



UNIVERSITI PUTRA MALAYSIA

***GENETIC DIVERSITY AND HERITABILITY ESTIMATE OF JATROPHA
CURCAS L. ACCESSIONS USING AGRO-MORPHOLOGICAL AND
MOLECULAR MARKERS***

IBRAHIM WASIU AROLU

ITA 2012 8

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**MASTER OF SCIENCE
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By

IBRAHIM WASIU AROLU

**Thesis submitted to the School of Graduate Studies, Universiti Putra Malaysia,
in Fulfillment of the Requirements for the Degree of Master of Science**

December 2012

DEDICATION

This thesis is dedicated to Allah, the almighty God, His Prophet (Salahu Alay Wasalam), his beloved companions and all those that follow their footsteps till the Day of Judgment.



Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfillment of the requirement for the degree of Master of Science

GENETIC DIVERSITY AND HERITABILITY ESTIMATE OF *JATROPHA CURCAS* L. ACCESSIONS USING MOLECULAR AND AGRO-MORPHOLOGICAL MARKERS

By

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December 2012

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Institute: Institute of Tropical Agriculture

Genetic diversity analysis is the measure of genetic relationship among individual germplasm existing in a population. This research work aims at studying the genetic diversity, heritability pattern and genetic advances in *Jatropha curcas* germplasm and finally to identify promising groups of accessions that will be used as parent in the future breeding and improvement program. Forty-eight accessions of *Jatropha curcas* collected from the state of Kelantan, Selangor and Terengganu were planted using randomized complete block design (RCBD). Eleven agro-morphological traits including seed yield/ha were evaluated. Heritability values, principal component analysis were calculated. Cluster analysis was carried out to determine the diversity of *Jatropha curcas*. Ten ISSR primers were also used to determine molecular diversity in the three populations. In this study, all the morphological traits showed wide variability with highly significant differences among the 48 accessions except for seed width. Positive and significant correlation coefficients were observed among collar diameter, number of

secondary branches and number of primary branches. Positive relationship was also observed among seed yield/ha, oil yield/ha and total number of seeds. High broad sense heritability was observed for all traits except for seed width and number of primary branch. The highest heritability was recorded for collar diameter (89.40%), while the least value for this parameter was seed width (-0.02%). Cluster analysis using agromorphological markers and ISSR markers partitions the 48 accessions into 11 and distinct groups at coefficient of 1.1 and 0.6 respectively. From this molecular study, the 48 accessions were clustered into 11 groups at a coefficient of 0.65 without any regard for their geographical origin. The clusters were also formed at medium range coefficient. The mean values of number of alleles, number of effective alleles, shannon's information index, expected heterozygosity and percentage polymorphic loci are 1.93, 1.69, 0.56, 0.38 and 96% respectively. The percentage variation within and among the populations as shown by analysis of molecular variance are 94% and 6% respectively. The principal component analysis revealed that about 75% of total variation as a result of the first three components with PC1, PC2 and PC3 having 61.69, 8.68 and 5.07%, respectively. The three dimensional principal component analysis does not show any distinct relationship among these accessions at a very low coefficient. From the analysis of genetic diversity pattern and estimation of heritability, it can be concluded that collar diameter, number of primary branches, seed yield/accession are useful traits upon which selection can be made. Therefore, accession from cluster II (Accessions B-01-04 and T-01-09) and cluster X (Accessions D-02-02) recommended as parent groups for future breeding programmes.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Master Sains

**Kepelbagaian Genetik dan Anggaran Kebolehwarisan dalam Akses
Jatropha curcas menggunakan Penanda Agro-morfologi dan Molekular**

By

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Analisa kepelbagaian genetik adalah pengukur kepada hubungan genetik di kalangan individu germplasma yang wujud di dalam sebuah populasi. Kajian ini bertujuan untuk mengkaji kepelbagaian genetik, corak kebolehwarisan dan kemajuan genetik dalam germplasma *Jatropha curcas* dan akhirnya mengenalpasti kumpulan aksesori yang boleh digunakan sebagai induk dalam program penambahbaikan dimasa depan. Empat puluh lapan aksesori *Jatropha curcas* dikumpul daripada tiga negeri (Kelantan, Selangor dan Terengganu) di Semenanjung Malaysia telah ditanam menggunakan rekabentuk blok penuh terawak (RCBD). Sebelas sifat agro-morfologi termasuk hasil biji/ha dikumpul untuk tiga tahun. Daripada ini, komponen kebolehwarisan dan analisis komponen utama juga telah dikira. Analisis kluster telah dijalankan untuk membahagikan aksesori kepada kumpulan yang berlainan. Sepuluh primer ISSR digunakan serentak untuk menerokai tiga populasi. Dari kajian ini, semua ciri mendapati menunjukkan variabiliti yang luas dan perbezaan yang amat ketara dikalangan 48 aksesori kecuali untuk lebar biji. Pekali korelasi yang positif yang bererti didapati di kalangan diameter kolar, bilangan cabang

sekunder dan bilangan cabang utama. Hubungan positif juga ditemui di kalangan hasil biji/ha, hasil minyak/ha dan jumlah bilangan biji. Kebolehwarisan luas yang tinggi ditemui dalam semua sifat kecuali untuk lebar biji dan jumlah bilangan cabang utama. Kebolehwarisan yang tertinggi dicatatkan untuk diameter kolar (89.40%) manakala nilai yang rendah untuk parameter ini adalah lebar biji (-0.02%). Analisis kluster menggunakan penanda agro-morfologi dan penanda ISSR membahagikan 48 aksesori kepada 11 kluster dan perbezaan kluster masing-masing pada pekali 1.1 dan 0.6. Dari kajian molekular ini, 48 aksesori diasingkan kepada 11 kumpulan pada pekali 0.65 tanpa berasaskan geografi asal-usul mereka. Kluster tersebut telah dibentuk dengan julat nilai pekali yang sederhana. Nilai min bilangan alel, bilangan alel yang efektif, indeks maklumat Shannon, heterozigositi dan peratusan lokus polimorfik adalah 1,93, 1,69, 0.56, 0.38 dan 96% masing-masing. Peratusan variasi dalam dan di kalangan populasi seperti yang ditunjukkan oleh analisis varians molekular adalah 94% dan 6% masing-masing. Analisis komponen prinsipal memberikan kira-kira 75% jumlah variasi adalah sebagai hasil daripada tiga komponen pertama dengan PC1, PC2 dan PC3 mempunyai 61,69, 8,68 dan 5.07% masing-masing. Juga tiga dimensi analisis komponen prinsipal tidak menunjukkan sebarang hubungan yang berbeza di kalangan aksesori pada pekali yang sangat rendah. Selepas meneliti analisis corak kepelbagaian genetik dan anggaran kebolehwarisan, ianya dapat disimpulkan bahawa kolar diameter, bilangan dahan utama, hasil biji/aksesori adalah ciri yang berguna untuk pemilihan akan boleh dibuat. Oleh itu, aksesori dari kluster II (Aksesori B-01-04 dan T-01-09) dan kluster X (Aksesori D-02-02) adalah disyorkan sebagai kelompok induk untuk program pembiakbakaan masa depan.

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I certify that a Thesis Examination Committee has met on 28 December, 2012 to conduct the final examination of Ibrahim Wasiu Arolu on his thesis entitled “Genetic diversity and Heritability Estimate in *Jatropha curcas* L. Accessions using Agromorphological and Molecular markers” in accordance with the Universities and University Colleges Act 1971 and the Constitution of the Universiti Putra Malaysia [P.U.(A) 106] 15 March 1998. The Committee recommends that the student be awarded the Master of Science.

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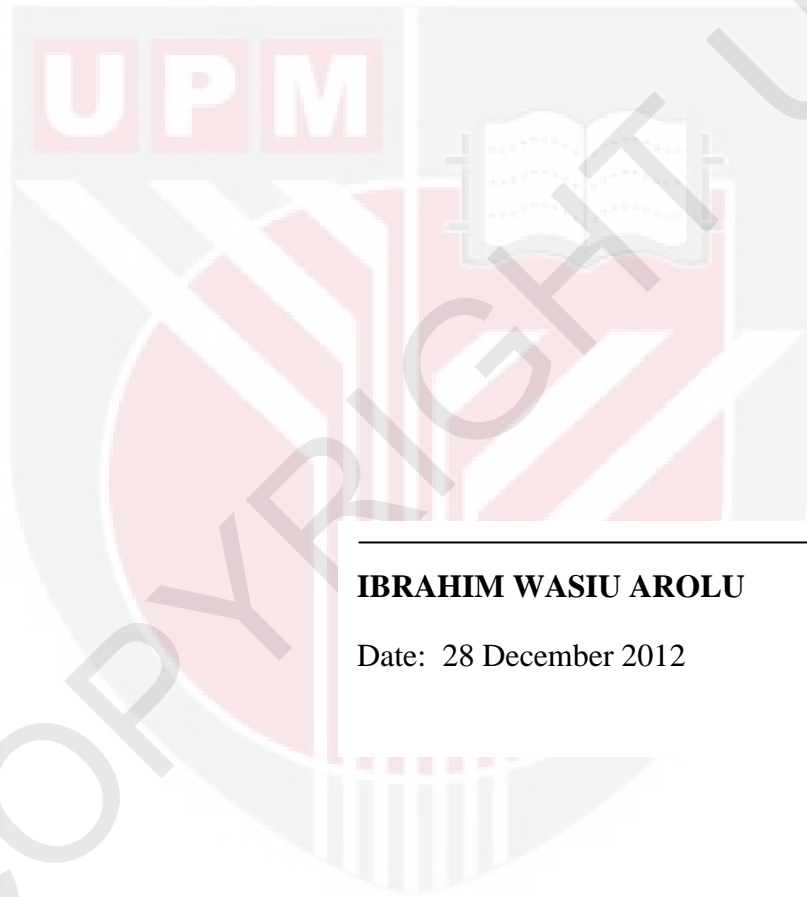
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DECLARATION

I declare that the thesis is my original work except for quotations and citations which have been duly acknowledged. I also declare that it has not been previously or concurrently submitted for any other degree at Universiti Putra Malaysia or other institutions.



IBRAHIM WASIU AROLU

Date: 28 December 2012

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