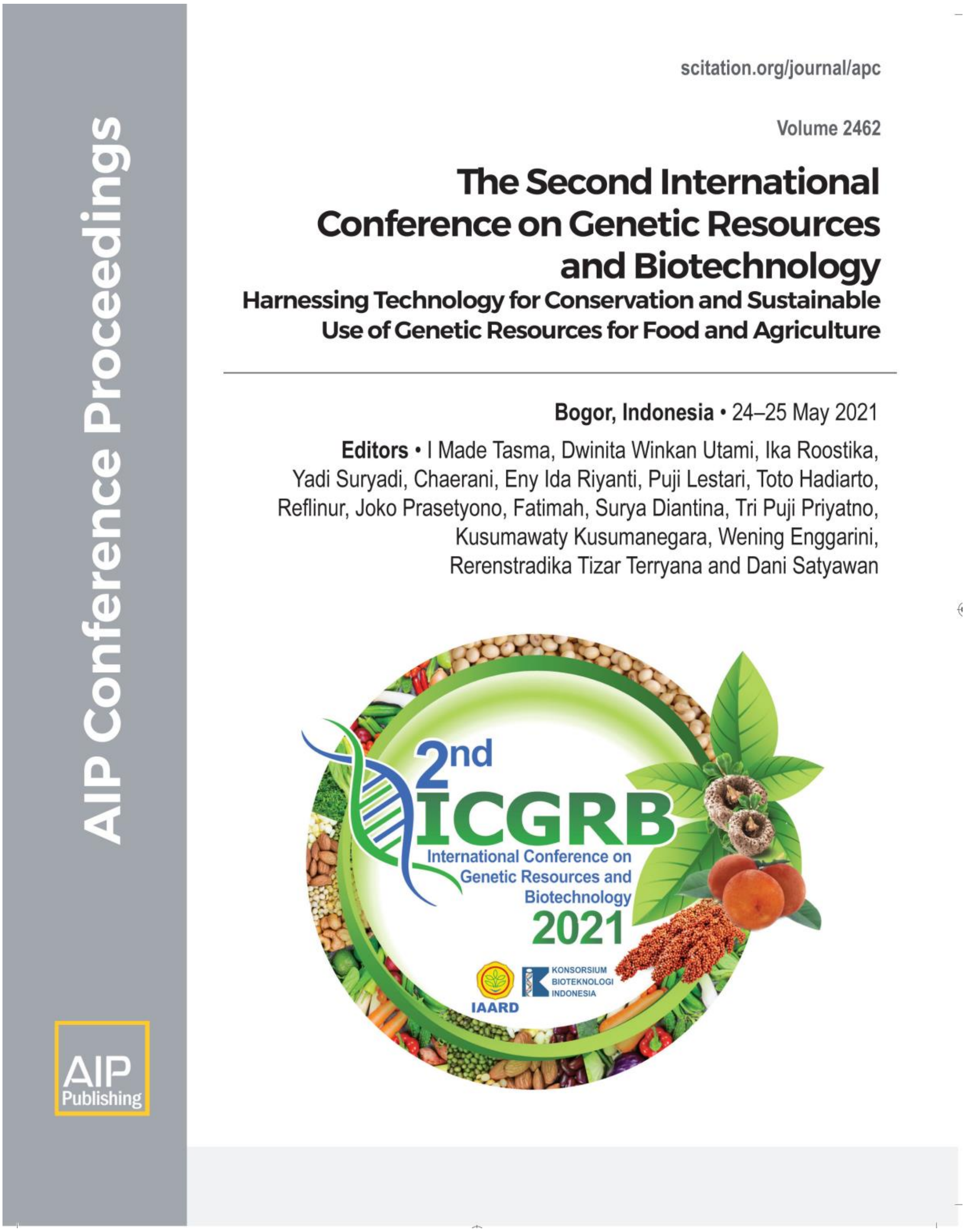

January 2022

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

Steering, Scientific and Organizing Committees

Steering Committee

Chair:

Dr. Ir. Fadjry Djufry, M.Si , *Director General of Indonesian Agency for Agricultural Research and Development (IAARD), Ministry of Agriculture, Indonesia*

Vice Chair:

Ir. Mastur Ph.D, *Director of Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Ministry of Agriculture, Indonesia*

Dr. Siswa Setyahadi, *Head of Indonesian Biotechnology Consortium, Indonesia*

Secretary:

Dr. Sustiprijatno, *Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Ministry of Agriculture, Indonesia*

Scientific Committee

Prof. Dr. M. Sabran, *Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Ministry of Agriculture, Indonesia*

Prof. Dr. Bahagiawati A., *Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Ministry of Agriculture, Indonesia*

Prof. Endang Gati Lestari, *Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Ministry of Agriculture, Indonesia*

Associate Prof. Endang Septiningsih, *Texas A & M University, USA*

Dr. Prakit Somta, *Kasetsart University, Thailand*

Dr. Laosatit Kularb, *Kasetsart University, Thailand*

Dr. Back Ki Kim, *Seoul National University, South Korea*

Dr. Iswari Saraswati Dewi, *Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Ministry of Agriculture, Indonesia*

Dr. Puji Lestari, *Indonesian Center for Rice Research, IAARD, Ministry of Agriculture, Indonesia*

Dr. Dani Satyawan, *Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Ministry of Agriculture, Indonesia*

Dr. Alina Akhdiya, *Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Ministry of Agriculture, Indonesia*

Ir. Tri Puji Priyatno, PhD, *Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Ministry of Agriculture, Indonesia*

Dr. Ir. Ragapadmi Purnamaningsih, *Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Ministry of Agriculture, Indonesia*

Dr. Nurul Hidayatun, *Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Ministry of Agriculture, Indonesia*

The Second International Conference on Genetic Resources and Biotechnology
AIP Conf. Proc. 2462, 010002-1–010002-3; https://doi.org/10.1063/12.0008934
Published by AIP Publishing. 978-0-7354-4172-9/$30.00

Organizing Committee

Chair	:	Dr. Toto Hadiarto
Vice Chair	:	Dr. Dani Satyawan
Secretary	:	Dr. Wening Enggarini
		Rerenstradika Tizar Terryana, M.Si
Treasurer	:	Dra. Sih Parmiyatni
		Ma’sumah, S.Si
Publication and documentation:		
		Dr. Hakim Kurniawan
		Endo Kristiyono, M.T.I.
		Andika Bakti, S.I.Kom
		Ansori
Logistic	:	Wawan, M.Si.
		M. Hasni Zulfikar

Preface: The Second International Conference on Genetic Resources and Biotechnology

Cite as: AIP Conference Proceedings **2462**, 010001 (2022); https://doi.org/10.1063/12.0006897
Published Online: 19 January 2022

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 24^{th}-25^{th} of May 2021virtually 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

AIP Conf. Proc. 2462, 010001-1–010001-1; https://doi.org/10.1063/12.0006897
Published by AIP Publishing. 978-0-7354-4172-9/$30.00

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

PREV

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

PRELIMINARY

AIP Conference Proceedings **2462**, 010001 (2022); https://doi.org/10.1063/12.0006897

-
    - PDF
    - E-READER
    - ADD TO FAVORITES
    - SHARE
    - EXPORT CITATION

FreeJanuary 2022

Committees: The Second International Conference on Genetic Resources and Biotechnology

AIP Conference Proceedings **2462**, 010002 (2022); https://doi.org/10.1063/12.0008934

-
    - PDF
    - E-READER
    - ADD TO FAVORITES
    - SHARE
    - EXPORT CITATION

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

FreeJanuary 2022

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

- SHOW ABSTRACT
-
    - PDF
    - E-READER
    - ADD TO FAVORITES
    - SHARE
    - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER

- ADD TO FAVORITES
- SHARE
- EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT

-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT

-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

Identifying potential seedless citrus accessions through floral structure and pollen performance

Baiq Dina Mariana, Anis Andrini and Sri Andayani
AIP Conference Proceedings **2462**, 020021 (2022); https://doi.org/10.1063/5.0076922

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT

-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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 Aswidinnoor and Hakim Kurniawan
AIP Conference Proceedings **2462**, 020023 (2022); https://doi.org/10.1063/5.0075706

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

Setyorini Widyayanti, Sutarno, Endang Wisnu Wiranti and Kristamtini
AIP Conference Proceedings **2462**, 020024 (2022); https://doi.org/10.1063/5.0075721

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT

-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

Andri Fadillah Martin, Dyah Retno Wulandari, Tri Muji Ermayanti, Betalini Widhi Hapsari, Erwin Al Hafiizh and Laela Sari
AIP Conference Proceedings **2462**, 020029 (2022); https://doi.org/10.1063/5.0075173

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER

- ADD TO FAVORITES
- SHARE
- EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

Tatik Khusniati, Ika, Harry Noviardi and Sulistiani
AIP Conference Proceedings **2462**, 020035 (2022); https://doi.org/10.1063/5.0076004

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

Rinda Kirana, Catur Hermanto, Reflinur and Derek W. Barchenger
AIP Conference Proceedings **2462**, 020036 (2022); https://doi.org/10.1063/5.0075186

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

The growth of garlic internal sprout on different storage condition

Chotimatul Azmi, Imas Rita Saadah, Nazly Aswani and Asih Kartasih Karjadi
AIP Conference Proceedings **2462**, 020037 (2022); https://doi.org/10.1063/5.0075180

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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
AIP Conference Proceedings **2462**, 020038 (2022); https://doi.org/10.1063/5.0077390

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

APPLICATION OF GENOMICS AND MOLECULAR MARKERS FOR GENETIC RESOURCE CONSERVATION AND CROP ADAPTATION TO CLIMATE CHANGE

FreeJanuary 2022

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

Muhamad Sabran, Dwinita Wikan Utami and Susilawati
AIP Conference Proceedings **2462**, 030001 (2022); https://doi.org/10.1063/5.0075202

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

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
AIP Conference Proceedings **2462**, 030003 (2022); https://doi.org/10.1063/5.0075665

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

Joko Prasetiyono, Tio Fadel Rafsanjani, Tri Aminingsih, Tasliah and Sugiono Moeljopawiro
AIP Conference Proceedings **2462**, 030004 (2022); https://doi.org/10.1063/5.0075660

- SHOW ABSTRACT

-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

Tasliah, Kurniawan Rudi Trijatmiko and Joko Prasetiyono
AIP Conference Proceedings **2462**, 030006 (2022); https://doi.org/10.1063/5.0075661

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

Hybrid purity assessment in F_1 hybrids segregating for phytophthora root rot resistance genes of chili pepper (*Capsicum annuum* L.)

Fatimah, Reflinur, Joko Prasetiyono, Wartono, Kristianto Nugroho, Rinda Kirana, Dani Satyawan, Rerenstradika Tizar Terryana, Aqwin Polosoro, Puji Lestari and I. Made Tasma
AIP Conference Proceedings **2462**, 030007 (2022); https://doi.org/10.1063/5.0075160

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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
AIP Conference Proceedings **2462**, 030008 (2022); https://doi.org/10.1063/5.0075392

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT

-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

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

PREV

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES

- SHARE
- EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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
AIP Conference Proceedings **2462**, 040006 (2022); https://doi.org/10.1063/5.0075603

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

The effect of $FeSO_4$ concentration on the callus growth of two chili (*Capsicum annuum* 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

- SHOW ABSTRACT
-
  - PDF

- E-READER
- ADD TO FAVORITES
- SHARE
- EXPORT CITATION

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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 Hafiizh and Tri Muji Ermayanti
AIP Conference Proceedings **2462**, 060002 (2022); https://doi.org/10.1063/5.0075503

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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
AIP Conference Proceedings **2462**, 060009 (2022); https://doi.org/10.1063/5.0075712

- SHOW ABSTRACT

-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

FreeJanuary 2022

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

- SHOW ABSTRACT
-
  - PDF
  - E-READER
  - ADD TO FAVORITES
  - SHARE
  - EXPORT CITATION

Characterization of genomic variation on three Indonesian oil palm genotypes analyzed using next-generation sequencing HiSeq

Cite as: AIP Conference Proceedings **2462**, 030008 (2022); https://doi.org/10.1063/5.0075392
Published Online: 19 January 2022

I. Made Tasma, Habib Rijzaani, Dani Satyawan, et al.

Characterization of Genomic Variation on Three Indonesian Oil Palm Genotypes Analyzed Using Next-Generation Sequencing HiSeq

I Made Tasma[1, a)], Habib Rijzaani[1], Dani Satyawan[1], Ida Rosdianti[1], Edy Supriyanto[2] and Razak Purba[2]

[1]*Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Jln. Tentara Pelajar No. 3A, Bogor 16111, West Java, Indonesia*
[2]*Indonesian Oil Palm Research Institute (IOPRI), Jln. Brigjen Katamso No. 51, Medan 20158, North Sumatra, Indonesia*

[a)]Corresponding author: imade.tasma@gmail.com

Abstract. Oil palm is an important estate crop and Indonesia is the largest palm oil producer in the world. Since the average yield is relatively low, a more efficient breeding program that utilizes the latest technological developments in DNA analysis is necessary. The objectives of this study were to (1) characterize genomic variations of three Indonesian oil palm genotypes based on whole genome sequencing using next-generation sequencing (NGS) HiSeq; (2) provide genomic data resources for future oil palm breeding program. Whole genome sequencing was performed on three Indonesian oil palm genotypes (Dura, Pisifera, and *Elaeis oleifera* from Brazil). Sequence data were aligned with that of the *Eg5* genome reference sequences. The average sequence coverage depth for all loci was 34 and more than 95% of the genome was sequenced at least ten times. Comparison of the sequences revealed 3,735,311 sequence changes, an average of one sequence change per 197 bases. Among these changes, 3,371,088 were SNPs and 364,233 were insertions and deletions (indels). DNA variations found within exons total 329,087. Of these, 214,068 SNPs variations were capable of causing modification in the amino acid composition of the encoded proteins (nonsynonymous mutations). A genomic database was constructed to manage DNA variations resulted from this study. The SNPs collected from this study should be useful for constructing high density oil palm SNP chip to expedite future national oil palm breeding program.

INTRODUCTION

Oil palm (*Elaeis guineensis*) is the most important estate crop in Indonesia. Indonesia is the largest palm oil producer of the world, even though it is not a native plant of this country. However, oil palm annual average yield is still low. There is a huge gap between the theoretical oil palm yield potential of about 18 t/ha/year [1] compared to that of the Indonesian oil palm yield average of about 4 t/ha/year [2]. This yield gap should be narrowed down by developing high yielding oil palm variety by applying a modern breeding method, e.g. molecular breeding based on genomic data.

Oil palm genome reference sequences of two oil palm genotypes have been constructed and are publicly accessible [3, 4], i.e. the ones derived from *E. guineensis* and *E. oleifera*. These reference genome sequences are important fundamental resources to enable in identifying genetic variations across oil palm genetic resources to obtain the ones important for breeding purposes and to develop molecular markers as well as gene discovery useful for breeding purposes.

Recent development of biotechnology techniques that utilize DNA-based tools, such as marker-assisted selection and genomic selection, should be explored to improve the speed and efficiency of oil palm breeding programs. Next-generation sequencing (NGS) technology has capabilities to sequence whole complexed genomes such as oil palm that has genome size of about 1.8 GB in a shorter time with lower per unit data sequencing cost [5, 6]. This opens

The Second International Conference on Genetic Resources and Biotechnology
AIP Conf. Proc. 2462, 030008-1–030008-6; https://doi.org/10.1063/5.0075392
Published by AIP Publishing. 978-0-7354-4172-9/$30.00

the way to re-sequence every genotype of oil palm collection to comprehensively understand the genetic make-up of each oil palm genotype through resequencing the genome simultaneously. By resequencing, one will be able to discover the genetic variations of the targeted traits and identify the plants having the genes and alleles to be used in a breeding program of that particular trait. In summary, the use of NGS can assist the design of a large number of DNA markers, which would be useful for fine mapping, genome-wide association studies and genomic selection of important characters targeted for breeding purposes [7].

This study was intended to assist future oil breeding programs in Indonesia by characterizing the genomes of local oil palm genotypes. Whole genome sequencing was performed on three selected local genotypes in order to (1) identify genetic mutations across the three oil palm genotypes by comparing to the oil palm reference genome sequence *Eg5*, and (2) to identify allelic variation that changes amino acid sequences and the variations of which should be useful for the development of DNA markers and gene discovery for future oil palm breeding programs in Indonesia.

MATERIALS AND METHODS

Plant Materials

The plant materials consisted of three oil palm genotypes from Indonesia, namely Dura, Pisifera, and a genotype of *E. oleifera* (originated from Brazil). The three genotypes were selected based on several criteria, such as the presence of useful traits, their utilization in breeding programs, and genetic diversity according to a previous phylogenetic study using simple sequence repeat (SSR) markers [8–10]. The oil palm genotypes were obtained from the collection of the Indonesian Oil Palm Research Institute (IOPRI), Medan, Indonesia.

Genomic DNA Isolation and Library Construction

Genomic DNAs of the three oil palm genotypes used in this study were isolated from young leaf using CTAB buffer by following the method of Michiels *et al*. [11] with small modification as reported by Satyawan and Tasma [12]. DNA concentration and purity were then measured using a nanodrop spectrophotometer (Thermo Scientific, USA). DNA was also electrophoresed in 1% agarose gel [13] and the DNA bands were visualized with a ChemiDoc (Bio-Rad, USA). Genomic DNA library construction was conducted using the Illumina TruSeq DNA low throughput (LT) protocol (Illumina Inc., USA) using a recommended procedure [14, 15]. In brief, the procedure included DNA fragmentation, DNA end modification, adenylation of 3’ end, adaptor ligation and purification, PCR amplification, and validation of the constructed oil palm genomic library. The library concentration and quality were measured using RT-PCR method.

Whole Genome Sequencing of Three Oil Palm Genotypes

Genome sequencing process of the constructed oil palm genomic libraries consisted of two steps, i.e. DNA clusterization in a DNA cluster platform (cBot) and sequencing of the clustered genomic DNA using an NGS HiSeq 2000. DNA cluster generation was conducted using the cluster generation protocol, reagents, and kits from Illumina (Illumina Inc., USA) [16]. The sequencing of the clustered libraries was performed using sequencing reagents and kit from Illumina (Illumina Inc., USA) according to the sequencing procedure as previously reported [15, 17]. A paired-end genome deep sequencing method was accomplished for the three oil palm genotypes using a total of 200 cycles for both sequencing reads.

Detection of DNA Variations across Oil Palm Genome

The quality of sequence data resulted from this study were analyzed and the good quality sequence data were aligned to that of the *Eg5* oil palm genome reference sequence [3]. The reference sequence was downloaded from Phytozome (www.phytozome.net). The sequence alignment was done by using Bowtie2 [18]. The sequence alignments were followed by single-nucleotide polymorphism (SNP) calling using the program mpileup in Samtools [19]. Annotation of the locations and predicted effects of the SNPs was performed using SNPEff [20]. Phylogenetic analysis and tree construction were carried out using DarWin [21]. Tree drawing was generated in Dendroscope [22].

RESULTS AND DISCUSSIONS

Sequencing Depth

The average sequence coverage depth for all loci was 34, and more than 95% of the genome was sequenced at least ten times. This average depth exceeding 30 times was the *de facto* standard [23] and the type of genome sequence coverage was classified as a deep sequencing data [24]. The coverage obtained from this study is very excellent to be used to obtain high quality SNPs and insertions and deletions (indels) as the more sequence overlapping would be obtained within the identified SNP or indel that increase SNP/indel discovery accuracy. The identified SNPs/indels, therefore, should be more reliable for further analysis and future breeding application purposes.

Analysis of Genomic DNA Variations

In total, we identified 3,735,311 sequence differences from all three genome sequences of Dura, Pisifera, and Brazilian *E. oleifera* with an average of one sequence change per 197 bases (Table 1). Among these variations, 3,371,088 were SNPs and 364,233 were indels. The number of variations varied in different parts across oil palm chromosomes. The DNA variations were observed in different regions across the oil palm genomes. The majority of the genome variations were discovered outside protein coding regions (exons). These included the intergenic region (upstream region, downstream region, and intron) (Table 2). DNA variations located within the gene sequences (exon, intron, and untranslated regions) were 19.39% (Table 2, Fig. 1). Among the genic SNPs discovered, only 329,087 (8.25%) sequence changes were located in exons (Table 2).

TABLE 1. The number of DNA changes and the rate of DNA changes detected in each of the oil palm chromosomes after comparison three genome sequences of Dura, Pisifera, and Brazilian *Elaeis oleifera*.

Chromosome	Length	Changes	Change rate
EG5_Chr1	68,432,966	325,213	210
EG5_Chr2	65,556,141	347,672	188
EG5_Chr3	60,058,032	300,326	199
EG5_Chr4	57,248,047	291,200	196
EG5_Chr5	51,953,839	282,277	184
EG5_Chr6	44,354,769	200,964	220
EG5_Chr7	43,453,266	211,879	205
EG5_Chr8	40,192,799	198,996	201
EG5_Chr9	38,054,796	182,000	209
EG5_Chr10	31,889,635	147,495	216
EG5_Chr11	30,067,610	157,672	190
EG5_Chr12	28,799,275	169,641	169
EG5_Chr13	27,816,170	147,132	189
EG5_Chr14	24,378,543	139,278	175
EG5_Chr15	24,313,565	125,175	194
EG5_Chr16	21,370,583	108,391	197
Total/average	**657,940,036**	**3,735,311**	**197**

TABLE 2. Number of DNA variations observed across chromosomal regions.

Chromosome region	Number of DNA variations observed	%
Upstream	584,063	13.06
Downstream	551,772	12.34
Intergenic	2,782,751	54.31
Intron	492,316	11.01
Exon	329,087	8.25
Not identified*	4,234	0.11
Splice site acceptor	84	0.01
Splice site donor	85	0.01

*The location of DNA variations in the chromosome cannot be determined.

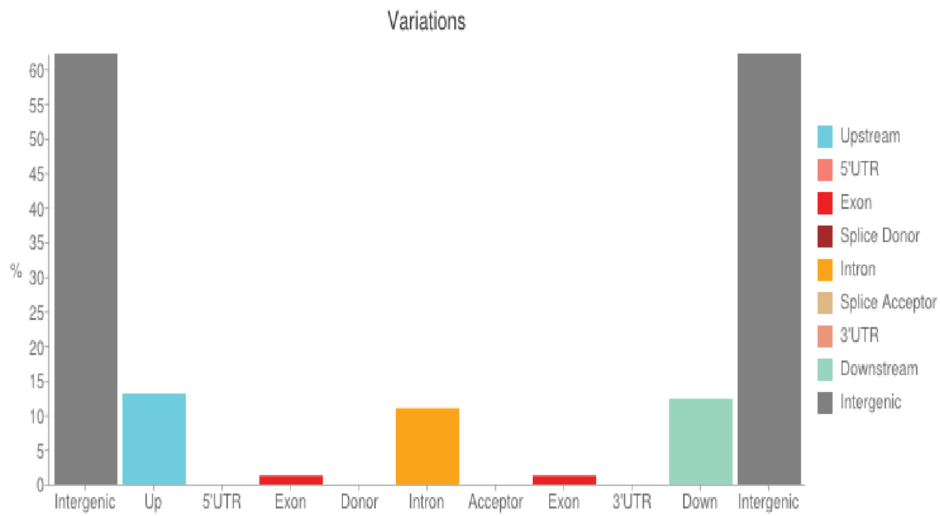

FIGURE 1. Distribution of genomic variation observed across the oil palm chromosomes based on next-gen re-sequence data of three Indonesian oil palm genotypes.

Observation of Exon-Based SNP Variations

To assist future research in fine mapping and gene identification using quantitative trait loci (QTL) mapping and association studies, sequence variations in exon regions were further characterized (Table 3). For breeding and gene discovery purposes, characterization of DNA variations located within the genic regions should be of utmost interest.

Out of 832,783 genic SNPs identified from this study, 322,788 SNPs were located within the exon (Table 3). Of those, 108,720 SNPs were synonymous (i.e. do not change amino acid composition of the encoded proteins) and thus did not affect gene function. The other 214,068 SNPs were nonsynonymous (i.e. cause the changes of amino acid composition of the proteins encoded by the genes containing the SNPs). This later type of SNPs certainly affects the protein composition, and might, therefore, affect the gene function. The majority of the nonsynonymous SNPs (188,949) were missense mutations (mutations that change amino acid) and the rest caused either change in stop and start codons or splice sites (Table 3) during RNA processing. These latest SNP types also significantly affect gene function through the loss of functions of the genes containing such types of SNPs.

A lower number of genic indels were also observed. Among 219,126 identified, only 6,299 indels were located within the exons. The remaining majority was located within introns that were spliced out during RNA processing. The majority of the exon indels caused protein frameshift that might cause those proteins not to function properly. Table 3 also categorizes the non-silent mutations according to their effect on mRNA/protein composition and lists the number of mutations of each type. This information is important for further analysis of such mutations for the ones who are interested in functional genomics of such gene mutations.

TABLE 3. Number and types of DNA sequence variations detected based the sequence data of the three Indonesian oil palm genotypes.

Types of DNA variation	Number of DNA variations observed
Number of total variants	
SNP	3,371,088
Indel	364,233
Genic SNPs	
In introns	509,995
In exon	322,788
Synonymous	108,720
Nonsynonymous	214,068
Missense	108,499
Start codons gained	8,133
Start codons lost	616
Stop codons gained	10,078
Stop codons lost	1,355
Splice site acceptor	2,536
Splice site donor	2,401
Genic indels	
In introns	212,827
In exon	6,299
Frameshift	5,359
Codon change plus codon deletion	173
Codon change plus codon insertion	304
Codon deletion	260
Codon insertion	203

Genome Database of the Oil Palm Genomic Variation

A genomic database termed as The Indonesian Center for Agricultural Genomics (ICAG) (http://genome.pertanian.go.id) was constructed to house the genomic data of eight Indonesian important crops including oil palm and an animal species (cow) [25, 26]. The database contents have been regularly updated to incorporate new developed data into the database. These include the incorporation of 96 SNP markers into the database resulted from an IAARD oil palm SNP marker development project [26]. The genomic data may be accessible to the scientific community interested in genetic data such as that for DNA marker development, gene discovery, as well as for searching other types of DNA variations that might be useful resources for genetic studies as well as for supporting future oil palm cultivar development.

CONCLUSION

A total of three Indonesian oil palm genotypes (Dura, Pisifera, and *E. oleifera* from Brazil) were sequenced their whole genomes using NGS HiSeq. The average sequence coverage depth was 34 and more than 95% of the genome was sequenced at least ten times. Comparison of the sequences to that of the *Eg5* oil palm reference genome sequence revealed 3,735,311 sequence variations with an average of one sequence change per 197 bases. A total of 3,371,088 SNPs and 364,233 indels were discovered from this study. Among the SNPs discovered a total of 329,087 were variations within the exon and 214,068 SNPs of the DNA variations were capable of causing mutations that would modify the amino acid composition of the encoded proteins. A genomic database was constructed to manage DNA variations resulted from this study. The SNPs and indels collected from this study should be useful for future oil palm breeding program.

ACKNOWLEDGMENTS

This study was funded by the 2012–2014 Indonesian Government Grant from the Indonesian Agency for Agricultural Research and Development, Ministry of Agriculture.

REFERENCES

1. R. Singh, S. G. Tan, J. M. Panandam, R. A. Rahman, L. C. Ooi and E. T. Low, BMC Plant Biol. **9**, 114–123 (2009).
2. I. M. Tasma, Perspektif **15**, 46–68 (2016).
3. R. Singh, M. Ong-Abdullah, E. T. L. Low, M. A. Manaf, R. Rosli, R. Nookiah, L. C. L. Ooi, S. E. Ooi, K. L. Chan, M. A. Halim *et al.*, Nature **500**, 335–339 (2013).
4. J. Jin, M. Leel, B. Bai, Y. Sun, J. Qu, Rahmadsyah, Y. Alfiko, C. H. Lim, A. Suwanto, M. Sugiharti, L. Wong, J. Ye, N. H. Chua and G. H. Yue, DNA Res. **23**, 1–7 (2016).
5. S. C. Schuster, Nat. Method **5**, 16–18 (2008).
6. J. Zhang, R. Chiodini, A. Badr and G. Zhang, J. Genet. Genomics **38**, 95–109 (2011).
7. D. Chagne, R. N. Crowhurst, M. Troggio *et al.*, PLoS One **7**, e31745 (2012).
8. I. M. Tasma, A. Warsun, D. Satyawan, Syafaruddin and B. Martono, J. AgroBiogen **9**, 19–27 (2013).
9. I. M. Tasma and S. Arumsari, J. Littri. **19**, 194–202 (2013).
10. I. M. Tasma, Bul. Palma **15**, 1–13 (2014).
11. A. N. Michiels, V. D. E. Wim, M. Tucker, R. Liesbet and L. Van Andre, Analyt. Biochem. **315**, 85–89 (2003).
12. D. Satyawan and I. M. Tasma, Bul. Ris. Tan. Indust. **2**, 411–419 (2012).
13. J. Sambrook, E. F. Fritch and T. Maniatis, *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, New York, 1989), 422 pp.
14. I. M. Tasma, D. Satyawan, H. Rijzaani and Rubiyo, Bul. Ris. Tan. Remp. Aneka Tan. Indust. **3**, 99–108 (2012).
15. I. M. Tasma, D. Satyawan and H. Rijzaani, J. AgroBiogen **11**, 7 (2015).
16. S. Quail, Nat. Methods **5**, 1005–1010 (2008).
17. D. Satyawan, H. Rijzaani and I. M. Tasma, Plant Genet. Resour. **S1**, S109–S113 (2014).
18. B. Langmead and S. L. Salzberg, Nat. Methods **9**, 357–359 (2012).
19. H. Li, B. Handsaker, A. Wysoker *et al.*, Bioinformatics **25**, 2078–2079 (2009).
20. P. Cingolani, A. Platts, M. Coon *et al.*, Fly **6**, 80–92 (2012).
21. X. Perrier and J. Jacquemoud-Collet, Nat. Methods **5**, 1005–1010 (2006).
22. D. H. Huson and C. Scornavacca, Syst. Biol. **61**, 1061–1067 (2012).
23. S. M. Ahn, T. H. Kim, S. Lee, D. Kim, H. Ghang, B. C. Kim, S. Y. Kim, W. Y. Kim, D. Park, Y. S. Lee, S. Kim *et al.*, Genome Res. **19**, 1622–1629 (2009).
24. D. Sims, I. Sudbery, N. E. Llott, A. Heger and C. P Ponting, Nat. Rev. **15**, 121–132 (2009).
25. H. Rijzaani, P. Lestari, T. P. Priyatno and I. M. Tasma, Warta Balitbangtan **38**, 2–6 (2016).
26. P. Lestari, H. Kurniawan, H. Rijzaani, D. Satyawan, E. Kristyanto, R. T. Terryana, K. Nugroho, D. W. Utami, I. M. Tasma, Mastur, Sustiprijatno and M. A. Istiadi, *Situs Web Pusat Genom Pertanian Indonesia: Media Akses Informasi Genomik Pertanian Indonesia* (IAARD Press, Jakarta, 2020), 94 pp.