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2016

*"The Future of Tropical
Horticulture"*



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FOREWORD

The International Seminar on Tropical Horticulture 2016 was held in IPB International Convention Center, Bogor, Indonesia 28 – 29 November 2016. This seminar was organized by Center of Excellence for Tropical Horticulture Studies (PKHT), Center of Excellence in University (PUI-PT), Bogor Agricultural University (IPB), and supported by an excellent collaboration with International Tropical Fruits Network (TF Net).

We're very glad to know the fact that the seminar displayed a very wide discussion about tropical horticulture with delegates from 5 countries (Taiwan, Thailand, Malaysia, Japan and Indonesia) as keynote speech and participants. 24 papers were selected to be included in this proceeding from 28 oral and 31 poster presentation.

This proceeding is contained of three sub chapter, that is fruits, vegetables and miscellaneous. There are 9 papers of fruits chapter, 12 papers of vegetables chapter and 3 papers of miscellaneous chapter. We wish to thank Sanjeet Kumar, Ph.D, Prof. Sobir, Prof Masayoshi Shigyo, Dr. Mohd Desa Haji Hassim, Parson Saradhulhat, Ph.D for being keynote speech at this international seminar and all participants for very lively atmosphere during and after the seminar.

Bogor, May 2017

Editor

Dr. Darda Efendi
Dr. Awang Maharijaya

SYMPOSIUM PROGRAM

28 November 2016

07.30 – 09.00	<i>Registration desk open and morning coffee</i>
09.00 – 09.30	Welcome addresses Dr. Darda Efendi , Director of Center for Tropical Horticulture Studies, Indonesia Prof. Herry Suhardiyanto , Rector of Bogor Agricultural University, Indonesia
09.30 – 12.00 (20 minutes presentation + 10 minutes discussion)	Session 1: Introductory Topics Dr. Sanjeet Kumar , World Vegetable Center, Taiwan <i>“Science and Art of Tropical Horticulture: Stories, Impacts and Prospects”</i> Prof. Sobir , Indonesian Center of Excellence for Tropical Horticulture <i>“Tropical Horticulture: Past, Present and Future”</i> Gregori Hambali, MSc , Mekarsari, Indonesia <i>“Managing Tropical Fruit Collection”</i>
12.00 – 13.00	<i>Lunch</i>
13.00 – 14.30 (20 minutes presentation + 10 minutes discussion)	Session 2: Opportunity in Tropical Horticulture Industry Prof. Muhammad Firdaus , Bogor Agricultural University <i>“Enhancing the Competitiveness of Tropical Horticulture Products”</i> Dr. Mohd Desa Haji Hassim , International Tropical Fruit Network, Selangor, Malaysia <i>“Issues and Challenges in The Global Tropical Fruit Market”</i> Parson Saradhuldat, Ph.D. , Department of Horticulture, Kasetsart University, Thailand <i>“Tropical Horticulture Business in Thailand”</i>
14.30 – 16.00 (20 minutes presentation + 10 minutes discussion)	Session 3: Quality of Horticultural Products Dr. Darda Efendi , Center for Tropical Horticulture Studies, Indonesia <i>“Quality Issues in Tropical Horticultural Products”</i>

	<p>Tatas H. P. Brotosudarmo, PhD, Ma Chung University <i>“Non-optical and optical spectroscopy as metabolomics platforms for determining the quality of horticultural products”</i></p> <p>Dr. Irmanida Batubara, Tropical Biopharmaca Research Center <i>“ Quality Control on Herbal Medicine”</i></p>
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29 November 2016

07.30 – 08.30	<i>Registration desk open</i>	
08.30 – 10.15	Parallel session 1	Parallel session 2
10.15 – 10.30	<i>Coffee Break and Poster Session</i>	
10.30 – 12.15	Parallel session 3	Parallel session 4
12.15 – 13.00	<i>Lunch</i>	
13.00 – 15.00 (@20 minutes presentation + 10 minutes discussion)	<p>Session 4 : Technology Needs for Improving Horticulture in The Tropics</p> <p>Prof. Masayoshi Shigyo, Yamaguchi University, Japan <i>“Proposal for a forwarding model in order to encourage social interaction among HRs and/or PGRs via platform operation based on research collaboration in Indonesian vegetable crops”</i></p> <p>Prof. Sri Hendrastuti Hidayat, Department of Plant Protection. Faculty of Agriculture. Bogor Agricultural University <i>“Integrated Disease Management for Vegetable Crops: Concepts and Practices”</i></p> <p>Dr. Catur Hermanto, Indonesian Vegetables Research Institute (IVEGRI) <i>“Pest And Disease Threats and Challenges For Future Vegetable In The Tropic”</i></p>	
15.00 – 16.00	<i>Concluding and Remarks</i>	
16.00 – 18.00	<i>Farewell Drink</i>	

ORAL PRESENTATION SCHEDULE

Tuesday, November 29th 2016

Paralel 1

TIME	PRESENTER NAME	CODE	TITLE
08.30 – 08.45	Slamet Susanto	OP 1	Prolong Shelflife of Seedless Pummelo (<i>Citrus maxima</i> (L.) Osbeck) Fruit During Storage
08.45 – 09.00	Dini Hervani	OP 2	Cryopreservation of Long-term Plant Germplasm Storage
09.00 – 09.15	Sulassih	OP 3	Variability of Jackfruit Based on Morphology and Molecular ISSR
09.15 – 09.30	Ahmad Solikin	OP 4	Characterization of Local Durian Varieties In Central Java Using Molecular Markers Inter Simple Sequence Repeats (ISSR)
09.30 – 09.45	Nelinda	OP 5	Packaging Design and Postharvest Treatment to Maintain the Quality of Rambutan (<i>Nephelium Lappaceum</i> L.) in Distribution System
09.45 – 10.00	Maxmilyand Leiwakabessy	OP 6	Disease Incidence and Molecular Analysis of Banana Bunchy Top Virus in Bogor, West Java
10.00 – 10.15	Ajmir Akmal	OP 7	Transpiration rate of relationship fruit with Gamboge of Mangosteen (<i>Garcinia mangostana</i> L.)

Paralel 2

TIME	PRESENTER NAME	CODE	TITLE
08.30 – 08.45	Juang Gema Kartika	OP 8	Growth and Production of Some <i>Moringa oleifera</i> Lam. Accession at Several Harvesting Interval
08.45 – 09.00	Lutfi Izhar	OP 9	Conservation Agriculture with Soil Health: Optimal Fosfor Fertilizer Rate for Tomato (<i>Lycopersicon esculentum</i> Mill. L) on Inceptisols
09.00 – 09.15	Adhitya Mahendra K	OP 10	Stakeholders Analysis in Seed Provision System Development Originated from True Seed of Shallot
09.15 – 09.30	Endro Gunawan	OP 11	Policy Analysis on Shallot Stock Seed Program Though The Botanical Seed (<i>True Shallot Seed</i>) TSS
09.30 – 09.45	Ali Asgar	OP 12	Integrating Understanding of Indigenous Vegetable Nutrients and Benefits
09.45 – 10.00	Marlin	OP 13	Metabolite Changes in Shallot (<i>Allium cepa</i> var <i>aggregatum</i>) during Vernalization
10.00 – 10.15	Suhesti Kusuma Dewi	OP 14	The Effects of Vernalization and Photoperiod on Flowering of Shallot (<i>Allium cepa</i> var. <i>ascalonicum</i> Baker) in Lowland Area

Paralel 3

TIME	PRESENTER NAME	CODE	TITLE
10.30 – 10.45	Satriyas Ilyas	OP 15	Study of Phenology and Determination of Seed Physiological Maturity of Long Bean (<i>Vigna sinensis</i> L.) Based on Heat Unit
10.45 – 11.00	Endah Retno Palupi	OP 16	Chromosome Number Estimation of Diploid, Autotetraploid and Triploid Hybrid 'Rejang' Banana Using Protoplast from Male Flower (anther)
11.00 – 11.15	Yudiwanti Wahyu	OP 17	Performance of Some First Generation Corn Populations derived from Selfing and Sibbing for Developing Baby Corn Varieties
11.15 – 11.30	Ady Daryanto	OP 18	Inheritance of Chili Pepper Resistance Against Infestation of <i>Aphis gossypii</i> Glover (Hemiptera: Aphididae)
11.30 – 11.45	Edi Santosa	OP 19	Variation in Floral Morphology of Agamosporous <i>Amorphophallus Muelleri</i> Blume of Natural and Gibberellins Treatment
11.45 – 12.00	Kusuma Darma	OP 20	The Eco-Friendly Technology to Control Pests and Diseases of Shallot
12.00 – 12.15	Filemon Yusuf	OP 21	Phylogenetic Study of Indigenous Pulses Based on Morphological and Inter Simple Sequence Repeat (ISSR) Markers

Paralel 4

TIME	PRESENTER NAME	CODE	TITLE
10.30 – 10.45	Ririh Sekar Mardisiwi	OP 22	Growth and Production of Black Cumin (<i>Nigella sativa</i> L.) at Several Composition Media and Watering Interval
10.45 – 11.00	Evi Setiawati	OP 23	Growth and Production of Black Cumin (<i>Nigella sativa</i> L.) at Shade Levels and Nitrogen Doses
11.00 – 11.15	Tatik Raisawati	OP 24	The Nutritional Value and Total Flavonoid Content of <i>Sonchus arvensis</i> L. Leave
11.15 – 11.30	Dewi Sukma	OP 25	Diversity Analysis of Phalaenopsis by Using SNAP Marker
11.30 – 11.45	Widya Sari	OP 26	Morphological, Molecular Characteristics and Pathogenicity of <i>Fusarium</i> spp. from Some Cultivars of Banana
11.45 – 12.00	Juwartina Ida Royani	OP 27	In Vitro Shoots Multiplication of Sapodilla (<i>Manilkara zapotta</i> Van Royen) with Modified MS Media
12.00 – 12.15	Willy B. Suwarno	OP 28	Melon Breeding: Past Experience and Future Challenge

Table of Content

Fruits

Evaluation of Morphological and Cytological Character of F1 Diploid Hybrid Banana Sapon and <i>Musa acuminata</i> var. <i>tomentosa</i> (K.Sch) Nasution Diyah Martanti, Tri Handayani and Yuyu Suryasari Poerba	1
Fruit Plants of Kalimantan : Results of Field Exploration and Conservation Sudarmono.....	9
Melon Breeding: Past Experiences and Future Challenges Willy B. Suwarno, Sobir, and Endang Gunawan	16
In vitro shoots multiplication of Sapodilla (<i>Manilkara zapotta</i> Van Royen) with modified MS media Juwartina Ida Royani.....	24
Confirmation Number of Chromosome Diploid, Autotetraploid and Triploid Hybrid 'Rejang' Banana Using Digested Anther Tri Handayani, Diyah Martanti, Yuyu S. Poerba, Witjaksono	31
Disease Incidence and Molecular Analysis of Banana Bunchy Top Virus in Bogor, West Java Maxmilyand Leiwakabessy, Sari Nurulita, Sri Hendrastuti Hidayat	37
The Potential of Liquid Smoke Coconut Shell in Extending The Shelf Life of Tropical Fruits Ira Mulyawanti, Sari Intan Kailaku and Andi Nur Alamsyah.....	46
The Effects of The Application of Edible Coating, Antimicrobial Agent, Packaging and Absorber on Snake Fruit (<i>Salacca edualis</i> REINW) Sari Intan Kailaku, Ira Mulyawanti, Asep W Permana and Evi Savitri Iriani	50
Packaging Design and Postharvest Treatment to Maintain the Quality of Rambutan (<i>Nephelium Lappaceum</i> L.) in Distribution System Nelinda, Emmy Darmawati, Ridwan Rachmat, Lilik Pujantoro Eko Nugroho	57
Characterization of Local Durian Varieties in Central Java Using Molecular Markers Inter Simple Sequence Repeats (ISSR) Ahmad Solikin, Amin Retnoningsih, and Enni S. Rahayu.....	65

Vegetables

Shallot Varieties Adaptation in Napu Highlands, Central Sulawesi Saidah, Abdi Negara and Yogi P Rahardjo.....	77
Collection and Characterization of Shallot Germplasm in Effort to Support National Food Security Ita Aprilia, Erviana Eka Pratiwi, Awang Maharijaya, Sobir, Heri Harti	81
Optimum Fertilizer of Shallot on Andisol and Latosol Soils Gina Aliya Sopha, Suwandi.....	86

Effect of Organic Fertilization on The Growth and Yields of New Onion Varieties in Limited Land I Ketut Suwitra dan Yogi P. Raharjo	94
Interaction Between Varieties and Plastic Mulch on Shallot Growth in Dryland South Kalimantan Lelya Pramudyani	98
Effect of <i>Trichoderma</i> and <i>Penicillium</i> Application (Isolated From Pine Rhizosphere) to The Shallot Growth Shinta Hartanto dan Eti Heni Krestini	107
The Effects of Vernalization and Photoperiod on Flowering of Shallot (<i>Allium cepa</i> var. <i>ascalonicum</i> Baker) in Lowland Area Suhesti Kusumadewi, Hamim, Sobir.....	112
Metabolite Changes in Shallot (<i>Allium cepa</i> var <i>aggregatum</i>) during Vernalization Marlin, Awang Maharijaya, Sobir, Agus Purwito.....	118
Stakeholders Analysis in the Development of Seed Provision System Originating from True Seed of Shallot Adhitya Marendra Kiloes, Puspitasari, and Turyono.....	124
Policy Analysis on Shallot Stock Seed Program through The Botanical Seed (True Shallot Seed/TSS) Endro Gunawan and Rima Setiani.....	131
The Dynamic of Shallot Production, Supply and Price after the Implementation of Horticulture Import Regulations Puspitasari and Adhitya Marendra Kiloes	136
Characterization and Resistance to Bacterial Wilt Diseases (<i>Ralstonia solanacearum</i>) of 20 Eggplant (<i>Solanum melongena</i> L.) Genotypes Heri Harti, Teni Widia, Pritha, Awang Maharijaya.....	143

Miscellaneous

Cryopreservation for Long-term Plant Germplasm Storage Dini Hervani, Darda Efendi, M. Rahmad Suhartanto, Bambang S. Purwoko	149
Good Manufacturing Practices (GMP) for Fresh-Cut Fruits and Vegetables Sari Intan Kailaku, Ira Mulyawanti and Andi Nur Alam Syah	154
Breeding of Anthurium (<i>Anthurium andreanum</i>) : A strategy to produce new clones as tropical ornamental plants Ridho Kurniati, Kurnia Yuniyanto, Suskandari Kartikaningrum	161

Melon Breeding: Past Experiences and Future Challenges

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Abstract

Melon (*Cucumis melo* L.) is a species with the largest genetic diversity among others in the Cucurbitaceae family, and therefore providing opportunities for plant breeders to develop new, improved varieties. *C. melo* var *reticulatus* (North American cantaloupes), *C. melo* var *inodorus* (honeydews), and *C. melo* var *cantalupensis* (European cantaloupes) are the most widely known among at least eight cultivar groups. Melon is a cross pollinated species where most of pollination events are performed by bees. F₁ hybrid is the most common type of varieties could be found in the market today. Some important fruit traits in melon include: fruit weight, sugar content, flesh color and texture, rind appearance and hardness, and shelf-life. An ideotype of large fruit with an attracting orange or green, sweet and crisp flesh are more demanded nowadays for Indonesian market. Additionally, obtaining varieties resistant to main pests and diseases are of importance as well. We have been conducting a melon breeding program aimed for quality fruits at the Center for Tropical Horticulture Studies, Bogor Agricultural University (IPB), and two honeydew varieties has been released. Recently we identified a melon genotype (IPB Meta 9) exhibiting good resistance to downy mildew and can be utilized in a breeding program. Future challenges include shifts in consumer preferences, for example, small-size fruits may be more preferred for personal or small family consumptions.

Keywords: breeding, fruit quality, melon

1. Genetic diversity of melon

Melon (*Cucumis melo* L.) is a cross-pollinated diploid species ($2n=2x=24$) with the largest genetic diversity among other species in the Cucurbitaceae family (Dutt and Saran, 1994; Nayar and Singh, 1994). Wild species of *Cucumis* occur in Africa. Secondary centers of diversity include Persia, Southern Russia, Iran, Afghanistan, India, and China. Cucumber (*Cucumis sativus* L.) is known as a close relative to melon based on combined chloroplast and nuclear data (Renner *et al.* 2007). The *C. melo* species has at least eight cultivar groups or botanical varieties, i.e. *C. melo* var. *reticulatus* (North American cantaloupe or muskmelon), *C. melo* var. *inodorus* (honeydew), *C. melo* var. *cantalupensis* (European cantaloupe), *C. melo* var. *makuwa* (oriental melon), *C. melo* var. *flexosus* (snake melon), *C. melo* var. *conomon*, *C. melo* var. *chito*, and *C. melo* var. *dudaim* (Robinson and Decker-Walters, 1999). *Reticulatus*, *inodorus*, and *cantalupensis* are the most widely known cultivar groups in many countries including in Indonesia. *Reticulatus* melons typically have thick, netted rind, moderate shelf-life, green or orange thick flesh with firm texture, and mature fruit slips from the stem. *Inodorus* melon generally have smooth (non-netted) rind, long shelf-life, flesh color of white, green, or orange, crisp flesh texture, and mature fruits does not slip from the stem. *Cantalupensis* melons typically have strong aroma, short shelf-life, juicy flesh, and vertical sections in the rind.

Our previous study evaluating a diverse collection consisting of 30 melon genotypes (13 F₁ hybrid varieties, 4 F₂ populations, 6 open pollinated varieties, and 7 inbred lines) indicated a good opportunity for breeding new, improved varieties. These genotypes can be classified into the reticulatus (12 genotypes), inodorus (8 genotypes), and makuwa (3 genotype) groups; however we found some reticulatus genotypes with some cantalupensis group's characteristics (e.g. stronger aroma, shorter shelf-life, juicier flesh), and therefore we put those into the 'cantalupensis-like' group (7 genotypes). Fruit appearance of some of the genotypes are shown in Figure 1. F₁ hybrids selected based on fruit weight and sugar content are: Action, Autumn Favor, and Monami Red from the reticulatus group; Jade Flower from the inodorus group, and Hales' Best from the cantalupensis-like group.



Figure 1. Genetic diversity of fruit appearance among melon genotypes

2. Flower types and pollination

Most cantaloupes and honeydews cultivars are andromonocious, i.e. has both male and hermaphrodite flowers in one plant (Robinson and Decker-Walters, 1999). Male flowers appear on the main and secondary branches, whereas hermaphrodite flowers appear on the secondary or higher order branches. Monoecious cultivars (having male and female flowers in one plant) are less common, although are more desirable for hybrid seed production because emasculation (removing anthers) from the female plants would not be required. Monoecious is dominant to andromonocious and the difference among these are controlled by a pair of alleles (More and Seshadri, 1994).

Main pollinating agent for melon plants is honey bees and the outcrossing amount is 5 – 70%. Higher fruit set (98%) occurred under natural pollination as compared to hand pollination

(68%) (Munshi and Alvarez, 2005). From a study of melon pollination in an area containing two cantaloupe genotypes, greater number of bee moves between the two strains were observed than that within the same strain (Foster and Levin, 1967).

Steps involved in making crosses among melon genotypes are described in Figure 2. Emasculation of hermaphrodite flowers of an andromonic parent should be performed one day before anthesis. Both male and hermaphrodite flowers need to be covered. Hand pollination should be done in early morning (e.g. by about 6 AM in Bogor, Indonesia) to avoid undesirable pollen contaminations by bees.



Figure 2. Steps involved in making a controlled crossing among melon genotypes: emasculating of a hermaphrodite flower on a female parent plant, before anthesis (a-f), pollination, performed the next morning (g-j), covering (k), and labelling (l).

3. Breeding objectives and methods

Ideally, breeding objectives are set to meet a melon ideotype demanded by consumers. The other less ideal practice is, the objectives may be set by the breeders and later the new released varieties will be advertised to the consumers. Fruit traits could be of most importance for consumers, and therefore the breeders should put considerable efforts into them. Some important fruit traits are: high sugar content, high yield, thick flesh, crisp flesh texture, attractive flesh color (usually green or orange), no unpleasant after-taste, hard rind for transportations, long shelf life, and good-looking dense net (for cantaloupes). No less important are breeding for pest and disease resistance. Important diseases in tropical regions include powdery mildew, downy mildew, bacterial wilt, and viruses. Additionally, breeding for adaptation to marginal environments, for example, drought tolerance, acid soil tolerance, or salinity tolerance could be of important considerations as well.

Because melon is a cross-pollinated species, its breeding programs could be targeted for developing improved open-pollinated varieties (OPVs) or hybrid varieties. Hybrid varieties are more common nowadays than OPVs even though their seed price are more expensive. Most melon hybrids available in the market are single crosses resulting from controlled mating of two inbred lines. Three-way cross and double cross varieties of melon hybrids are rarely available. An advantage of the single cross hybrid is theoretically more uniform than the other type of hybrids and the OPVs. Additionally, a hybrid melon variety may possess a specific combination of desirable traits (in our example, flesh and rind color) from its female and male parents. Characterizations of the traits may utilize a well developed descriptor such as from (IPGRI, 2003).

Breeding improved melon varieties involves four important practical steps: (1) development of base populations, (2) development of inbred lines, (3) generation of hybrids through controlled mating among inbred lines, (4) evaluation of the hybrids. A base population is a segregating population that can be derived from a controlled mating among two genotypes (for example, see (Zuniga *et al.* 1999)), or from a topcross. Inbred lines can be developed from base populations following the pedigree breeding method (Robinson, 2000). In our example illustrated in Figure 3, we have two F_2 base populations named A and B. Manual self-pollinations (selfing) were conducted in selected plants from each populations, and the resulting fruit would contain S_1 seeds. The S_1 seeds from each fruit were kept separately and planted in groups in the following season. Selections were made among and within groups, and the selected S_1 plants were selfed to produce S_2 seeds. In a practical breeding program for fruit traits, we selfed a number of plants and then perform selection based fruits performance later. These processes continue until at least S_7 generation. The S_7 s or more advanced generations have homozygous genotypes in most of the loci, and hence can be considered as inbred lines. Genetic diversity within an inbred line theoretically are small, among lines derived from the same base population are larger, and among lines from different base populations are even larger. The hybrids, therefore, are suggested to be produced by crossing the lines derived from different base populations for obtaining aimed combinations of the traits as well as some amount of heterosis. Studies reported positive heterosis for fruit shape in melon (Fernandez-Silva *et al.* 2009; Jose *et al.* 2005).

Inbreeding depression are a phenomena typically observed during development of inbred lines of a cross pollinated species. We observed somewhat higher inbreeding depression level for fruit weight in *reticulatus* (netted) groups than in *inodorus*; whereas for sugar content, we did not notice a considerable level of such a depression.

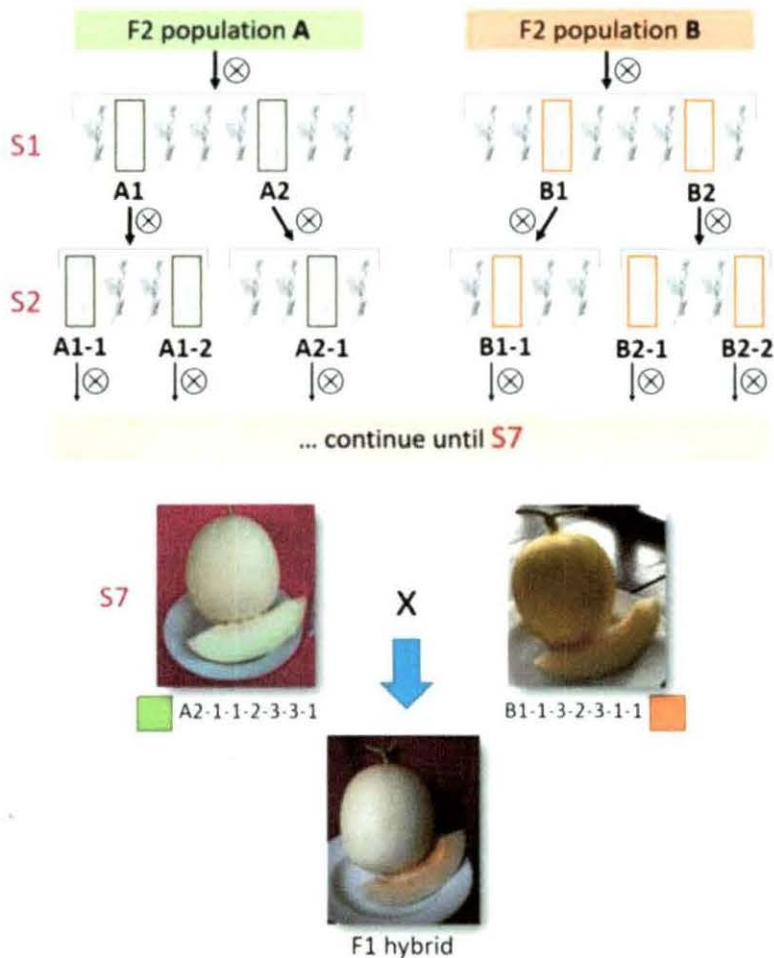


Figure 3. Illustration of steps involved in hybrids melon breeding

Our previous study evaluating 29 melon genotypes showed that fruit weight was positively correlated with fruit diameter ($r=0.96$, $P<0.01$), flesh thickness ($r=0.82$, $P<0.01$), fruit length ($r=0.67$, $P<0.01$), and rind thickness ($r=0.49$, $P<0.01$). We performed a path analysis for partitioning the correlation coefficients into direct and indirect effects, using fruit weight as an independent variable (Y), and stem diameter, days to harvest, fruit length, fruit perimeter, rind thickness, and flesh thickness as dependent variables (X). The direct effects of fruit perimeter on fruit weight were positive and large (0.83), while the indirect effects through the other X's are negligible. Altogether, these six X traits could explain 96% of the total variability of fruit weight.

4. Future challenges

The demand for melon fruits implies the necessity of quality seeds production of improved varieties. Changes on consumer preferences need to be anticipated through development of new, unique varieties with excellent tasting quality. Small-size melon cultivars will perhaps be popular for small family or personal consumptions.

Planting melon in tropical regions faces the challenges on dealing with pest and diseases. Downy mildews and viruses, among other diseases, are regarded as very important melon diseases leading to considerable economic losses, and hence breeding melon varieties resistant to these diseases could be among the top priorities. The 'IPB Meta 9' melon genotype from our breeding program showed moderate resistance to downy mildew (Huda and Suwarno, 2016). Its fruits, however, are small (less than 500 g on average) with thin and sweet white flesh. This implies that subsequent breeding activities are needed to introduce the resistance to another genotypes, and/or to 'fix' some undesirable characteristics possessed by this genotypes.

Our breeding experience suggested that breeding *reticulatus* (cantaloupe; netted) melons are more challenging somewhat than breeding *inodorus* (honeydew; non-netted) melons in terms of achieving uniformity of the lines. The cantaloupes unfortunately are still more popular than the honeydews in Indonesia, and therefore varieties from both groups need to be bred still. Large-size cantaloupes with sweet, orange thick flesh, and strong rind are on market demand at present and also in near future, we predict. Breeding honeydews could be aimed for obtaining fruits with thick, sweet and crisp flesh, along with unique rind appearance. Additionally, breeding for nutrients could also be an interesting option as melon is a good source of vitamin C. We recently observed a considerable range of genetic diversity for vitamin C concentrations among several melon genotypes in our breeding program.

Finding genes controlling a trait of interest is simply challenging; however genotyping tools are becoming more available recently. Marker-assisted selection could be an option for accelerating the breeding process, especially for traits that are controlled by single or few genes. Gene-finding approaches such as QTL or association mapping requires both genotypic and phenotypic data. Several recent studies have been conducted for studying QTL controlling important traits in melon, for example fruit traits (Monforte *et al.* 2004; Ramamurthy and Waters, 2015; Wang *et al.* 2016), fruit ripening and fruit softening (Moreno *et al.* 2008, Vegas *et al.* 2013), yield-related traits (Zalapa *et al.* 2007), powdery mildew resistance (Fukino *et al.* 2008; Wang *et al.* 2016), cucumber mosaic cucumovirus resistance (Dogimont *et al.* 2000), aphids and whiteflies resistance (Boissot *et al.* 2010).

Phenotyping of low-heritability, polygenic quantitative traits unfortunately are typically difficult. Measuring tolerance to abiotic stresses are not simple because a relatively small shift on the stress level may lead to a dramatic change on the phenotype. Even more difficult is that, another stress (e.g. heat) can be confounded with the stress-of-interest (e.g. drought) if the experiment is not controlled properly. Utilization of computer-aided, precision phenotyping which are becoming more popular could be a good opportunity for obtaining more accurate phenotypic data. Some of the tools are not very expensive (for example, using scanner and/or computer imaging devices along with a relevant software for quantifying color components as RGB) and could be of practical use in a breeding program.

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