

The Second International Conference on Genetic Resources and Biotechnology

Harnessing Technology for Conservation and Sustainable Use of Genetic Resources for Food and Agriculture

Bogor, Indonesia • 24–25 May 2021

Editors • I Made Tasma, Dwinita Winkan Utami, Ika Roostika,
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January 2022

THE SECOND INTERNATIONAL CONFERENCE ON GENETIC RESOURCES
AND BIOTECHNOLOGY: Harnessing Technology for Conservation and Sustainable
Use of Genetic Resources for Food and Agriculture

Committees: The Second International Conference on Genetic Resources and Biotechnology

Cite as: AIP Conference Proceedings **2462**, 010002 (2022); <https://doi.org/10.1063/12.0008934>
Published Online: 19 January 2022



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Preface: The Second International Conference on Genetic Resources and Biotechnology

The Second International Conference on Genetic Resources and Biotechnology, which is the continuation of the first event held in 2018, focuses on topics related to advances in biotechnology to create more opportunities for effective conservation and sustainable utilization of genetic resources for food and agriculture. This year conference's theme is Harnessing Technology for Conservation and Sustainable Use of Genetic Resources for Food and Agriculture. The conference was organized by Indonesian Agency for Agricultural Research and Development (IAARD), Ministry of Agriculture, Indonesia, in collaboration with Indonesian Biotechnology Consortium and held on 24th-25th of May 2021 virtually due to the pandemic of COVID-19.

The conference aims to share and exchange current scientific information and technological developments on biotechnology and their applications for conservation and sustainable use of genetic, to encourage and promote quality, efficiency, and modernization of management and utilization of genetic resources, and to facilitate national and international collaboration among participants. There are five scopes discussed in this conference. They are effective management of conservation and sustainable use of genetic resources for food and agriculture, application of genomics and molecular markers for genetic resource conservation and crop adaptation to climate change, application of innovative crop improvement techniques for conservation and sustainable use of plant genetic resources for food and agriculture, plant cell and tissue culture for conservation and effective utilization of genetic resources, and the use of microbial genetic resources as biological control agents of agricultural pests and diseases, and for soil bioremediation.

Five speakers from the United States of America, Japan, India and Indonesia were invited to discuss about their expertise and knowledge on relevant subjects in the plenary sessions. This conference was attended by more than 100 participants including 75 presenters and 44 listeners worldwide. They came from diverse governmental, private, or academic institutions and also scientific communities. The presented materials have undergone peer review processes and only qualified papers were selected. Furthermore, all papers were subjected to double blind peer-review and expected to meet the scientific criteria of significance and academic excellence to be published in a conference proceedings indexed in a well-known, reputable service.

We would like to express our sincere gratitude to our speakers, presenters and all participants for their contributions in this conference. We would also like to express our appreciation for the generosity of our sponsors that support this conference: PT CropLife, PT ITS Science Indonesia, PT Fajar Mas Murni and PT Prima Instrument Analitika. Lastly, special thanks to all committee members for their exceptional work and contributions in the conference and publication.

Chair of Organizing Committee

Dr. Toto Hadiarto

Table of Contents

THE SECOND INTERNATIONAL CONFERENCE ON GENETIC RESOURCES AND BIOTECHNOLOGY: Harnessing Technology for Conservation and Sustainable Use of Genetic Resources for Food and Agriculture



Conference date: 24–25 May 2021

Location: Bogor, Indonesia

ISBN: 978-0-7354-4172-9

Editors:

I Made Tasma, Dwinita Winkan Utami, Ika Roostika, Yadi Suryadi, Chaerani, Eny Ida Riyanti, Puji Lestari, Toto Hadiarto, Reflinur, Joko Prasetyono, Fatimah, Surya Diantina, Tru Puji Priyanto, Kusumawaty Kusumanegara, Wening Enggarini, Rerenstradika Tizar Terryana and Dani Satyawan

Volume number: 2462

Published: Jan 19, 2022

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- [20](#)
- [50](#)

- [100](#)
- [all](#)

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EFFECTIVE MANAGEMENT OF CONSERVATION AND SUSTAINABLE USE OF GENETIC RESOURCES FOR FOOD AND AGRICULTURE

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Harnessing plant genetic resources through biotechnology for food security in Indonesia

[Mastur](#), [Reflinur](#), [Nurul Hidayatun](#), [Sustiprijatno](#), [Fatimah](#), [Tri Puji Priyatno](#) and [Puji Lestari](#)
AIP Conference Proceedings **2462**, 020001 (2022); <https://doi.org/10.1063/5.0075671>

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DNA barcoding of *Vatica bantamensis*, a critically endangered tree endemic to Banten, Indonesia

[Muhammad Rifqi Hariri](#), [Iyan Robiansyah](#), [Dipta Sumeru Rinandio](#), [Dodo](#), [Desi Siti Sundari](#), [Cecep H. Sukmawan](#) and [Bayuntoro Ardi](#)
AIP Conference Proceedings **2462**, 020002 (2022); <https://doi.org/10.1063/5.0075529>

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Genetic parameters of agronomic traits in soybean (*Glycine max* [L.] Merrill) genotypes tolerant to drought

[Made J. Mejaya](#), [Suhartina](#), [Purwantoro](#), [Novita Nugrahaeni](#) and [Titik Sundari](#)
AIP Conference Proceedings **2462**, 020003 (2022); <https://doi.org/10.1063/5.0075159>

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Yield stability performance of soybean (*Glycine max* [L.] Merrill) lines tolerant to drought

[Suhartina](#), [Purwantoro](#), [Novita Nugrahaeni](#), [Abdullah Taufiq](#) and [Made Jana Mejaya](#)
AIP Conference Proceedings **2462**, 020004 (2022); <https://doi.org/10.1063/5.0075158>

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Polymorphisms and associations of the *RACK1* genes with antibody response to Newcastle disease in KUB chickens

[Ifa Manzila](#), [Puji Lestari](#), [Tike Sartika](#), [Tri Puji Priyatno](#), [Risa Indriani](#), [Kristianto Nugroho](#) and [Rerenstradika Tizar Terryana](#)

AIP Conference Proceedings **2462**, 020005 (2022); <https://doi.org/10.1063/5.0075622>

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Rice grain quality evaluation of promising lines of rice under irrigation and for salinity tolerance

[Dody D. Handoko](#), [Nafisah](#), [Aris Hairmansis](#), [Trias Sitaresmi](#), [Heni Safitri](#), [Satoto](#), [Ali Imamuddin](#), [Cucu Gunarsih](#) and [Untung Susanto](#)

AIP Conference Proceedings **2462**, 020006 (2022); <https://doi.org/10.1063/5.0075956>

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FreeJanuary 2022

Existing diversity profile for kernel characteristics of maize germplasm in IAARD-ICABIOGRAD gene bank

[Andari Risliawati](#), [Sobir](#), [Trikoesoemaningtyas](#), [Willy B. Suwarno](#) and [Puji Lestari](#)
AIP Conference Proceedings **2462**, 020007 (2022); <https://doi.org/10.1063/5.0075178>

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Characterization of Japansche citroen rootstock somaclones and *in vitro* selection for aluminium tolerance

[Deden Sukmadjaja](#), [Mia Kosmiatin](#) and [Tiwi Wati](#)
AIP Conference Proceedings **2462**, 020008 (2022); <https://doi.org/10.1063/5.0077888>

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FreeJanuary 2022

Resistance to brown planthoppers (*Nilaparvata lugens* Stål) in rice accessions originated from Sumatra Island, Indonesia

[Dodin Koswanudin](#), [Nurul Hidayatun](#) and [Muhamad Ace Suhendar](#)
AIP Conference Proceedings **2462**, 020009 (2022); <https://doi.org/10.1063/5.0075680>

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Morphological identification of underutilized local fruits in Kutai Barat Regency to support their conservation and sustainable use

[Fitri Handayani](#), [Nurbani](#) and [Asep Pebriandi](#)

AIP Conference Proceedings **2462**, 020010 (2022); <https://doi.org/10.1063/5.0075594>

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Genetic resources of adlay (*Coix lacryma-jobi* L.) in East Kalimantan as source of functional food

[Fitri Handayani](#), [Muhammad Amin](#) and [Muhammad Taufiq Ratule](#)

AIP Conference Proceedings **2462**, 020011 (2022); <https://doi.org/10.1063/5.0075593>

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-
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Screening of soybean genotypes resistance to rust disease (*Phakopsora pachyrhizi*)

[Sumartini](#) and [Kurnia Paramita Sari](#)

AIP Conference Proceedings **2462**, 020012 (2022); <https://doi.org/10.1063/5.0075674>

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Identification of soybean promising lines resistant to pod-sucking bug, *Riptortus linearis* (Fabricius)

[M. Muchlish Adie](#), [Titik Sundari](#), [Kurnia Paramita Sari](#) and [Ayda Krisnawati](#)
AIP Conference Proceedings **2462**, 020013 (2022); <https://doi.org/10.1063/5.0075343>

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Variation in pod shattering resistance among black soybean genotypes associated with agronomic traits

[Ayda Krisnawati](#), [Titik Sundari](#) and [M. Muchlish Adie](#)
AIP Conference Proceedings **2462**, 020014 (2022); <https://doi.org/10.1063/5.0075338>

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Preliminary characterization and identification of genetic integrity of velvet bean germplasm in IAARD-ICABIOGRAD gene bank

Nurwita Dewi, Andari Risliawati and Nurul Hidayatun

AIP Conference Proceedings **2462**, 020015 (2022); <https://doi.org/10.1063/5.0076355>

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Plant parasitic nematodes infesting three minor legumes (velvet bean, lablab bean, and jack bean)

Chaerani, Try Zulchi P. Hariyadi and Nurwita Dewi

AIP Conference Proceedings **2462**, 020016 (2022); <https://doi.org/10.1063/5.0075204>

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Proactive management approach of seed PGRFA conservation during the pandemic of coronavirus disease (COVID-19) in Indonesia

Nurul Hidayatun, Andari Risliawati, Nurwita Dewi, Lina Herlina and Dodin Koswanudin

AIP Conference Proceedings **2462**, 020017 (2022); <https://doi.org/10.1063/5.0075531>

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Evaluation of mung bean accessions in saline soil based on quantitative morphological characters

[Trustinah](#), [Ratri Tri Hapsari](#), [Rudi Iswanto](#) and [Rudy Soehendi](#)

AIP Conference Proceedings **2462**, 020018 (2022); <https://doi.org/10.1063/5.0075324>

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Screening and evaluation of 100 upland rice accessions for developing high-yielding upland rice varieties tolerant against acid soil

[Lina Herlina](#) and [Yusi N. Andarini](#)

AIP Conference Proceedings **2462**, 020019 (2022); <https://doi.org/10.1063/5.0075550>

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Morphological characters of sugarcane mutant (*Saccharum officinarum* L.) from *in vitro* selection for drought stress

Rr. Sri Hartati, Sri Suhesti and Nurya Yuniyati

AIP Conference Proceedings **2462**, 020020 (2022); <https://doi.org/10.1063/5.0075656>

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Identifying potential seedless citrus accessions through floral structure and pollen performance

Baiq Dina Mariana, Anis Andrini and Sri Andayani

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Secondary characters based selection of Indonesian kenaf (*Hibiscus cannabinus* L.) germplasm for developing superior varieties

Taufiq Hidayat R. S., Marjani, Nurindah, Muhammad Rasyidur Ridho, Cynthia Lestari Hertianti and Widya Fatriasari

AIP Conference Proceedings **2462**, 020022 (2022); <https://doi.org/10.1063/5.0075716>

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Genetic relationship of pigmented rice (*Oryza sativa* L.) collected from Eastern Indonesia based on morpho-agronomical traits and SSR markers

[Yusi Nurmalita Andarini](#), [Willy Bayuardi Suwarno](#), [Hajrial Aswidinnor](#) and [Hakim Kurniawan](#)
AIP Conference Proceedings **2462**, 020023 (2022); <https://doi.org/10.1063/5.0075706>

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Rejuvenation and morphological characterization of local rice from the province of Yogyakarta

[Setyorini Widyayanti](#), [Sutarno](#), [Endang Wisnu Wiranti](#) and [Kristamtini](#)
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Characterization of plant architecture and yield trait of castor (*Ricinus communis* L.) germplasm suitable for mechanical harvesting

[Tantri Dyah Ayu Anggraeni](#) and [Rully Dyah Purwati](#)

AIP Conference Proceedings **2462**, 020025 (2022); <https://doi.org/10.1063/5.0075155>

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Characterization and interrelationships of the number of vessel bundles with yield components in various genotypes of soybean (*Glycine max* [L.] Merrill)

[Anna S. Karyawati](#) and [Dyah P. Fitrawantio](#)

AIP Conference Proceedings **2462**, 020026 (2022); <https://doi.org/10.1063/5.0075693>

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Tuber starch content of edible canna (*Canna indica* L.) from different geographical origins

[Surya Diantina](#), [Randy Sanjaya](#), [Kristina Dwi Atmini](#), [Ace Suhendar](#) and [Dodin Koswanudin](#)

AIP Conference Proceedings **2462**, 020027 (2022); <https://doi.org/10.1063/5.0075922>

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The diversity of morpho-agronomic characters and identification of early maturity cassava (*Manihot esculenta* Crantz.) germplasm

[Tinuk Sri Wahyuni](#), [Kartika Noerwijati](#) and [Made J. Mejaya](#)
AIP Conference Proceedings **2462**, 020028 (2022); <https://doi.org/10.1063/5.0075658>

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Radiosensitivity and phenotypic characterization of gamma ray-induced mutant population of four *Capsicum annum* L. cultivars grown in screen house

[Andri Fadillah Martin](#), [Dyah Retno Wulandari](#), [Tri Muji Ermayanti](#), [Betolini Widhi Hapsari](#), [Erwin Al Hafiih](#) and [Laela Sari](#)
AIP Conference Proceedings **2462**, 020029 (2022); <https://doi.org/10.1063/5.0075173>

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Morphological performances of mutant butterfly pea (*Clitoria ternatea* L.)

[Try Zulchi](#), [Ali Husni](#), [Dwinita Wikan Utami](#), [Reflinur](#), [Mia Kosmiatin](#), [Tarkus Suganda](#) and [Agung Karuniawan](#)

AIP Conference Proceedings **2462**, 020030 (2022); <https://doi.org/10.1063/5.0075592>

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Screening of beta carotene and its correlation with tuber flesh color in sweet potato

[Kristina Dwi Atmini](#), [Surya Diantina](#), [Muhamad Sabda](#) and [Dodin Koswanudin](#)

AIP Conference Proceedings **2462**, 020031 (2022); <https://doi.org/10.1063/5.0075618>

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Evaluation of morpho-agronomical characters and grain quality of red rice lines

[Heni Safitri](#) and [Puji Lestari](#)

AIP Conference Proceedings **2462**, 020032 (2022); <https://doi.org/10.1063/5.0078807>

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Growth variation and relationship of clove progenies of high-yielding mother trees collected from various regions in Indonesia

[Mariana Susilowati](#), [Sri Wahyuni](#), [Adi Setiadi](#) and [Nurliani Bermawie](#)

AIP Conference Proceedings **2462**, 020033 (2022); <https://doi.org/10.1063/5.0075824>

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Screening on bast fiber plants resistant to spiral stem borer, *Agrilus acutus* (Coleoptera: Buprestidae)

[Sujak](#), [Nurindah](#), [Dwi Adi Sunarto](#), [Marjani](#) and [Nurul Hidayah](#)

AIP Conference Proceedings **2462**, 020034 (2022); <https://doi.org/10.1063/5.0075691>

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Characteristic of indigenous *Leuconostoc mesenteroides* EN 17-11 protease and its stability during storage at cold and freezing temperatures

[Tatik Khusniati](#), [Ika](#), [Harry Noviard](#) and [Sulistiani](#)

AIP Conference Proceedings **2462**, 020035 (2022); <https://doi.org/10.1063/5.0076004>

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Performance of introduced lines based on morphological markers for diversity enrichment of Indonesian chili pepper (*Capsicum annum* L.) varieties

[Rinda Kirana](#), [Catur Hermanto](#), [Reflinur](#) and [Derek W. Barchenger](#)

AIP Conference Proceedings **2462**, 020036 (2022); <https://doi.org/10.1063/5.0075186>

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The growth of garlic internal sprout on different storage condition

[Chotimatul Azmi](#), [Imas Rita Saadah](#), [Nazly Aswani](#) and [Asih Kartasih Karjadi](#)

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Genetic diversity analysis of *Castanopsis argentea* using random amplified polymorphic DNA markers

Muhammad Imam Surya, Lily Ismaini, Decky Indrawan Junaedi, Aisyah Handayani, Taufikurrahman Nasution, Muhammad Efendi, Andes Hamuraby Rozak, Zaenal Mutaqien, Musyarofah Zuhri, Imawan Wahyu Hidayat, Fitri Kurniawati, Vandra Kurniawan, Dwinda Mariska Putri and Risha Amilia Pratiwi
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APPLICATION OF GENOMICS AND MOLECULAR MARKERS FOR GENETIC RESOURCE CONSERVATION AND CROP ADAPTATION TO CLIMATE CHANGE

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Current status of tidal swamp rice varieties and its improvement for Fe toxicity tolerance and biofortification

Muhamad Sabran, Dwinita Wikan Utami and Susilawati
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Agroforensic, a new emerging study using molecular marker technique

[Edy Listanto](#), [Ahmad Warsun](#), [Ahmad Dadang](#), [Eny Ida Riyanti](#), [Saptowo Jumali](#)

[Pardal](#), [Sustiprijatno](#) and [Mastur](#)

AIP Conference Proceedings **2462**, 030002 (2022); <https://doi.org/10.1063/5.0075164>

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FreeJanuary 2022

Molecular diversity comparison in local rice accessions originated from Kalimantan and other islands of Indonesia

[Puji Lestari](#), [Rerenstradika Tizar Terryana](#), [Kristianto Nugroho](#), [Andari Risliawati](#), [Nurul](#)

[Hidayatun](#), [Priatna Sasmita](#), [Yudhi Sastro](#), [I. Gusti Komang Dana Arsana](#) and [Ikhwani](#)

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Genetic variation of Adan, a Krayan local rice mutant, using microsatellite markers

[Joko Prasetyono](#), [Tio Fadel Rafsanjani](#), [Tri Aminingsih](#), [Tasliah](#) and [Sugiono Moeljopawiro](#)

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The genome sequence of Ciherang, an Indonesian rice mega variety, revealed the footprints of modern rice breeding

[Ida Rosdianti](#), [Dani Satyawati](#), [Muhamad Yunus](#) and [Dwinita Wikan Utami](#)
AIP Conference Proceedings **2462**, 030005 (2022); <https://doi.org/10.1063/5.0075676>

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Field adaptation and molecular characterization of Code-*qTSN4* and Code-*qDTH8* rice lines at two different locations

[Tasliah](#), [Kurniawan Rudi Trijatmiko](#) and [Joko Prasetyono](#)
AIP Conference Proceedings **2462**, 030006 (2022); <https://doi.org/10.1063/5.0075661>

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Hybrid purity assessment in F₁ hybrids segregating for phytophthora root rot resistance genes of chili pepper (*Capsicum annuum* L.)

[Fatimah](#), [Reflinur](#), [Joko Prasetyono](#), [Wartono](#), [Kristianto Nugroho](#), [Rinda Kirana](#), [Dani Satyawan](#), [Rerenstradika Tizar Terryana](#), [Aqwin Polosoro](#), [Puji Lestari](#) and [I. Made Tasma](#)
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Characterization of genomic variation on three Indonesian oil palm genotypes analyzed using next-generation sequencing HiSeq

[I. Made Tasma](#), [Habib Rijzaani](#), [Dani Satyawan](#), [Ida Rosdianti](#), [Edy Supriyanto](#) and [Razak Purba](#)
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Cytological and molecular identifications of seedless tangerine derived from endosperm culture

[Chaireni Martasari](#), [Mia Kosmiatin](#), [Ali Husni](#), [Kurniawan Budiarto](#) and [Innez Candri Gilang Purnama](#)
AIP Conference Proceedings **2462**, 030009 (2022); <https://doi.org/10.1063/5.0076395>

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Improvement of sex determination of salak plant using sequence characterized amplified regions

Reflinur, Ma'sumah, Namira Nur Arfa, Budi Setiadi Daryono and Azis Natawijaya
AIP Conference Proceedings **2462**, 030010 (2022); <https://doi.org/10.1063/5.0075698>

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-
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Table of Contents

THE SECOND INTERNATIONAL CONFERENCE ON GENETIC RESOURCES AND BIOTECHNOLOGY: Harnessing Technology for Conservation and Sustainable Use of Genetic Resources for Food and Agriculture



Conference date: 24–25 May 2021
Location: Bogor, Indonesia
ISBN: 978-0-7354-4172-9
Editors:

I Made Tasma, Dwinita Winkan Utami, Ika Roostika, Yadi Suryadi, Chaerani, Eny Ida Riyanti, Puji Lestari, Toto Hadiarto, Reflinur, Joko Prasetyono, Fatimah, Surya Diantina, Tru Puji Priyanto, Kusumawaty Kusumanegara, Wening Enggarini, Rerenstradika Tizar Terryana and Dani Satyawan

Volume number: 2462

Published: Jan 19, 2022

DISPLAY :

- [20](#)
- [50](#)

- [100](#)
- [all](#)

APPLICATION OF INNOVATIVE CROP IMPROVEMENT TECHNIQUES FOR CONSERVATION AND SUSTAINABLE USE OF PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE

FreeJanuary 2022

Design and *in vitro* test of sgRNA for the CRISPR/Cas9 plasmid construct of the *SQS* gene of *Artemisia annua* L.

Sri Koerniati

AIP Conference Proceedings **2462**, 040001 (2022); <https://doi.org/10.1063/5.0075695>

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FreeJanuary 2022

The efficacy of genetically modified (GM) corn Bt11 against *Ostrinia furnacalis* (Guenee) and *Helicoverpa armigera* (Hubner)

Bahagiawati and Diani Damayanti

AIP Conference Proceedings **2462**, 040002 (2022); <https://doi.org/10.1063/5.0075312>

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Construction and introduction of OsAER1::LeAlaAT cassette to improve the nitrogen use efficiency in rice cv. Mekongga

Atmitri Sisharmini, Aniversari Apriana, Intan Kamila, Aqwin Polosoro, Wening Enggarini, Tri Joko Santoso, Toto Hadiarto, Bahagiawati A. Husin and Kurniawan Rudi Trijatmiko

AIP Conference Proceedings **2462**, 040003 (2022); <https://doi.org/10.1063/5.0075458>

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FreeJanuary 2022

Environmental safety assessment of genetically engineered potato resistant to late blight caused by *Phytophthora infestans*

Alberta Dinar Ambarwati, Eny Ida Riyanti, Edy Listanto, Tri Joko Santoso, Toto Hadiarto and Kusmana

AIP Conference Proceedings **2462**, 040004 (2022); <https://doi.org/10.1063/5.0075612>

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Backcrossing of soybean lines containing aluminium tolerance gene into superior soybean variety, Biosoy

[Saptowo J. Pardal](#), [Amalia Prihaningsih](#), [Suharsono](#), [Ratna Utari](#) and [Riri Sundasari](#)
AIP Conference Proceedings **2462**, 040005 (2022); <https://doi.org/10.1063/5.0075187>

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Phenotypic and genetic stability evaluation of the targeted *GA20ox-2* gene mutation in CRISPR/Cas9 mutant rice derived from Mentong cultivar

[Aniversari Apriana](#), [Tri Joko Santoso](#), [Atmitri Sisharmini](#), [Reflinur](#), [A. Dinar Ambarwati](#), [Toto Hadiarto](#), [Sustiprijatno](#) and [Nuryati](#)
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FreeJanuary 2022

Transformation of *csp* gene into tobacco plant mediated by *Agrobacterium tumefaciens*

[Sustiprijatno](#), [Seagames Waluyo](#) and [Suharsono](#)

AIP Conference Proceedings **2462**, 040007 (2022); <https://doi.org/10.1063/5.0075571>

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PLANT CELL AND TISSUE CULTURE FOR CONSERVATION AND EFFECTIVE UTILIZATION OF GENETIC RESOURCES

FreeJanuary 2022

The application of gamma ray irradiation to increase triterpenoid compounds in embryogenic calli of *Centella asiatica* L. Urban

[Ika Roostika](#), [Suci Rahayu](#) and [Nurliani Bermawie](#)

AIP Conference Proceedings **2462**, 050001 (2022); <https://doi.org/10.1063/5.0076402>

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FreeJanuary 2022

The effect of FeSO₄ concentration on the callus growth of two chili (*Capsicum annum* L.) varieties

[Rossa Yunita](#), [Endang Gati Lestari](#), [Iswari S. Dewi](#), [Mastur](#) and [Bambang Sapta Purwoko](#)

AIP Conference Proceedings **2462**, 050002 (2022); <https://doi.org/10.1063/5.0075223>

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FreeJanuary 2022

Evaluation of ratooning ability in several sweet sorghum (*Sorghum bicolor* [L.] Moench) mutant lines

[Endang Gati Lestari](#), [Iswari Saraswati Dewi](#), [Rossa Yunita](#) and [Amin Nur](#)

AIP Conference Proceedings **2462**, 050003 (2022); <https://doi.org/10.1063/5.0075542>

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FreeJanuary 2022

Response of gamma ray irradiation derived-cultures of three sugarcane varieties to drought stress induced by polyethylene glycol

[Ragapadmi Purnamaningsih](#) and [Suci Rahayu](#)

AIP Conference Proceedings **2462**, 050004 (2022); <https://doi.org/10.1063/5.0075185>

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-
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Sucrose and putrescine increased callus induction in tomato anther culture

Iswari Saraswati Dewi, Imam Nur Kholis, Bambang Sapta Purwoko and Ratna Ningsih
AIP Conference Proceedings **2462**, 050005 (2022); <https://doi.org/10.1063/5.0075666>

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-
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Field evaluation of elephant grass mutant lines (*Pennisetum purpureum* Schumach.) in highlands

Ali Husni, Muhammad Rifay, Mia Kosmiatin and Vyta W. Hanifah
AIP Conference Proceedings **2462**, 050006 (2022); <https://doi.org/10.1063/5.0076418>

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FreeJanuary 2022

Increasing drought tolerance of sugarcane through gamma ray irradiation and *in vitro* selection

Sri Suhesti, Syafaruddin, I. Ketut Ardana, Endang Hadipoentyanti and Rr. Sri Hartati
AIP Conference Proceedings **2462**, 050007 (2022); <https://doi.org/10.1063/5.0076155>

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Cells density affects cell production of *Citrus limonia* in flask and air-lift bioreactor cultures and limonin farming

Dita Agisimanto, Farida Yulianti and Hidayatul Arisah

AIP Conference Proceedings **2462**, 050008 (2022); <https://doi.org/10.1063/5.0075651>

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THE USE OF MICROBIAL GENETIC RESOURCES AS BIOLOGICAL CONTROL AGENTS OF AGRICULTURAL PESTS AND DISEASES, AND FOR SOIL BIOREMEDIATION

FreeJanuary 2022

In Silico functional prediction of CAS2, a protein specifically expressed in appressorium and required for pathogenicity of *Colletotrichum gloeosporioides*

Tri Puji Priyatno, Farah Diba Abu Bakar, Rohaiza Ahmad Redzuan, Abdul Munir Abdul Murad and Ifa Manzila

AIP Conference Proceedings **2462**, 060001 (2022); <https://doi.org/10.1063/5.0075625>

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Biofertilizer increases nutrient use efficiency (NUE) of nitrogen, phosphorus, and potassium at leaves level of *Artemisia annua* L.

Wiguna Rahman, Arthur A. Lelono, Erwin Al Hafiih and Tri Muji Ermayanti

AIP Conference Proceedings **2462**, 060002 (2022); <https://doi.org/10.1063/5.0075503>

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FreeJanuary 2022

Effect of nitrogen fixation and phosphate solubilizing bacteria on growth and yield of lowland rice in different soil type

Ikhwani, Higa Afza, Siti Yuriyah and Waluyo

AIP Conference Proceedings **2462**, 060003 (2022); <https://doi.org/10.1063/5.0077914>

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Morphological, physiological, and molecular identification and characterization of yeast isolated from Indonesian fruits and woods

Rerenstradika Tizar Terryana, Nazhirotul Ilmiyah, Inda Setyawati, Titin Haryati, Karden Mulya, Eny Ida Riyanti, Yudi Sastro and Puji Lestari

AIP Conference Proceedings **2462**, 060004 (2022); <https://doi.org/10.1063/5.0075170>

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The effect of coating application using chitosan enzymatic depolymerization on anthracnose disease suppression in mango (*Mangifera indica* L.) cv. ‘Arumanis’

[Yadi Suryadi, Dwi Ningsih Susilowati, I. Made Samudra, Alina Akhdiya and Karsinah](#)
AIP Conference Proceedings **2462**, 060005 (2022); <https://doi.org/10.1063/5.0075183>

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Understanding yeast tolerance as cell factory for bioethanol production from lignocellulosic biomass

[Eny Ida Riyanti and Edy Listanto](#)
AIP Conference Proceedings **2462**, 060006 (2022); <https://doi.org/10.1063/5.0075157>

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Isolation and pathogenicity test of fusarium basal rot and purple blotch fungal pathogens from shallot and *Allium* spp

Chaerani, Ragapadmi Purnamaningsih and Suci Rahayu

AIP Conference Proceedings **2462**, 060007 (2022); <https://doi.org/10.1063/5.0075209>

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Morphological characters and efficacy of thirteen entomopathogenic fungi of *Aschersonia aleyrodis* Webber isolates on whitefly (*Bemisia tabaci* Gennadius)

Yusmani Prayogo, Marida Santi Yudha Ika Bayu, Sri Wahyuni Indiati and Made Jana Mejaya

AIP Conference Proceedings **2462**, 060008 (2022); <https://doi.org/10.1063/5.0076067>

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Physicochemical characteristics of yoghurt from various beans and cereals

Heny Herawati, Diana Nur Afifah, Eni Kusumaningtyas, Sri Usmiati, Agus S. Soemantri, Miskiyah, Elmi Kamsiati and Muchamad Bachtiar

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The potential use of zeolite and exopolysaccharide bacteria for reduction of degradation and carbon emission on oil palm plantation in tropical peatland

[Laksmita P. Santi](#), [Haryo T. Prakoso](#) and [Donny N. Kalbuadi](#)
AIP Conference Proceedings **2462**, 060010 (2022); <https://doi.org/10.1063/5.0075506>

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Application of phosphate solubilizing microbes to promote the effectiveness of rock phosphate on cacao seedling growth in acid soil

[Kurnia Dewi Sasmita](#), [Iswandi Anas](#), [Syaiful Anwar](#), [Sudirman Yahya](#) and [Gunawan Djajakirana](#)
AIP Conference Proceedings **2462**, 060011 (2022); <https://doi.org/10.1063/5.0075843>

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Cite as: AIP Conference Proceedings 2462, 020015 (2022); <https://doi.org/10.1063/5.0076355>
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Preliminary Characterization and Identification of Genetic Integrity of Velvet Bean Germplasm in IAARD-ICABIOGRAD Gene Bank

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Abstract. Velvet bean (*Mucuna pruriens* [L.] DC.) is a tropical legume native to Africa and tropical Asia. In Indonesia, this plant is not widely cultivated, although, in some areas in Java, the community processed and fermented the pulse into a food called *tempeh benguk*. Besides being alternative for protein source, velvet bean can be used as herbal medicine. For decades, IAARD-ICABIOGRAD Gene Bank has been conserved the germplasm of velvet bean from some areas in Indonesia. However, morphological variability of the germplasm has not been reported. The research aimed to describes of phenotypic diversity among velvet bean accessions and focuses on morpho-agronomical characters. A total of 14 characters were observed from 9 accessions using plant descriptor. During the characterization, we found genetic mixture under the same accession. Therefore, we split these mixtures into different accession and assigned a new accession number for them, thus total accessions to be analyzed were 13 accessions. From clustering analysis, we found that these accessions were grouped into four clusters. Accession Koro Rawe Wonogiri was found to be the most distinct genotypes among accessions observed. Further comprehensive characterization should be conducted to reveal more information about diversity among velvet bean germplasm in IAARD-ICABIOGRAD Gene Bank.

INTRODUCTION

Velvet bean (*Mucuna pruriens* [L.] DC.) is an annual leguminous plant belonging to the family Fabaceae (Leguminoceae). It is indigenous of the tropics, especially Africa, India, and the West Indies. The plant is a self-pollinated, climbing shrub with long vines, have white or purple flower colors. The seed coat is hard, thick, and glossy. The pods or legumes are hard, curved, hairy, and thick. In Indonesia, it is commonly known as *koro benguk* (Java) or *kowas* (Sunda). The central areas of velvet bean production are dryland areas in Central Java, Special Region of Yogyakarta, and East Java. Velvet bean is usually intercropped with food crops in dry land [1].

Velvet bean is rich in nutrition. It contains protein (28.25–29.53%), lipid (8.04–8.26%), and flavonoid [2, 3]. Protein content of velvet bean is lower than soybean protein, but carbohydrate and fiber content is higher [4]. Although velvet bean has good nutritional value, an important constrain for its widespread adoption is that it contains a variety of anti-nutritional factors, such as L-Dopa (3,4 dihydroxy phenylalanine) and HCN [2], and digestible enzymic inhibitors (antitrypsin and anti-amylase), phytates, and anti-hemagglutinin [4]. In fact, with appropriate treatment, the antinutrient can be controlled [5, 6].

According to previous studies, velvet bean also has a variety of medicinal properties. It can be used as antidiabetic, aphrodisiac, antineoplastic, antiepileptic, and antimicrobial activity [7], and neuro protective drugs [8] [9]. The nonprotein amino acid, L-DOPA has been extracted from the seed to provide commercial drugs for the treatment of Parkinson's disease [10, 11]. Study of Indonesian velvet bean as herbal medicine also has been conducted [12].

In Indonesia, velvet bean is categorized as underutilized legume. In southern Central Java, it is mainly used as food reserves during the dry season [1] and its utilization is still limited for making tempeh for daily consumption in

Special Region of Yogyakarta, Wonogiri and Sukoharjo Regencies, known as *tempeh benguk*. Tempeh benguk has a higher dietary fiber and isoflavone level than soybean tempeh [13]. In addition to food and medicine, velvet bean also can be used as ruminant feed, soil fertility improvement, and soil cover [14]. Several studies about conservation and diversity of Indonesian underutilized legumes have been conducted, but the velvet bean has not been specifically discussed [15–18].

For decade IAARD-ICABIOGRAD Gene Bank has been conserved more than 10 food crops seeds including velvet bean. However, the morphological variability of germplasm has not been reported yet. Lack of basic information about diversity, variability, and relationship among genotypes limits the effective utilization of velvet bean. The study reported here describes of phenotypic diversity among velvet bean accessions and focuses on morpho-agronomical characters.

MATERIALS AND METHODS

A total of nine accessions of velvet bean germplasm conserved in IAARD-ICABIOGRAD Gene Bank (Table 1) were characterized during 2019/2020 at Cikeumeuh Experimental Station, ICABIOGRAD, Bogor. Plant spacing was 75 cm × 50 cm and each accession was planted 3 rows. Spacing between accessions was twice of plant spacing. A 2 m height of bamboo stake were used to support the stem of the bean.

During characterization activity, we observed the genetic integrity among plants in the same accession as well as characterizing their morpho-agronomical characters. Four qualitative traits were observed, i.e. flower color, hair color of immature pod, pod hairs itchiness, and seed color. Moreover, ten quantitative traits were observed, i.e. days to flowering, days to first harvesting, pod width and length, number of seed per pod, seed weight per 10 pods, seed width, length, and thickness, and 100-seed weight.

Two main analyses were applied, i.e. Principal Component Analysis (PCA) and cluster analysis. PCA was carried out to identify which character that contributes to the diversity among accessions, followed by results visualization in biplot and corrplot graphic visualization, which were generated through ggplot2, FactoMineR, factoextra, and corrplot package in R software v.4.0.5. Meanwhile, cluster analysis to determine genetic relationship among accessions was performed using PBSTAT-CL web-based software (<https://pbstat.com/>). Average linkage was used as clustering method based on Gower distance [19].

TABLE 1. List of velvet bean germplasm conserved in IAARD-ICABIOGRAD Gene Bank.






No.	Accession number	Accession name	Origin
1	05040-00001	Lokal Purwokerto	Purwokerto
2	05040-00003	B. Hijau Banyumas	Banyumas
3	05040-00004	Lokal Purworejo	Purworejo
4	05040-00005	Lokal Wonogiri 5	Wonogiri
5	05040-00006	Lokal Wonogiri 6	Wonogiri
6	05040-00007	Lokal Pasuruan 7	Pasuruan
7	05040-00008	Lokal Pasuruan 8	Pasuruan
8	05040-00009	Lokal Madura	Madura
9	05040-00010	Koro Rawe Wonogiri	Wonogiri

RESULTS AND DISCUSSIONS

Monitoring of Genetic Integrity within Accessions

In general, the planting condition of velvet bean was conducted properly. The plants grow well and produce normal pod and seeds (Fig. 1). An optimal cultivation practice is important in germplasm characterization; thus, germplasm can perform their maximum genetic potential [20]. These potencies need to be discovered through germplasm characterization; thus, they can raise more valuable benefits for crop improvement [21]. Because of germplasm characterization is a dynamic activity and usually require a lot of resources, a genebank manager usually conduct preliminary characterization for their accessions [22]. Characterization of phenotypic diversity is an important first step in the conservation of plant species [20].

TABLE 2. List of velvet bean accessions that exhibit genetic mixture.

No.	Original Accession	Derived Accession
1.	Accession number : 05040-00001 Name : Lokal Purwokerto A Flower color : white Pod hair color : grayish-white	Accession number : 05040-00011 Name : Lokal Purwokerto B Flower color : purple Pod hair color : black
		
2.	Accession number : 05040-00004 Name : Lokal Purworejo A Seed color : white	Accession number : 05040-00012 Name : Lokal Purworejo B Seed color : white
		
3.	Accession number : 05040-00005 Name : Lokal Wonogiri 5A Seed color : white Seed shape : flat	Accession number : 05040-00013 Name : Lokal Wonogiri 5B Seed color : mottled Seed shape : round
		
4.	Accession number : 05040-00007 Name : Lokal Pasuruan 7A Seed size : small	Accession number : 05040-00014 Name : Lokal Pasuruan 7B Seed size : large
		

During this preliminary activity, identification of genetic mixture among plants within same accession should be carried out, particularly at generative and postharvest stage. In both stage of our study, we found four accessions that exhibit genetic mixture. Therefore, we split these mixtures into different accession and assigned a new accession number and name for them (Table 2). Generally, morphological traits become a handy marker to distinguish among

accessions and to identify the genetic integrity within accession. In this study, we utilized the hair color of immature pod, flower color, and seed color as phenotypic marker to assess the genetic integrity within accession.



FIGURE 1. Field condition of velvet bean at Cikeumeuh Experimental Station, ICABIOGRAD, Bogor.

Variability of Morpho-Agronomical Characters

Based on the result of genetic integrity, the total accessions to be observed for characterization become 13 accessions. These accessions showed variability on their morpho-agronomical characters. For qualitative traits, we observed 2 kinds color of the flower, 2 kinds color of immature hairs pod, 2 types of pod itchiness, and 3 kinds color of the seed (Table 3). White flower, greyish white of hairs pod, not itchy pod, and mottled seed become the major phenotype observed among accessions.

The quantitative traits result also varied among accessions (Table 4). Days to flowering ranged from 83–133 days after planting (DAP) and days to first harvesting ranged from 178–228 DAP among accessions. Lokal Purworejo B and Lokal Wonogiri 5 B have earlier flowering days than the others, while Lokal Pasuruan 8 and Lokal Madura have earlier harvesting level compared to others.

Seed character also varied among accessions (Table 5). Hundred-seed weight ranged from 60.00–122.10 g and seed weight per 10 pods ranged from 22.9–53.10 g. Koro Rawe Wonogiri has the smallest seed size and lighter seed weight than other accessions.

TABLE 3. Qualitative traits of velvet bean germplasm in IAARD-ICABIOGRAD Gene Bank.

Accession number	Accession name	Flower color	Hairs color of immature pod	Pod itchiness	Seed color
05040-00001	Lokal Purwokerto A	White	Greyish white	No	Mottled
05040-00003	B. Hijau Banyumas	Purple	Greyish white	No	Mottled
05040-00004	Lokal Purworejo A	White	Black	No	White
05040-00005	Lokal Wonogiri 5A	White	Black	No	White
05040-00006	Lokal Wonogiri 6	White	Greyish white	No	Mottled
05040-00007	Lokal Pasuruan 7A	White	Greyish white	No	Mottled
05040-00008	Lokal Pasuruan 8	White	Black	No	White
05040-00009	Lokal Madura	White	Black	No	White
05040-00010	Koro Rawe Wonogiri	Purple	Greyish white	Yes	Redish black
05040-00011*	Lokal Purwokerto B*	Purple	Black	No	Mottled
05040-00012*	Lokal Purworejo B*	White	Black	No	Mottled
05040-00013*	Lokal Wonogiri 5B*	White	Black	No	Mottled
05040-00014*	Lokal Pasuruan 7B*	White	Greyish white	No	Mottled

*New accession number and names assigned as result of the monitoring of genetic integrity among velvet bean germplasm.

TABLE 4. Agronomic and pod characters of velvet bean germplasm in IAARD-ICABIOGRAD Gene Bank.

Accession number	Accession name	Days to flowering (DAP)	Days to first harvesting (DAP)	Pod length (cm)	Pod width (cm)	Number of seed per pod
05040-00001	Lokal Purwokerto A	126	205	8.80	1.77	5.20
05040-00003	B. Hijau Banyumas	130	228	10.50	1.75	5.90
05040-00004	Lokal Purworejo A	120	188	9.51	1.67	5.30
05040-00005	Lokal Wonogiri 5A	130	220	9.15	1.72	4.50
05040-00006	Lokal Wonogiri 6	133	205	8.70	1.60	4.90
05040-00007	Lokal Pasuruan 7A	110	205	9.95	1.82	5.67
05040-00008	Lokal Pasuruan 8	97	178	9.33	1.79	5.70
05040-00009	Lokal Madura	99	178	10.64	1.62	5.83
05040-00010	Koro Rawe Wonogiri	120	189	7.93	1.69	4.75
05040-00011*	Lokal Purwokerto B*	125	205	9.67	2.63	5.60
05040-00012*	Lokal Purworejo B*	83	197	8.91	1.59	5.50
05040-00013*	Lokal Wonogiri 5B*	89	181	10.25	1.77	5.24
05040-00014*	Lokal Pasuruan 7B*	90	178	10.04	1.70	5.71
Average		111.69	196.69	9.49	1.78	5.37
Standard error		5.26	4.67	0.25	0.10	0.14

*New accession number and names assigned as result of the monitoring of genetic integrity among velvet bean germplasm. DAP = days after planting.

TABLE 5. Seed characters of velvet bean germplasm in IAARD-ICABIOGRAD Gene Bank.

Accession number	Accession name	Seed length (mm)	Seed width (mm)	Seed thickness (mm)	100-seed weight (g)	Seed weight per 10 pods (g)
05040-00001	Lokal Purwokerto A	14.03	10.37	7.08	86.21	42.60
05040-00003	B. Hijau Banyumas	15.78	11.50	8.41	92.21	35.00
05040-00004	Lokal Purworejo A	16.26	11.99	9.41	113.38	46.60
05040-00005	Lokal Wonogiri 5A	14.34	10.91	6.62	101.44	53.10
05040-00006	Lokal Wonogiri 6	15.38	11.35	7.89	97.64	45.00
05040-00007	Lokal Pasuruan 7A	15.47	11.52	7.88	94.06	33.30
05040-00008	Lokal Pasuruan 8	14.68	11.20	8.48	122.10	41.80
05040-00009	Lokal Madura	14.92	11.36	8.80	101.68	39.00
05040-00010	Koro Rawe Wonogiri	14.86	10.39	6.65	60.00	22.90
05040-00011*	Lokal Purwokerto B*	13.88	10.02	7.66	100.84	39.50
05040-00012*	Lokal Purworejo B*	14.08	10.40	7.42	71.84	35.90
05040-00013*	Lokal Wonogiri 5B*	14.54	11.57	13.11	89.00	33.20
05040-00014*	Lokal Pasuruan 7B*	15.69	11.33	6.99	100.97	43.10
Average		14.92	11.07	8.18	94.72	39.31
Standard error		0.20	0.17	0.61	5.45	2.60

*New accession number and names assigned as result of the monitoring of genetic integrity among velvet bean germplasm.

Principal Component Analysis of Quantitative Traits

A total of 10 Principal Components (PCs) were resulted from the analysis with total contribution to the variation of 100%. Generally only PCs with eigenvalue above 1 are used and in our study this meant PC1 to PC4 were eligible. However, since there was one character, i.e. seed thickness, had major contribution on component 5, principal component analysis eventually resulted in five PCs with total contribution to diversity of 91.11% (Table 6).

The first two PCs explained total variation only of 54.37% with almost all characters were drawn in both PCs, except for the pod width (PW) character (Fig. 2). The total variation in this study that can be explained by the PCA analysis was lower than previous report on Indian velvet bean, i.e. 66.34% for the first two PCs. However, some characters agreed with that report in term of major contribution in the first two PCs [23]. These characters were pod length, seed length, seed width, seed thickness, and 100-seed weight. Based on this agreement we can stated that the pod and seed characters are varied among velvet bean germplasm, thus may be applied to distinguish among accessions, especially for monitoring genetic integrity.

TABLE 6. The principal component result of velvet bean germplasm based on 10 agronomical characters.

Character	PC1	PC2	PC3	PC4	PC5
Days to flowering (DAP)	6.701	25.589	0.007	9.265	4.104
Days to first harvesting (DAP)	6.364	15.388	1.156	22.774	1.143
Pod length (cm)	18.550	0.037	10.289	6.004	0.213
Pod width (cm)	1.659	0.001	44.761	1.031	3.357
Number of seed per pod	11.365	2.947	13.948	8.213	21.703
Seed weight per 10 pods (g)	0.384	26.693	1.332	27.797	0.422
Seed length (mm)	10.790	6.693	12.443	11.483	5.263
Seed width (mm)	21.560	4.852	8.296	0.993	2.040
Seed thickness (mm)	12.122	3.261	0.010	0.000	61.390
100-seed weight (g)	10.505	14.539	7.759	12.441	0.363
Eigenvalue	3.33	2.11	1.68	1.16	0.83
Percentage of variance	33.29	21.07	16.84	11.65	8.26
Cumulative percentage of variance	33.29	54.37	71.21	82.85	91.11

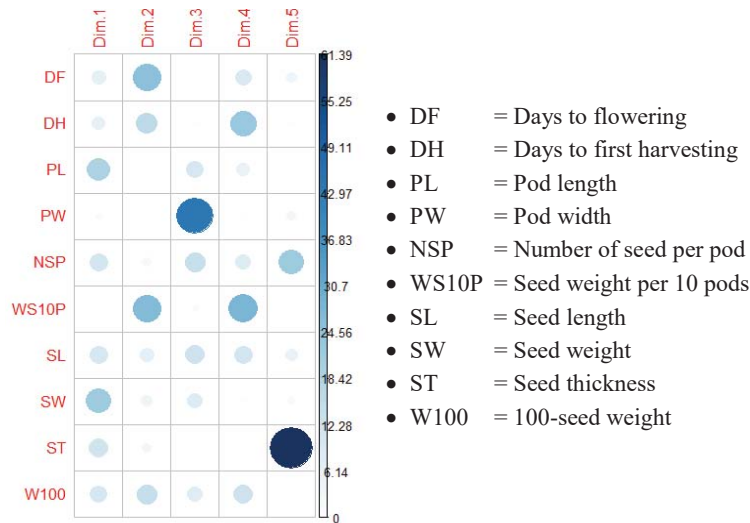


FIGURE 2. Correlation plot showing contribution of each character on the first five components. The value at the axis showed the percentage of character contribution to each PC, higher values are represented by darker color and *vice versa*.

Among 10 quantitative characters observed, only 3 characters that had major contribution to specific PCs, i.e. pod width, seed weight per 10 pods, and seed thickness (Fig. 2). Pod width contributed on PC1, seed weight per 10 pods contributed to PC2 and PC4, and seed thickness contributed to PC5. Meanwhile, the rest characters were contributed relatively equal on fifth PCs. Therefore, it was quite difficult to determine a particular character as group identity in further performing cluster analysis. In the study of ornamental chili lines evaluation, several

morphological characters were identified to be specific through PCA analysis and can be used as marker for the released of new variety [24]. Therefore, more comprehensive characterization on morphological and agronomical characters should be done as well for velvet bean germplasm at IAARD-ICABIOGRAD Gene Bank to obtain a better result.

The biplot analysis was conducted to know further relationship among accessions and associate characters in general. There are four information can be obtained from a biplot analysis, i.e. relationship among accessions, variability of the characters, correlation among characters, and relative position of accession to character [25]. In term of relationship among accessions, the result showed that a wide genetic distance was prevalent among accessions, indicated by the wide spread of the accession in the biplot graphic (Fig. 3). This may occur by exchange or distribution of accessions among regions as reported by similar result in cowpea [26] and mung bean [27].

The lines in biplot graphic showed the information for the variables or characters observed in the study. The result indicated that several characters had higher contribution to the diversity on PC1 and PC2 than others, i.e. days to first flowering, pod length, seed width, and seed weight per 10 pods. These characters had longer line than others. Correlation among characters can be seen from the line's direction. The result showed that seed length and seed weight correlated with 100-seed weight, meant that longer and wider seed are heavy. In the study that has been reported in several cocoa hybrids, the hybrid with bigger seed has better germination and growth vigor in the field [28]. Another character correlation was also inferred by days to flowering and days to first harvesting, meant that all accessions had same period of generative stage (fast flowering, fast harvesting, and oppositely).

From the relative position of the accessions to the lines in the biplot graphic, the result showed that some accessions grouped in the same group with particular characters (Fig. 3). Accessions Lokal Wonogiri 5A and Lokal Wonogiri 6 were in the same group and characterized by days to flowering and days to first harvesting. While accessions Lokal Hijau Banyumas and Lokal Purworejo A were grouped together with 100-seed weight as the group identity. From this biplot we can also inferred that velvet bean from East Java Province, i.e. Madura and Pasuruan, grouped together and had same characteristic in number of seed per pod.

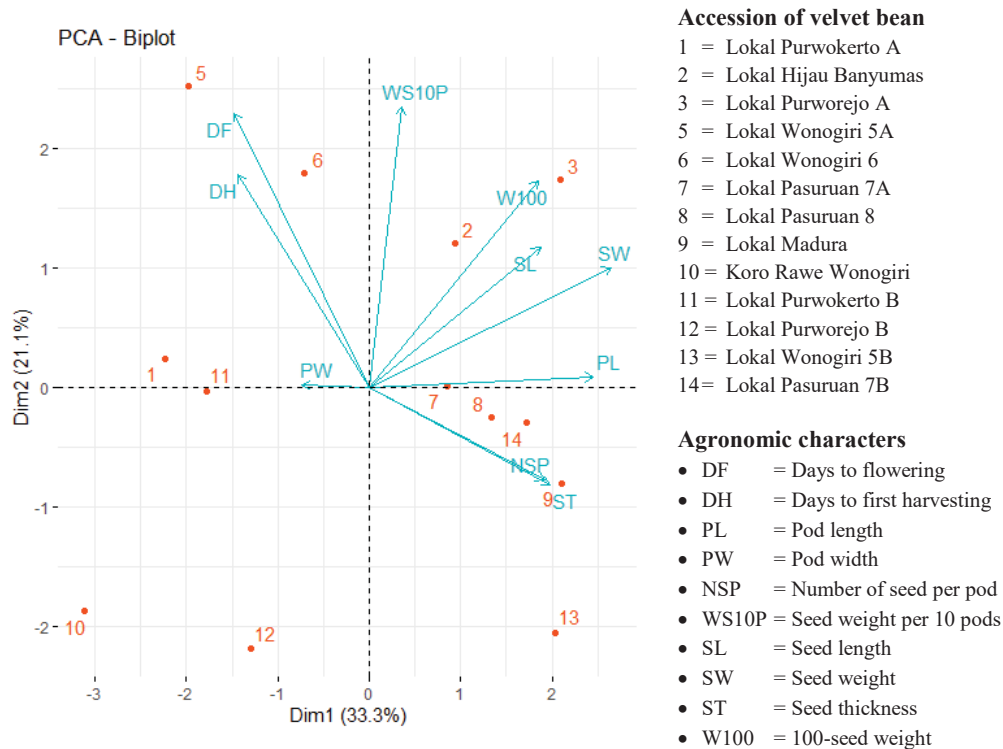


FIGURE 3. Biplot of 13 accessions based on 10 agronomic characters of the first two principal components.

Cluster Analysis among Accessions

The dendrogram generate from morpho-agronomical characters from 13 accessions of velvet bean is given in Fig 4. Average linkage was used as clustering method based on Gower distance. At 0.34 coefficient dissimilarity, the accessions were group into four clusters. Cluster profile is in Table 7.

TABLE 7. Cluster profile of 13 accessions of velvet bean.

Cluster	Number of accessions	Name of accessions
I	1	Koro Rawe Wonogiri
II	1	Lokal Purwokerto B
III	6	Lokal Wonogiri 5 B, Lokal Purworejo B, Lokal Wonogiri 5A, Lokal Madura, Lokal Pasuruan 8, Lokal Purworejo A
IV	5	Lokal Hijau Banyumas, Lokal Pasuruan 7B, Lokal Pasuruan 7A, Lokal Wonogiri 6 and Lokal Puwokerto A

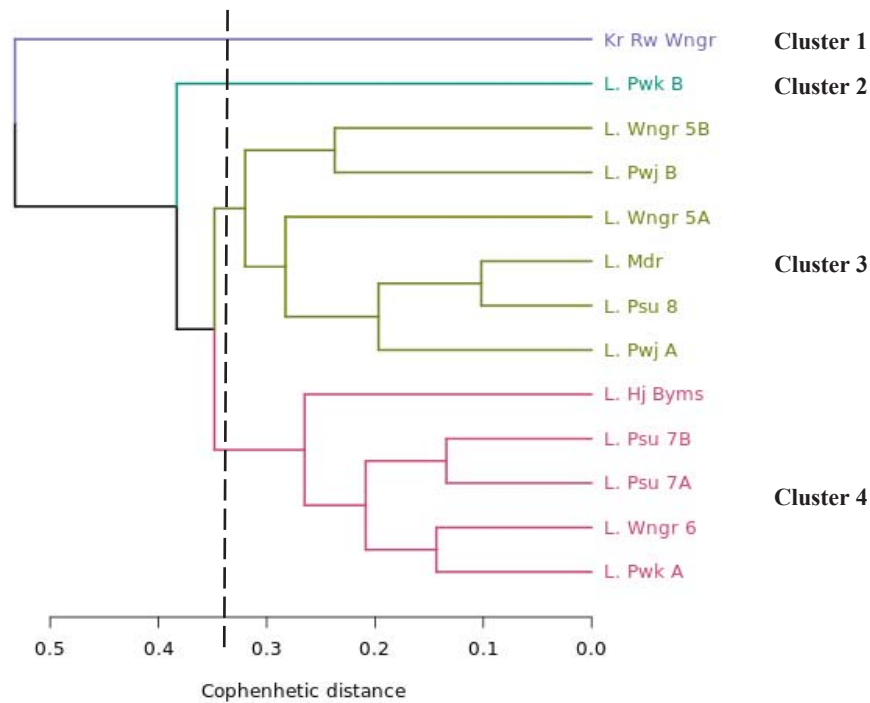


FIGURE 4. Dendrogram of dissimilarity of velvet bean germplasm conserved by IAARD-ICABIOGRAD Gene Bank based on 13 morpho-agronomical characters.

The dendrogram tends to group some of accession with similar morphological traits into the same cluster. Cluster I (Koro Rawe Wonogiri) is indicated by itchy hair pod and reddish black seed color. Cluster II (Lokal Purwokerto B) is indicated by purple flower color and mottled seed color. Cluster I and II were not clustered with any cluster formed. Cluster III was the largest consist of 6 accessions or 46.15% of the accessions belong to this cluster indicated by white flower color and black hairs pod color of immature pod. Cluster IV consist of 5 accessions (38.46%) as greyish-white hairs pod color of immature pod and mottled seed color.

TABLE 8. Average value of 4 clusters of 10 characters quantitative in 13 accessions of velvet bean.

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Average
Days to flowering	120	125	103.00	117.8	115.27
Days to first harvesting	189	205	190.33	203.2	199.84
Pod length (cm)	7.93	9.67	9.63	9.60	9.63
Pod width (cm)	1.69	2.63	1.69	1.73	2.02
Number of seed per pod	4.75	5.60	5.35	5.48	5.47
Seed weight per 10 pods (g)	22.90	39.50	41.60	39.80	40.30
Seed length (mm)	14.86	13.88	14.80	15.27	14.65
Seed width (mm)	10.39	10.02	11.24	11.21	10.82
Seed thickness (mm)	6.65	7.66	8.97	7.65	8.09
100-seed weight (g)	60.00	100.84	99.91	94.22	98.32

The cluster mean value of quantitative characters has been presented in Table 8. The mean data of observation revealed that differences in cluster mean value had existed. Cluster I had one accession (Koro Rawe Wonogiri) which was characterized as having above average value for days to flowering and seed length. Cluster II also had one accession (Lokal Purwokerto B) that almost all characters having above average value except seed characters (seed weight per 10 pods, seed length, seed width, and seed thickness). Cluster III had 6 accessions which characterized having above for seed character such as seed weight per 10 pods, seed length, seed width, seed thickness, and 100-seed weight. Cluster IV consisted of 5 accessions which having above average value for days to flowering, days to first harvesting, number of seed per pod and seed width.

Dendrogram from this study does not distinct grouping according to geographical origin. This also reported in Indian *Mucuna* germplasm which also cannot differentiate the germplasm observed based on their area origin [29].

CONCLUSION

On the velvet bean germplasm accessions were have variations based on morpho-agronomical characters. PC analysis was indicated that flowering days, pod length, seed width, and seed weight per 10 pods highly contributed to the diversity. The clustering analysis, the accessions were grouped into four clusters. Accession Koro Rawe Wonogiri was the most distinct genotype among accessions observed. The further comprehensive characterization which includes yield components should be carried out to reveal more information about diversity among velvet bean germplasm in IAARD-ICABIOGRAD Gene Bank.

ACKNOWLEDGMENTS

Authors thank Suparjo for preparing the seed, Jumanta for maintaining the seed integrity, and DIPA ICABIOGRAD fiscal year of 2019 for financial support of this study.

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