected for further analysis. Genotyping of three lines (IL9, IL12, and IL55) revealed that three lines had four, four and two *O. glaberrima* homozygous segments, respectively. Among identified three lines (IL9, IL12 and IL55) showing significant difference with Milyang 23, IL9 performed better than Milyang 23 for all the traits measured in 20% PEG treated conditions. Although, IL9 and IL12 showed improved drought tolerance at seedling and vegetative stages, they performed poor under drought stress at reproductive stage. Whereas, IL55 was found no significant difference for control and treatment in SPP and FER. This result indicates that IL55 will be a good resource for drought tolerance breeding in rice. These materials would be useful not only in developing drought tolerant lines in the breeding program but also for fine-mapping the genes/QTLs for drought tolerance. This work was carried out with the support of ″Golden Seed Project″ (Project No. PJ00993301), Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), Rural Development Administration (RDA) and Korea Forest Service (KFS), Republic of Korea.

Keywords: drought tolerance, QTL, polyethylene glycol, rice, O.glaberrima, introgression lines

SP-LL37, Human Antimicrobial Peptide, Imparts Improved Disease Resistance in Transgenic Rice

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ABSTRACT

Rice is a staple food to more than half of the world's population, andreceivesheavy production lossesdue to variouspathogens.Breeding using biotechnology can easily obtain the desired properties as well as reduce the time and expense required. Promotion of antimicrobial methods using AMPs is controlled by a single gene which confers resistance to various microorganisms. hCAP18 / LL37 isolated from humans is a multifunctional antimicrobial peptide in the cathelicid in family. To prevent degradation by the protease in the plant, the vicil in gene was fused to the N-terminal adjusted to the pGD1 promoter to allow intercellular secretion.Through the tobacco transient assay, the cellular localization of the SP-LL37-GFP fusion protein was determined to be mainly the intercellular space. A total of 472 transgenic lines with introduction of SP-LL37 were created by agrobacterium-mediated transformation. Of these, 181 lines were selected as having a single copy via Taqman PCR utilizing thenos gene probe. For the selection of intergenic lines, the genome adjacent side of the RB or LB was digested with BfaI enzyme. FSTs analysis through IPCR identified 16 integeniclines (13%). The results of the ELISA assay and RT-PCR analysis for the level of LL37 expression indicated formation ofa band for LL37 RNA at 10 times higher level compared to the non-transformant proteins, confirming stable expression. The *in vivo* test for resistance to bacterial leaf blight revealedthe WT plants to suffer from lesions 4.5 to 5 times larger than those found on the transformants,with lesions of about 10.8cm in WT two weeks after inoculation.Inoculation experiment was performed to investigate the effects of over-expression of transgenic SP-LL37 on pathogenic fungi.The four transgeniclines tested showed remarkably little disease lesions up on infection,covering only3.1 to 9.0%.Breeding combining biotechnology with multi-function genes has been continuing for over 30 years,while it is still subject to doubt regarding reliability problems. This is because of lack of understanding of the people, and high mistrust. To ensure the relative homogeneity of the transgenic and WT as a first step, the SP-LL37 introduced as intergenic objects were selected. In addition, the introduction of transgenic SP-LL37 was carried out to obtain resistance to bacterial leaf blight and blast fungus. Transgenic LL37,which confers resistance against a broad-spectrum of phytopathogens for crop development, is a suitable candidate. Stable expression using a signal peptide is the best strategy for intercellular secretion of AMPs in plants. ***Keywords: GM plants, antimicrobial peptide, Signal peptide, intergenic, bacterial leaf blight, rice blast fungus***

Improvement of Tolerance to Heat Stress in Rice Seeds Under Hot Water Disinfection by Reducing their Water Contents

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ABSTRACT

Hot water disinfection of rice seeds has recently received increased attention as a clean and useful farming technique, because it uses no expensive agricultural chemicals and does not produce harmful waste fluid. The general method of this technique is to disinfect the rice seeds in hot water at 60°C for 10 minutes. In Japan, the automatic system (SATAKE) for hot water disinfection was established and 2,000 kg of rice seeds could be treated by using this system within one-hour. However, some diseases cannot be controlled efficiently by the disinfection at 60°C for 10 minutes. In addition, the seeds of several rice cultivars are sensitive to heat-shock and could not germinate after disinfection by the method. Therefore, it is required to increase the heat tolerance in seeds of these cultivars and to treat with higher tempreture for disinfection with high efficiency. In the present report, we examined the effects of reducing the water content in seeds on their heat tolerances. The water content in seeds of a *Japonica* rice cultivar "Hitomebore" was 12.5%, and the germination rate of these seeds after immersion in hot water at 70°C for 10 minutes was 76.7%. When the water content in the seeds was reduced to less than 8% by drying before the hot water treatment, more than 90% of the seeds germinated. Such an effect of seed pre-drying was confirmed in *Indica* cultivar "Kasalath" and "IR 58". These results indicate that reducing water contents in rice seeds including *Japonica* and *Indica* is effective for strengthening their tolerance to a high temperature.

Keywords:* *rice, seeds, hot-water disinfection, heat-tolerance, seed water-contents, clean farming technique

Circadian Clock and Photoperiodic Flowering Genes in Adzuki Bean [*Vignaangularis* (Willd.) Ohwi&H.Ohashi]

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ABSTRACT

Adzuki bean [*Vignaangularis* (Willd.) Ohwi&H.Ohashi] is one of important legume crops cultivated in East Asia and northern South Asia. Despite its agronomic importance, a lack of available sequence information has led to difficulty in improvement of important agronomic traits in Adzuki bean. In the present study, de novo assemblyof transcript sequences produced by short read sequencing constructed 59,860 full-length protein coding sequences in Adzuki bean. These sequences were subjected to a BLASTP search for identification of putative homologues of the 85 Arabidopsis genes involved in the circadian clock and photoperiodic flowering pathway. A large portion of these Arabidopsis genes were represented in adzuki bean. However, there were no cDNA homologues of six genes including *FLOWER LOCUSD* (*FD*) and *LFY* (*LEAFY)*. Furthermore, phylogenic relationship of 25high homologous matches to *CONSTANS* (*CO*) or *CONSTANS-LIKE* (*COL*) of Arabidopsis indicated the lack of *CO*orthologues in Adzuki bean. *FLOWER LOCUS T* (*FT*) and its homologs were identified to have two homologous counterparts in Adzuki bean and these Adzuki bean homologues showed the leaf-specific transcript abundance. This study may provide primary genetic resources for improvement of Adzuki bean with better flowering and fruiting performance in response to environmental changes.

Keywords:Adzuki bean,de novo assembly, transcript, circadian clock, photoperiod, flowering gene

The Diversity of Physical Quality, Lipid Content and Flavor in Cacao Derived from Kolaka, Southeast Sulawesi

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ABSTRACT

Cacao (*Theobroma cacao* L.) is considered as one of important export commodity in Indonesia, which make Indonesia as the third largest cacao producers worldwide after Cote d'Ivoire and Ghana. In order to increase the exports value, the quality of cocoa beans should be a major concern. In present study, we examined the physical quality, lipid content and flavor of 11 cacao genotypes which obtained from Kolaka, Southeast Sulawesi. A total of 100 cacao beans were randomly selected to measure the length, width, thickness, weight of 100 cacao beans, weight of one cacao bean and number of beans per 100 g. Moreover, ± 500 g of cacao beans from each genotype were also used for testing the lipid content and flavor. All of the data were then analyzed using analysis of variance and NTSYS program. The result showed that two genotypes, IAARD 7 and IAARD 9, have higher value of all physical quality characters tested. According to the size of the seed weight, which is expressed by the number of seeds per 100 g sample, both of genotypes are included in AA criteria. In addition, IAARD 1 and IAARD 9, which have total lipid content 57.95% and 57.87%, respectively, were higher than the other genotypes. Besides, IAARD 9 also showed the highest preference value (6.83), which is similar to released varieties (Sulawesi 2). An UPGMA clustering dendrogram, which analyzed based on physical quality, classified all the genotypes into three groups. In which, IAARD 7 and IAARD 9 were clustered together in group three. This result indicates that these two genotypes are considered as the promising genotypes that shown by good physical quality, high lipid content as well as high preference value.

Key words: cacao, diversity, physical quality, lipid content, flavor, promising genotypes

Combining Ability of some Commercial Dura and Pisifera Oil Palm Parents in Thailand

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ABSTRACT

An experiment was conducted to study the variability in 20 oil palm hybrids obtained from crosses between seven Dura and eight Pisifera parents from Golden Tenera Limited Partnership. Two commercial cultivars, viz. 'Surat 2' and 'Univanich' were grown as checks. All 22 entries were evaluated in the field of Hong Sila Agriculture and Industry Company Limited, Khao Phanom District, Krabi Province. The experiment was laid out in a randomized complete block design with four replications to collect data on bunch and yield components for a total of three years during January 2011 to January 2013. An analysis of variance showed significant differences between hybrid progenies and check cultivars, among check cultivars, and among hybrid progenies. The Dura parents that showed the highest general combining ability were D43/9 and D8/9, while the Pisifera male parent was P5/21. The cross D15/14 × P5/21 was the best combination giving high specific combining ability for yield with 31.18 percent of oil to bunch ratio (O/B).

Keywords:* *oil palm, general combining ability, specific combining ability, Tenera hybrids, yield components, bunch analysis

Genetic Variability and Heritability Analysis of Cassava (*Manihot esculenta* Crantz) Mutants at the M_1V_3 Generation

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ABSTRACT

Cassava (*Manihot esculenta* Crantz) is a potential crop for food, feed, and industry. Cassava breeding though conventional approaches are hampered with some limitations which resulted in a low number of superior cassava varieties. Recently, some cassava mutant lines with higher yield and starch content were already developed and several mutant lines serve as important genetic materials for cassava breeding program. The objective of this research was to identify cassava mutants from gamma ray irradiation and to estimate the heritability at the M_1V_3 generation. The irradiated cassava varieties were Jame-jame and Ratim (local genotypes from Halmahera), UJ-5, Malang-4 and Adira-4 (national varieties). The results showed that the Gamma irradiation increased the variability of the five genotypes of cassava. Heritability estimation used for the next generation cassava mutant. The characters with high heritability estimation score from all genotypes were number of long leaf, long petiole, diameter rod, plant branching, number of roots, number of economic roots and tuber weigh. Based on the stability test, characters plant height and plant branching were characters with high heritability.

Keywords: characterization, cassava mutant, heritability, local genotype, M1V3 generasion, stability

Establishment Numbers of SalinityTolerant Rice Varieties Ciherang, Inpari 13 and Inpara 3 by Induced mutation and *in vitro* Selection

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ABSTRACT

Induced mutation combined with *in vitro* selection can be used to assemble the salinity tolerant rice varieties. The purpose of this study is to get the numbers putative mutant somaclone salinity tolerant rice mutation induction and in vitro selection. The varieties used are Ciherang, Inpari 13, Inpara 3. This study comprises four main activities embryogenic callus induction, induction of mutation and selection in vitro, regeneration buds, acclimatization. Results of the study were 29 putative mutants somaclone numbers derived from rice varieties Ciherang. 39 numbers somaclone putative mutant derived from rice Inpari 13 and 42 number somaclone putative mutant derived from rice varieties Inpari 13.

Key word: In vitro selection, mutation, mutan, Oryza sativa L

Sequential Morphological Characters of Triploids and Tetraploids Produced by Colchicines on Bud and Flower of *Phalaenopsis amabilis* Using Principle Component Analysis

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ABSTRACT

Sequential Principle Component Analysis executed on study of morphological characters using plant diameter, leaf number, length and width of diploids, triploids and tetraploids produced by applying colchicines on bud and flower of *Phalaenopsis amabilis* from 4, 5, 6, 7, 8, and 9 month after acclimatization (MAA). The treatment were 50 ppm colchicines on bud and then selfed pollinated, 500, and 1000 ppm colchicines applied on the bud then the flower was selfed pollinated or crossed with normal flower, and 50 and 500 ppm colchicines applied on selfed pollinated and castrated flower for 3 and 5 days. Cluster analysis using R program resulted in three clusters with 45, 50, and 55% of Gower's dissimilarity on 9 MAA. Combination of morphological characters showed that the diploids distributed more evenly, but the triploids and tetraploids clumped together despite its treatments. Principal Component Analysis (PCA) and dendrograms were more synchronized on 8 and 9 MAA. The differences occurred caused by individual plant was genetically different. This outcome showed that triploids and tetraploids of *Phalaenopsis amabilis* were more uniformed than the diploids.

Keywords: diploid, moth orchid, PCA, polyploid, uniform

Detection of Traits and Genes Related to the Promotion of Root System Development in the Rice by Inoculation of Biofertilizer

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ABSTRACT

Bacillus pumilus strain TUAT1 is known as a plant growth promoting rhizobacteria. It is reported that the inoculation of TUAT1 to rice seedling brings increase of 10~20% in the yield. It is also known that TUAT1 promotes the root system development through the increase in number of the crown root in rice. However, the mechanisms of promotion of rice root system development by TUAT1 are poorly understood. In this study, in order to obtain clues to elucidate such promotion mechanisms, we tried to detect changes in trait and gene expression in rice seedlings inoculated with TUAT1. The seedlings of *Oryza sativa* cv. Hitomebore were cultivated in a cell tray in the constant temperature room and inoculated with TUAT1 from germination stage. The shoot fresh weight, lateral root fresh weight, and elongation rate of seminal root were increased in the seedlings inoculated with TUAT1 as compared to control. Root hydraulic conductivity and concentrations of NO^{3-} and PO_4^{3-} in bleeding sap from cut stem were also increased. These results suggest that inoculation of TUAT1 to the rice seedlings activates root elongation and lateral root development and improves absorption of nourishment and water by root system. RT-qPCR analysis of several genes involved in root growth and development revealed that TUAT1 inoculation induced both *CRL5* activation and *WOX11* suppression in the basal portion of shoot where crown root initiation occurs. *CRL5* and *WOX11* are known as genes involved in the formation of rice crown root through control of the cytokinin signal. Thus, our results suggest that TUAT1 inoculation promotes rice crown root formation through suppression of cytokinin signal transduction by transcriptional control of *CRL5* and *WOX11*.

Keywords: biofertilizer, Bacillus. pumilus, Olyza sativa, root system development, CRL5, WOX11, cytokinin

High Temperature Tolerance Evaluation and Grouping Germplasm of Rice

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ABSTRACT

Global warming is one of the limiting production of crops, including rice as a main food crop in Indonesia. The objective of this research were to study the level of tolerance of rice germplasm against high temperature stress and classifying rice germplasm based on quantitative characters. Research was conducted in February-August 2013 at Greenhouse University Farm, Cikabayan (high temperature stress condition), and the drying floor University Farm (no high temperature stress condition), Cikabayan. Rice germplasm are 40 genotypes. The experiment used Augmented design in a randomized block design (three replications). Rice plants put into a greenhouse (average daily temperature of 41 ^{0}C / 22 ^{0}C), when it has entered a phase of early generative. High temperature tolerance parameters based on the value of the Mean productivity/MP, Geometric mean productivity/GMP, Tolerance to stress conditivity/TOL, and Stress tolerance index/STI. Grouping by Principal Component Analysis (PCA) and Cluster Analysis using software Star based on 12 quantitative characters. Germplasm rice has a different tolerance to high temperatures are tolerant (4 genotype), intermediate (19 genotypes) and sensitive (17 genotypes). Grouping is based on three main components (KUI, KUII, and KUIII) has highlighted the diversity of 83%. Grouping based KU1 and KU2 accordance with the results Cluster Analysis. Both the results of the analysis are group I (15 genotypes: tolerant, intermediate, sensitive), II (4 genotype: intermediate and sensitive) and III (1 genotype: sensitive). Crossbreeding to study inheritance to high temperatures and produce high diversity of rice in this population can be done between different groups.

Keywords: cluster analysis, genotype, intermediate, PCA, sensitive

Dianthus chinensis Haploid Plants Induced from Pseudofertilization Using Gamma Ray Irradiated Pollen

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ABSTRACT

The aim of the research was to obtain haploid plants by inducing gynogenesis with gamma-ray irradiated pollen for pollination. By using a model plant *Dianthus chinensis* L., haploid plants were successfully induced. The optimal pollen of *D. chinensis* 'D-chi14' for pseudofertilization was exposed to 200 Gray gamma rays using Co^{60} at a dose rate of 1 kRad/48 s and then used to fertilize 98 donor female flowers of *D. chinensis* 'D-chi11'. Ovules harvested from two weeks after fertilization were cultured *in vitro* on Murashige and Skoog (MS) medium supplemented with 0.5 mg L^{-1} 6-benzyladenine (BA), 0.01 mg L^{-1} α-naphthaleneacetic acid (NAA), 400 mg L^{-1} L-glutamine, 104 mg L^{-1} proline and 30% sucrose for shoot initiation. The shoots derived from the initiation stage were transferred into hormone free MS medium for further growth both proliferation and root formation. The rooted plants (34 plants) were successfully transferred into *ex vitro* condition using sterile coco peat and 16 of them grew well in plastic house. Plants were successfully analyzed for their ploidy level, 11 diploid and 5 haploid per 98 flowers pollinated with inactivated pollen and 2 of them overcoming chromosome doubling spontaneously. The double haploid plants are useful in production of F_1 *D. chinensis* hybrids.

Keywords: Dianthus chinensis L., gamma ray, pseudofertilization, haploid

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Fine Mapping of QTL Conferring Resistance to Bacterial Wilt in Pepper (*Capsicum annuum* L.) Using Genotyping by Sequencing

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ABSTRACT

Bacterial wilt (BW) caused by *Ralstonia solanacearum* is one of the most common soil-borne vascular diseases of many solanaceous crops such as pepper and tomato. This study aimed to identify QTL for bacterial wilt trait in a 188 F_8 recombinant inbred line (RIL) population obtained from a cross of ‘YCM334’ x ‘Taean’ using genotyping by sequencing (GBS) approach. For pathogen inoculations, *R. solanacearum* isolate WR-1 was cultured on NB medium at 28℃ for 48 h and a bacterial suspension was adjusted to 1×10^7 to 1×10^8 CFU/mL (A 600 = 0.3 to 0.4). Each RIL and the parents were sown in a 72-cell plastic tray filled with sterilized soil, and the seedlings were inoculated at the 6 to 8 leaf stage using soil-drenching (3 to 5 ml/ plant) inoculation methods with 3 replications. After 10 days post inoculation (dpi), each line was evaluated visually for occurrence of bacterial wilt ranging from 1 (most resistant) to 5 (most susceptible). For development of GBS markers, the construction of four 48-plex libraries from the RIL population is ongoing, and all four GBS libraries will have been sequenced on one lane each of Illumina HiSeq2000. High-density genetic map of pepper using SNPs markers from the GBS data and several QTL significantly associated with resistance to BW will be presented.

Keywords: pepper, bacterial wilt, genotyping by sequencing, genetic map, QTL, resistance

Finding Large Scale Insertion Between Wild Soybean and Cultivated Soybean

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ABSTRACT

Structural variations (SVs) are known as key factor of regulation, but they have been rarely discovered yet. Here, we predicted 23 SV candidates using NGS sequencing and some of SVs were validated by DNA amplifying. Disease resistance proteins, protein kinase and Leucine-rich repeat were detected on those candidates by homology search. The SV candidates were mainly detected on intergenic regions and 1kb downstream regions and many repeat sequences, which might promote SVs, were rich on the candidates. Repeat sequences might activate SVs. This study could contribute to introduce useful genes on SVs of wild soybeans into cultivated soybeans and the methods this study use could be applied to detect SVs for other organisms.

Keywords: structural variation, NGS, soybean, insertion

Zn Content of Ultra Early Maturing Elite Rice Lines in Indonesia

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ABSTRACT

The prefalence of Zn defficiency in Indonesia is around 30% that is very high. One major effort to overcome the problem is by genetically improve the Zn content in rice grain. On the othen hand, ultra early maturing rice variety (having less than 90 days growth duration) is being studies as one strategy to increase yield and crop index either in optimum and unfavorable rice agro-ecosystem. This research was aimed to study grain Zn content of ultra early maturing elite rice lines in Indonesia. It was tested 10 ultra early maturing elite rice lines along with 2 check varieites (Silugonggo and Inpari 13). The field experiment was conducted in irrigated rice field of ICRR experimental station in Sukamandi during WS 2014/2015, following randomized complete block design of four replications. Zn content of brown rice samples from each plot were measured using XRF machine Oxford Instrument X-Supreme that had been validated to ICP method. The results showed that all the lines had significantly higher Zn content compared to Silugonggo (20.55) and Inpari 13 (20.03). The four highest Zn content lines were UG-1 (27.30 ppm), B13031b-RS*2-2-1-13-2 (26.50 ppm), B27-6-2-1 (25.63 ppm), and BP156118-1b-11 (25.20 ppm). Out of them, B13031b-RS*2-2-1-13-2 (8.64 t/ha) had comparable yield with the check having the highest yield, Silugonggo (8.16 t/ha). All the four high Zn lines had earlier heading compared to Silugonggo (66 days) and Inpari 13 (73 days). Introducing new varieties having higher Zn content compared to the previous popular variety would hopefully reduce the prevalence of Zn defficiency in Indonesia.

Keywords: rice, Zn content, ultra early maturing, Indonesia

Selection of DNA Marker to BPH Resistance Gene *Bph3* for MAS

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ABSTRACT

Because of change in weather conditions in Korea, the occurrence of BPH was increasing. The development of rice varieties with different resistant genes to BPH is required. This study was carried out search of *Bph3* gene marker for development of *Bph3* gene hold rice varieties through Marker-assisted Selection (MAS). DNA was extracted from nine varieties with each of genes. For PCR, eight SSR markers near the *Bph3* gene of chromosome 6 were used. In eight SSR markers, RM586 is the most suitable markers for *Bph3* gene, because that marker represents different band location. To test the ability of RM586, we developed F_1 by crossing between an elite japonica cultivar Saenuri, which is highly susceptible to BPH and BG367-2 carrying *Bph3* gene and eighty BC_1F_1 lines were developed by backcross using Saenuri. The results showed that the eighty BC_1F_1 lines segregated in 1:1 ratio(resistant:susceptible) indicating the inheritance of monogenic dominant gene for BPH resistant. DNA of these were extracted for test of RM586 and they separated by electrophoresis. Each of lines(resistant:susceptible) forming a band of different sizes. The size of the PCR products generated as RM586 is easily analyzed by 2% agarose gel. Therefore, RM586 marker was identified as a marker suitable for use with the MAS to develop BPH resistant varieties with *Bph3* gene.

Keywords: BPH, Bph3, marker-assisted selection, RM586, DNA marker, resistant gene

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Modification of Starch Composition Using RNAi Targeting of *SSS1* Gene in Rice

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ABSTRACT

An increasing preference for good eating quality of rice among consumers has become one of the important considerations in rice breeding. Amylose content is a leading factor affecting eating quality of rice. Amylose composition is determined by the relative activity of soluble starch synthase (SSS) and granule-bound starch synthase (GBSS). This study focused on modifying the expression of SSSI gene which is responsible for amylopectin and amylose synthesis in rice by using RNA interference (RNAi) technology. The transgenic rice plants showed various amylose contents in rice grains. Favorable rice lines were selected according to genomic PCR, transgene expression and amylose contents analysis. A semi-quantitative RT-PCR was carried out to determine the expression level of SSSI gene after flowering of transgenic rice and wild type. Down-regulation of SSSI gene in transgenic plants was evident in the decreasing expression in rice grains. Accordingly, scanning electron microscopy (SEM) analysis revealed uniform size with smooth curves starch granules in down-regulation rice lines, in contrast with the non-uniform granules in wild type. Results indicated that RNAi-SSSI transgenic lines produced low amylose contents that fell between glutinous and non-glutinous rice. This study showed that down-regulation of endogenous SSSI may improve the eating quality in rice. This work was supported by a grant from the Next-Generation BioGreen 21 Program, RDA and iPET, Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea.

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Field Performance of Five Soybean Mutants Under Drought Stress Conditions and Molecular Analysis Using SSR Markers

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ABSTRACT

The objectives of this research were to evaluate (1) performances of soybean mutant lines under drought stress conditions and (2) the genetic diversity and relationship among the mutant lines using SSR markers. The field evaluation was conducted in the Mataran University Experimental Farm, West Nusatenggara, Indonesia. The experiment was set up in a randomized block design. Fife mutant lines and two control varieties were evaluated in four replicates. The experiment was conducted during the dry season of 2011 and 2012. Genetic distance among evaluated lines were determined based on allelic diversity analysis of 40 simple sequence repeat (SSR) loci. Cluster analysis was performed and dendrogram was constructed based on the SSR allele diversity data. Under drought stress conditions, two mutant lines (GK 3 and GK 8) performed better than the other lines. These mutant lines reuire 30.75 to 32 days to flower and 79.75 to 83.75 days to harvest. They also have relatively short plant height (28.25 and 23. 35 cm). Those mutant characters are better than those of the other three mutants, the original parents, and the control soybean species. Since the evaluated soybean mutant lines yielded more under drought stress conditions than the standard varieties, they could be used and registered as drought tolerance soybean mutants. Moreover, the evaluated soybean accessions showed a wide genetic distance. The eccessions were clustered into two groups according to their genetic background, such as group I (The Pandermen with three mutant lines) and group II (the Muria with two mutant lines). Nine out of 40 SSR loci evaluated (SATT126, SATT162, SATT244, SATT285, SATT383, SATT294, SATT511, SATT540, and SATT557) yielded polymorphic allele between the parents and their mutants and could be used to differentiate mutants from their parents. Therefore, these loci may be used for further analysis of soybean mutants in the future.

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Keyword : Soybean Mutant Line , Drop Condition, SSR Marker

Genetic Parameter Estimations of Yield Components Using Four Diallel Populations of Peppers (*Capsicum annuum* L.)

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ABSTRACT

Pepper is one of the most widely grown vegetables in the world. The need of pepper had been increasing which had led to the rapid development of pepper breeding programs especially to produce high yielding varieties. Genetic parameter estimations are needed to decide the most effective breeding method of pepper. This paper describes our study aimed at estimating the genetic parameters of yield components of peppers. Four populations of diallel crosses were used to estimate the pattern of additive and dominant variances followed by the calculations of narrow and broad sense of heritability. Our results showed that the additive-dominant model was more accurate to estimate the yield components of pepper. This pattern was similar on all populations used in this study. Additive genetic effects were mostly larger than that of non-additive for all parameters of yield component indicating that the type varieties of pepper can be developed through non-hybrid and hybrid breeding.

Keyword: additive, full diallel, heritability, hybrid, non-additive, breeding

A Study of Gene Action, Combining Ability, Heritability and Heterosis between Big and Curly Fruit Lines and Thirty Inbred Lines of *Capsicum annuum* L.

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ABSTRACT

Big and curly fruit lines of *Capsicum annum* L. were crossed according to Griffing's Method (Diallel) Method 1. The objectives of this study were to assess the general combining ability (GCA) and specific combining ability (SCA) of *C. Annuum* L. lines through diallelic crosses providing information about the genetic effect, heritability and heterosis on expression of yield and yield component traits. Thirty cross combination and six parent were evaluated in a randomized complete block design with three replications. The experiment was conducted at Leuwikopo experiment field, Department of Agronomy and Horticulture, Faculty of Agriculture, Bogor Agricultural University on October 2012 to April 2013. The GCA and SCA means square were significant for all traits. The higher values of mean squares associated to GCA indicates a strong contribution of additive genetic effects to the expression of some traits. C5 scored highly for GCA in some traits and can be used to developed an open pollinated variety. Estimates of heritability showed that some of the traits were highly heritable, and weight per plant trait should readily be improved by selection. The SCA of cross C2×C5, C5×C120, C19×C120, C120×C159 were found to be high, with progeny showing high positive heterosis for some traits, thereby indicating that those crosses has the potential to function as a superior cultivar within commercial breeding programmes.

Keywords: Capsicum annuum* L.*, additive, heritability, heterosis

Stability Analysis of Putative Mutant Soybean Lines (*Glycine max* (L.) Merr.) on Four Environments

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ABSTRACT

The research to develop high yielding varieties of soybean through mutation breeding by using gamma ray irradiation which conducted by BAU has produced M9 generation of putative mutant lines. The aim of this research was to evaluate the stability and adaptability of those putative mutant lines in some environments. Evaluation was done on 10 putative mutant lines and two national varieties as control, i.e. Argomulyo and Tanggamus, and conducted in Bogor and Purwakarta, each in two seasons. Randomized Complete Block Design (RCBD) with three replications was applied on each environment. Finlay-Wilkinson, Eberhart-Russell, and AMMI were applied to analyse stability and adaptability. The result showed that the dry seed weight per ha was influenced by interaction of genotype and environment. Based on Finlay-Wilkinson, Eberhart-Russell, and AMMI methods, M200-13-47-7 and M200-93-49-6 were stable lines with high adaptability (general adaptability), meanwhile M100-29A-42-14, M100-33-6-11 lines, and Argomulyo variety were stable lines with low adaptability in all environment. M100-46-44-6, M100-96-53-6, and M150-7B-41-10 lines had specific adaptation on marginal environment, meanwhile M200-39-64-4 line had specific adaptation on optimum environment. Based on AMMI method, Tanggamus variety was specific for Bogor 1; M150-29-44-10 line was specific for Bogor 2, and M200-93-49-13 line was spesific for Purwakarta 2.

Keywords: AMMI, Eberhart-Russell, Finlay-Wilkinson, putative mutant, stability

Performance and Variability of F5 Soybean Lines from Argomulyo x Tanggamus Developed by *Single Seed Decent*

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ABSTRACT

The objectives of this experiment was to obtain information on agronomic performance and variation of F5 soybean lines developed by *single seed descent* method from Argomulyo x Tanggamus. This experiment was conducted in an Augmented Design in Randomized Complete Block Design (RCBD) wiht genotype as the single factor. The genotypes tested were 125 F5 lines with no replication and 3 checks consisted of national variety Tanggamus, Argomulyo and Wilis replicated six times. This experiment was conducted at the experimental field and the Plant Breeding Laboratory, Department of Agronomy and Horticulture, Bogor Agricultural University from April to September 2014. Results of this experiment showed high variation among F5 lines in plant height, number of nodes per plant, number of productive nodes per plant, number of full pods per plant, and number of pods per plant. Those characters were not significantly different with Tanggamus and but was higher than Argomulyo. The highest heritability and broad sense genetic variation was found for plant height, number of nodes per plant, number of productive nodes per plant, number of full pods per plant, number of pods per plant, and weight seed per plant. The results showed that single seed decent method was able to maintain genetic variability amongs advanced soybean lines.

Keyword: agronomic performance, genetic variation, heritability, soybean

Inheritance Yield Component Character of Pepper (*Capsicum annuum* L.) Curly and Big Chili Pepper Crosses

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ABSTRACT

Inheritance yield components character of chili using curling and big chili pepper crosses to obtain generation F1 and F2 generation obtained from selfing F1 generation. The backcross generations BCP1 and BCP2 were obtained through crossing between F1 and the parents P1 and P2, respectively. The data obtained were generation analysis to get a phenotype variance, environment variance, genotype variance, additive variance and dominant variance. Join scaling test were estimated the mean effect of all possible homozygotes, additive, dominants, and epystatics interaction effect of additive-additive, additive-dominant, and dominant-dominant. Broad-sense heritability were high for fruit length, fruit weight, and thick of fruit flesh and moderate for yield per plant. Narrow-sense heritability were high for fruit weight and thick of fruit flesh, and moderate for yield per plant and fruit length. Appropriate genetic model for yield per plant is additive-dominant model with additive-dominant interaction. Appropriate genetic model for fruit length and fruit weight is additive-dominant model. Appropriate genetic model for thick of fruit flesh character is additive-dominant model with additive-dominant and dominant-dominant interaction model.

Keywords: genetic model, heritability, inheritance, yield component

Isolation and Identification of Peat Soils Phosphate Solvent Bacteria in Giam Siak Kecil Biosphere Conservation-Bukit Batu, Bengkalis, Riau

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ABSTRACT

Phosphate (P) is the essential nutrient which has an important role in the process of photosynthesis and root development. The availability of this element is limited in the tropical land. One of the alternative processes to improve the efficiency of phosphate availability in the soil is using phosphate solvent microorganisms. Phosphate solvent bacteria, is one of the microorganisms that has a role in providing the P element for plants. This study aims to obtain the phosphate solvent bacteria isolate and determine the potential of the bacteria in dissolving phosphate. This research was conducted at the Soil Laboratory of the Faculty of Agriculture, University of Riau, in October 2013 to May 2014. The study was conducted experimentally and descriptively by using peat soils samples derived from *Giam Siak Kecil* Biosphere Conservatory-*Bukit Batu*. The result of the isolation and bacteria selection, purified by streak plate method on Pikovskaya media, obtained 16 phosphate solvent bacteria isolates. The result of clear zone observation on Pikovskaya media, there are 7 isolates that have PSI index ≥ 2.5. Based on the result of morphology, physiology and biochemistry observation, the selected phosphate solvent bacteria, categorized seems like to the *Bacillus* sp. and *Pseudomonas sp*. genus.

Keywords: phosphate solvent bacteria, peat soil, Giam Siak Kecil Biosphere conservatory

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Stability Analysis on Leaf Spot Resistance of Peanut (*Arachis hypogaea* L.) Promising Lines Developed by BAU

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ABSTRACT

Evaluation was conducted on ten promising peanut lines which were resistant to leaf spot disease developed by BAU and four varieties to obtain information about their yield stability. The field experiment was conducted in four environments i.e. Bogor, Sumedang, Sukabumi and Kuningan in West Java, Indonesia. Randomized Complete Block Design (RCBD) with three replications was applied in each environment. Stability analyses was done using Finlay-Wilkinson, Eberhart-Russel, and AMMI (*Additive Main Effects Multiplicative Interaction*) methods. The results showed that genotype and interaction of genotype and environment were significantly affected the yield. GWS-73D genotype was stable according to the three methods of stability analyses. Based on the method of Finlay-Wilkinson and Eberhart-Russell, GWS-110A1, GWS-110A2 and GWS-134A were stable genotypes with high adaptability in all environments. Those genotypes showed average yield, respectively were 1.74, 1.62 and 1.55 ton.ha^{-1} which was higher than the total average (1.46 ton.ha^{-1}). Based on AMMI method, GWS-110A1 was specific genotype for Bogor, GWS-110A2 for Sukabumi, and GWS-134A for Kuningan. The AMMI method was the most appropriate stability method to analyze the stability of peanuts in this study.

Keywords: AMMI, Bogor, Eberhart-Russel, Finlay-Wilkinson, Kuningan, Sukabumi, Sumedang

Identification of Clubroot Resistance Qtls and Revision of Reference Genome Assembly in Cabbage Using a New Genotyping-By-Sequencing Map

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ABSTRACT

Clubrootcaused by Plasmodiophorabrassicaeis one of devastating diseases and leads to severe losses of yield and quality in Brassica crops. Many resistance genes and markers are available in B. rapa but less is known in B. oleracea. Therefore, it is important to identify resistance gene for clubroot disease in B. oleracea. In this study, we applied the genotyping-by-sequencing (GBS) technique to construct a high resolution genetic map and analyze clubroot resistance (CR) genes. A total of 18,187 GBS markers were identified between two parental lines, resistant and susceptible to the disease, of which 4,103 markers were genotyped with 78 F_2 plants. The markers were clustered into nine linkage groups spanning 879.9 cM with an average interval of 1.15cM. QTL survey based on triplication of clubroot resistance tests using $F_{2:3}$ progenies revealed that two and single major QTLs were resistant to P. brassicae race 2 and race 9, respectively. These three QTLs did not show collinearity with CR loci found in *B. rapa* but have roughly overlapped with CR loci identified in cabbage for resistance to race 4. In addition, high resolution genetic map helps to refine and curate the reported reference genome of cabbage and anchor the unplaced scaffolds to the reference assembly. Taken together, genetic map and QTLs obtained in this study will provide valuable information to facilitate in-depth genetic study for development of clubroot resistance and improvement of reference genome in cabbage. This research was supported by the Golden Seed Project (No. 213003-04-1-SB430), Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), Rural Development Administration (RDA) and Korea Forest Service (KFS), and the Bio & Medical Technology Development Program of the NRF funded by the Korean government, MSIP (NRF-2015M3A9A5030733)

Keywords:Clubroot, Brassica oleracea, Genotyping-by-sequencing, QTL, Genetic map

Establishment of Molecular Authentication System between *Panax ginseng* Cultivar Gumpoong and Landrace Hwangsook

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ABSTRACT

Panax ginseng is well known herb plant for its positive medicinal effects. From 700-year-old history, three landraces have been cultivated in Korea, of which Hwangsook (HS) is easily distinguished from the others by its yellow fruit instead of reddish color.Only ‘Gumpoong’ (GU) has been bred and developed into commercial cultivar from HS.However, it is difficult to distinguish GU and HSmorphologicallybefore harvesting their roots.In this study, we developed molecular method to authenticate GU and HS. From sequence comparison of chloroplast genome sequence, we applied two polymorphic markers from previous study and one newly designed dCAPS marker to total32 DNA samples of GU and HSindividuals, collected from two different places. While amplicons of individual GU sample has exact expected band profile of GU in three markers, the samples of HS showed both GU and HS genotypes. It is likely that each HS sample could not be authenticatedindividually due tocharacteristic of landrace, high genetic variation. Therefore, we applied bulked segregation analysis, which is using DNA pools of GU and HS individuals separately. As a result, we were able to distinguish GU from HS accurately. Pooling samples of HS showed both genotype bands, while pooling GU showed only GU type of band profiles. This marker system will be faster and accurate method and useful to the ginseng market from stopping fraud trading as well as the development of ginseng breeding. This research was supported by the grant funded by Next-Generation BioGreen21 Program (No. **PJ01103001**), Rural Development Administration, Republic of Korea and the Bio & Medical Technology Development Program of the NRF funded by the Korean government, MSIP (NRF-2015M3A9A5030733)

Keywords:Panax ginseng, landrace, cultivar, Bulked segregation analysis,Molecualr authentication

Diversity of Minor Food Legumes in Maluku Tenggara Barat District, Maluku Province, Indonesia

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ABSTRACT

The diversity of minor food legumes in Maluku Tenggara Barat (MTB) District, Maluku Province, was explored in this study. The objectives were: to assess the diversity of minor legume species with a high diversity based on their morphology and to determine diversity centers of the minor legumes in the district. This research used a survey method, with determination of sample sub-districts, villages and farmers by a purposive sampling. Four sub-districts, i.e. Wertamrian, Kormomolin, Selaru and Tanimbar Utara, with 8 sample villages, were selected. Morphological characterizations were based on the descriptor guides. The data were analyzed qualitatively, in the forms of figures (photographs taken) in addition to direct observation in the field. The results showed that there were six minor food legumes cultivated in MTB, i.e. 'kacang tunggak' [*Vigna unguiculata* (L.) Walp], 'kacang koro karatok' (*Phaseolus lanatus* L.), 'kacang gude' [*Cajanus cajan* (L.) Millsp], 'kacang komak' (*Lablab purpureus* L. Sweet), 'kacang uci' (*Vigna umbellata*) and 'kacang kecipir' (*Psophocarpus tetragonolobus*), with a diversity center in *Selaru Subdistrict*. The highest within-species diversity based on seed colors and shapes was found in *Vigna unguiculata* with 14 accessions, with a center in Tanimbar Utara Sub-District. Within-species diversities in *P. lanatus* with eight accessions, followed by *C. cajan* with six accessions, were found in the diversity center in Selaru Sub-District.

Keywords : diversity, minor food legumes, germplasm, Maluku Tenggara Barat

Estimation of Genetics Variance and Selection Sorghum (*Sorgum bicolor* (L.) Moench) in Leuwikopo Experimental Field, Darmaga

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ABSTRACT

Estimation of genetics variance and selection is one of most important factors in determining the success of plant breeding programs. This research was aimed to estimate genetics variance and to conduct selection form 3 F2 populations by potential yield and agronomy characters. This research was conducted in Leuwikopo Experimental Field Bogor Agriculture University from February to May 2015. This research used three F2 populations from the cross of P/I 10-90 x Numbu, P/I 150-20-A x Numbu, and P/I 150-20-A x Kawali. The qualitative characters evaluated using Mendelian ratio of F2 phenotypes and the quantitative characters were evaluated using analysis of skewness and curtosis. Selection was conducted at 10 % selection intensity and the differential selection was calculated for each character. The analysis of medelian ration showed that the qualitative characters of shorghum are controlled by epistatic gene action. The heritability of agronomic characters and yiled components of the three sorghum population was high.

***Key words:* heritability, mendelian ratio, selection, variance**