UNIVERSITI PUTRA MALAYSIA

DEVELOPMENT OF FUSARIUM WILT RESISTANT AND HIGH YIELDING WATERMELON (*Citrullus lanatus* L.) VARIETY THROUGH MARKER-ASSISTED BACKCROSS BREEDING

OLALEKAN KAZEEM KOLAPO

IPTSM 2019 9

DEVELOPMENT OF FUSARIUM WILT RESISTANT AND HIGH YIELDING WATERMELON (*Citrullus lanatus* L.) VARIETY THROUGH MARKER-ASSISTED BACKCROSS BREEDING

By

OLALEKAN KAZEEM KOLAPO

Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in fulfillment of the Requirements for the Degree of Doctor of Philosophy

February 2019

DEDICATION

This thesis is dedicated to the sweet memories of:
My parents; *Mr. Idris Olalekan Aminu* and *Mrs. Afsat Agbeke Olalekan- Aminu*
My mentor & father-like uncle, *Immam Dawood Tijani Adekilekun*, PhD
My spiritual father and guide; *Immam Asimiyu Igbayilola Ilobu*
and
My friend, brother and confidant; *Alh. (Omoba) Abdulwaheed Adewale Gbadebo.*
May Allah be pleased with their souls and count them among the dwellers of al jahnat firdaous. Aamiin.

Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfillment of the requirement for the degree of Doctor of Philosophy

DEVELOPMENT OF FUSARIUM WILT RESISTANT AND HIGH YIELDING WATERMELON (*Citrullus lanatus* L.) VARIETY THROUGH MARKER-ASSISTED BACKCROSS BREEDING

By

OLALEKAN KAZEEM KOLAPO

February 2019

Chairman : Professor Mohd Rafii Yusop, PhD
Institute : Tropical Agriculture and Food Security

One of the major production limiting diseases of watermelon (*Citrullus lanatus* L.) is Fusarium wilt (FW) caused by *Fusarium oxysporum* f. sp. *niveum* (FON). The use of disease-free cultivars is the preferred method of controlling the disease in a sustainable way. Watermelon is a major crop in Malaysia and the country spends about RM 10 million annually for the importation of its seeds to support local production. There is therefore the need to save this huge amount by breeding for local varieties that will be high yielding and Fusarium wilt resistant. In this study, the Fusarium wilt resistant inbred line CS-19 and susceptible inbred line BL-14 were crossed to generate the F_1 population. The subsequent two backcrosses and selfing led to the transfer of the resistance gene (*fo-1*) into the susceptible inbred line BL-14 using marker-assisted backcrossing (MABC) and the subsequent development of Fusarium wilt resistant lines that still retain the desirable qualities in BL-14. Eleven microsatellite markers linked to the Fusarium wilt resistance gene were selected and two of the markers, BVWS02309 and BVWS01133 located on chromosomes 1 and 9 respectively were used for the confirmation of Fusarium wilt resistant gene in F_1,BC_1F_1, BC_2F_1 and BC_2F_2 generations. From the 380 microsatellites markers screened, 78 were found polymorphic between the parents and used for recurrent parent genome (RPG) recovery in each backcross population. From the inheritance test conducted in BC_2F_1 and BC_2F_2 generations, the recurrent parent BL-14 scored 4.5 of the 0-5 scale, and this confirmed its susceptibility to the Fusarium wilt disease. In the BC_2F_1 generation, 72 of the 150 plants showed resistance while 78 plants showed susceptibility when inoculated with the virulent *Fusarium oxysporumniveum* isolate. Chi-square test ($\chi 2$) showed that the observed frequencies in the BC_2F_1 population fitted into the single gene model. The goodness of fit ($p=0.46$) to the expected test segregation ratio (1:1) indicated that the resistance is controlled by a single dominant gene. The plants resistant to the *Fusarium oxysporum niveum* isolate from BC_2F_1 population showed good fit with the two markers BVWS02309 ($\chi 2= 0.24$; $p= 0.6892$) and BVWS01133

($\chi 2$= 0.11; p= 0.8065), with expected segregation ratio (1:1) for single gene model. These two markers were found suitable for marker-assisted selection of *fo-1* gene against Fusarium wilt disease. The BC_2F_2 population phenotypically segregated into 3:1 ratio (resistant: susceptible). The genotypic segregation of the BC_2F_2 population using the two markers was in the ratio 1:2:1. This is a confirmation of the fact that resistance to Fusarium wilt disease in CS-19 is under the control of a single dominant gene. The RPG recovery analysis for the best improved lines ranged from 74.7 to 94.4% in BC_1F_1, 86.8 to 96.8% in BC_2F_1 and 95.1 to 96.9% in BC_2F_2 generations. The 96.14% average proportion of the recurrent parent genome in selected improved lines showed the close phenotypic resemblance to the recurrent parent BL-14. Ten homozygous lines carrying Fusarium wilt resistance gene with similar genome background to BL-14 were selected as the developed improved Fusarium wilt resistant breeding lines. The agro-morphological traits showed that there was no significant difference between the recurrent parent BL-14 and Fusarium wilt resistant improved lines developed. In conclusion, this study confirmed that Fusarium wilt resistance inbred line CS-19 is under the control of a single dominant gene and it is linked with SSR markers BVWS02309 and BVWS01133. This finding is recommended for use in marker-assisted selection for further development of Fusarium wilt resistant varieties with the newly developed resistant lines serving as source of resistance.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

PEMBANGUNAN VARIETI TEMBIKAI (*Citrullus lanatus* L.) RINTANG LAYU FUSARIUM DAN HASIL TINGGI MELALUI PEMBIAKBAKAAN KACUKBALIK BANTUAN PENANDA

Oleh

OLALEKAN KAZEEM KOLAPO

Februari 2019

Pengerusi : Profesor Mohd Rafii Yusop, PhD
Institut : Pertanian Tropika dan Sekuriti Makanan

Satu penyakit utama tembikai (*Citrullus lanatus* L.) yang menghadkan pengeluaran tanaman ini adalah layu Fusarium (FW), yang disebabkan oleh *Fusarium oxysporum* f. sp. *niveum* (FON). Penanaman mengunakan kultivar rintang penyakit merupakan kaedah yang terbaik bagi mengawal penyakit secara lestari. Tembikai adalah merupakan satu tanaman utama di Malaysia dan negara membelanjakan kira-kira RM10 juta setiap tahun untuk mengimport bijibenih, dan oleh itu adalah perlu untuk menjimatkan jumlah yang besar ini melalui pembiakbakaan varieti yang berhasil tinggi serta kerintangan terhadap layu Fusarium. Dalam kajian ini, kacukkan antara waris inbred rintang layu Fusarium CS-19 dan waris rentan BL-14 bagi memindahkan gen rintang (*fo-1*) ke dalam waris inbred rentan BL-14 untuk menghasilkan populasi F_1. Seterusnya dua generasi kacukan balik dan swa-kacuk bagi memindahkan gen (*fo-1*) rintang ke waris inbred rentan BL-14 melalui kacuk-balik bantuan penanda molekul (MABC) untuk membangunkan waris rintang penyakit layu Fusarium yang mana ciri-ciri baik BL-14 yang dikehendaki dikekalkan. Sebelas penanda mikrosatelit yang berkaitan rapat dengan gen rintangan Fusarium telah dipilih dan dua daripada penanda polimorfik ini; penanda SSR BVWS02309 dan BVWS01133 yang terletak pada kromosom 1 dan 9 masing-masing telah digunakan untuk pengesahan gen Fusarium rintang pada generasi F_1, BC_1F_1, BC_2F_1 dan BC_2F_2. Dari 380 penanda microsatelit yang telah disaring, 78 didapati polimorfik antara kedua-dua induk yang digunakan untuk pemulihan genom induk (BL-14) penerima (RPG) dalam setiap populasi kacukbalik. Melalui ujian pewarisan yang dilakukan pada pada generasi BC_2F_1 dan BC_2F_2, didapati bahawa induk BL-14 mencatatkan 4.5 dari skala 0-5, dan ini mengesahkan kerentananya terhadap penyakit layu Fusarium. Dalam generasi BC_2F_1, 72 dari 150 pokok menunjukkan kerintangan, manakala 78 pokok menunjukkan kerentanan apabila diinokulasi dengan isolat *Fusarium oxysporum niveum* yang virulen. Ujian Khi-square ($\chi 2$) menunjukkan bahawa frekuensi yang dicerap dalam populasi BC_2F_1 menepati model gen tunggal. Ketepatan padanan (p=0.69) kepada nisbah segregasi dijangkan

(1:1) menunjukkan bahawa kerintangan ini dikawal oleh gen tunggal. Pokok yang rintang terhadap isolat *Fusarium oxysporum niveum* dari populasi BC_2F_1 menunjukkan ketepatan padanan dengan dua penanda BVWS02309 ($\chi 2$= 0.24; p= 0.6892) dan BVWS01133 ($\chi 2$= 0.11; p= 0.8065), dengan nisbah segregasi dijangkakan (1:1) untuk model gen tunggal. Kedua-dua penanda ini didapati sesuai untuk pemilihan bantuan penanda gen *fo-1* terhadap penyakit layu Fusarium. Populasi BC_2F_2 secara fenotipnya bersegregasi kepada nisbah 3:1 (rintang: rentan). Segregasi genotip populasi BC_2F_2 menggunakan penanda SSR BVWS02309 dan BVWS01133 adalah mengikut nisbah 1:2:1. Ini mengesahkan bahawa kerintangan terhadap penyakit layu Fusarium pada CS-19 adalah di bawah kawalan gen dominan tunggal. Analisis pemulihan RPG untuk waris maju terbaik adalah dengan julat dari 74.7 hingga 94.4% dalam generasi BC_1F_1, 86.8.4 hingga 96.8% dalam generasi BC_2F_1 dan 95.1 hingga 96.9% dalam generasi BC_2F_2. Purata RPG 96.14% genom induk penerima pada waris maju terpilih menunjukkan persamaan fenotip yang menyerupai induk BL-14. Sepuluh waris homozaigus yang mengandungi gen kerintangan layu Fusarium dengan genom yang sama dengan BL-14 telah dipilih sebagai waris maju yang rintang layu Fusarium. Ciri-ciri agro-morfologi menunjukkan bahawa tidak terdapat perbezaan yang ketara antara induk BL-14 dan waris maju rintang Fusarium. Kesimpulannya, kajian ini mengesahkan bahawa waris inbred CS-19 adalah rintang layu Fusarium dengan kawalan gen dominan tunggal dan ia adalah boleh disahkan dengan penanda SSR, BVWS02309 dan BVWS01133. Hasil penemuan ini serta sepuluh waris maju rintang baharu yang dibangunkan ini adalah disyorkan untuk digunakan dalam pemilihan bantuan penanda seterusnya bagi membangunkan varieti tembikai yang rintang layu Fusarium.

ACKNOWLEDGEMENTS

My thanks and gratitude is firstly to Allah (SWT) for His unending rahmah before and during this programme, alhamdulilah. I look forward to more of this after the whole programme. The chairman of my supervisory committee; Prof. Dr. Mohd Rafii Yusop, deserves my deep and heartfelt appreciation. Words enough cannot capture how much he and his touch in this research work meant to me. I pray Allah in His infinite mercies continue to elevate and bless him. Also worthy of note is the input of other members of my supervisory committee in persons of Prof. Dr. Mahmud Tengku Muda Mohamed, Assoc. Prof. Dr. Khairulmazmi Ahmad and Dr. Azizah Misran. May your pool of knowledge and mercies never dry.

Special gratitude to the management of the Osun State University, Osogbo, Nigeria for granting me the PhD scholarship under the TETFUND's Academic Staff Training & Development Scheme. I also appreciate members of staff of the College of Agriculture, Osun State University; for the loving "push", the moral as well as spiritual support. May God bless and reward you all. The members of staff and students of the Laboratory of Climate-Smart Food Crop Production, Institute of Tropical Agriculture and Food Security (ITAFoS), UPM, are well acknowledged. Particular mention must be made of Drs. Ibrahim, Usman, Yusuff, Tanweer, Gous, Wendy and Raihanah, Messrs Azrul, Jamil, Hamis, Bello and Sam Chukwu ; thank you all and may Allah take us all to greater height, I am indeed grateful.

My siblings; Mrs Aminat Odebo, Alhaja Sadiat Adegbola, Messrs Taofeek and Mukail Olalekan and Alhaja Toyiba Afolake Balogun, their spouses and children, thanks immensely. May Allah further strengthen and bless the bond we share.

Many good people, too numerous to mention were of assistance in the course of this journey. Let me represent them by the following: HRM Oba Munirdeen Adesola Lawal, Timi of Edeland, Alh. Kola' Alimi (Alagba), Engr Habeeb Ajibola, Profs. Siyan Oyeweso, Clement Adebooye & Oguntola Alamu , Alhaja Dr. Bola Olaniyan, Dr. Ope Ajewole, Engr. Niyi Adedokun, Alhaja Mutiat Babalola & husband, Alh & Alhaja Ibrahim Awolowo, Alh. Pharm Muslihudeen Tijani, Engr. Miftahu Kola Olajide, Otunba 'Yomi Olajide, Alh. Raf. Adeoye, Mrs Adebola Ayeigboyin, Mrs Mustapha Bushra, Uztaz & Hajia Abdwasih Ayinde, Sis. Iyabo Adedigba and all my sprirtual fathers. I appreciate members of Inner Circle of Friends, UI, Ede Crystal Club, EMGS, Ede Old Students' Association, Alhaq Muslim Society Samanda, Minaret Family etc

Members of my "newly found family" in Malaysia are just too wonderful to be left out here; Drs. AbdulKabir Adedeji, Sures Kumar, Dimeji Bolarinwa, Monsur Salisu, Akeem Dauda (Dabak), Kolapo Shakiru, Taiwo Ambali, 'Toyin Olagunju and Omoba Ibrahim Akinfalabi. Messrs Muideen Ahmed, Abdfatah Arolu and indeed all "Tiwa n tiwa" members, thanks a lot & God bless you.

Last but certainly not the least, my deepest appreciation goes to my wife; Mrs. Idayat Idowu Olalekan-Kolkaz (2I), for the unalloyed love shown and sacrifice she made to keep the home front safe, secured & comfortable while I was away. May Allah reward you with long life and His pleasure on our "fruits"; Immam Daud Igbayilola, Jameelah Jayeola, Kawthar Kanyinsola and Labeeb Laoye. I love you all and shall continue to do.

Finally, to everyone that has contributed one way or the other in making me who I am today, I appreciate and pray God reward you in folds.

This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfillment of the requirement for the degree of Doctor of Philosophy. The members of the Supervisory Committee were as follows:

Mohd Rafii Bin Yusop, PhD
Professor
Institute of Tropical Agriculture and Food Security
Universiti Putra Malaysia
(Chairman)

Mahmud Tengku Muda Mohamed, PhD
Professor
Faculty of Agriculture
Universiti Putra Malaysia
(Member)

Khairulmazmi Ahmad, PhD
Associate Professor
Faculty of Agriculture
Universiti Putra Malaysia
(Member)

Azizah Misran, PhD
Senior Lecturer
Faculty of Agriculture
Universiti Putra Malaysia
(Member)

_____
ROBIAH BINTI YUNUS, PhD
Professor and Dean
School of Graduate Studies
Universiti Putra Malaysia

Date:

Declaration by graduate student

I hereby confirm that:

- this thesis is my original work;
- quotations, illustrations and citations have been duly referenced;
- THIS thesis has not been submitted previously or concurrently for any other degree at any other institutions;
- intellectual property from the thesis and copyright of thesis are fully-owned by Universiti Putra Malaysia, as according to the Universiti Putra Malaysia (Research) rules 2012;
- written permission must be obtained from supervisor and the office of Deputy Vice-chancellor (Research and Innovation) before thesis is published (in the form of written, printed or in electronic form including books, journals, modules, proceedings, popular writings, seminar papers, manuscripts, posters, reports, lecture notes, learning modules or any other materials) as stated in the Universiti Putra Malaysia (Research) rules 2012;
- there is no plagiarism or data falsification/fabrication in the thesis, and scholarly integrity is upheld as according to the University Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2012-2013) and the Universiti Putra Malaysia (Research) Rules 2012. The thesis has undergone plagiarism detection software.

Signature: _____ Date: _____

Name and Matric No.: Olalekan Kazeem Kolapo, GS40000

Declaration by Members of Supervisory Committee

This is to confirm that:

- The research conducted and the writing of this thesis was under our supervision,
- Supervision responsibilities as slated in Rule 41 in Rules 2003(Revision 2012-2013) were adhered to.

Signature: _____
Name of Chairman of Supervisory Committee: Professor Dr. Mohd Rafii Bin Yusop

Signature: _____
Name of Member of Supervisory Committee: Professor Dr. Mahmud Tengku Muda Mohamed

Signature: _____
Name of Member of Supervisory Committee: Associate Professor Dr. Khairulmazmi Ahmad

Signature: _____
Name of Member of Supervisory Committee: Dr. Azizah Misran

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS

QTL	Quantitative trait loci
DNA	Deoxyribonucleic acid
MAS	Marker-assisted selection
MABC	Marker-assisted backcross
SSR	Simple sequence repeat
PCR	Polymerase chain reaction
AFLP	Amplified fragment length polymorphism
RAPD	Randomly Amplified Polymorphic DNA
SNP	Single nucleotide polymorphism
CTAB	Cetyltrimethylammonium bromide
EDTA	Ethylenediamine Tetraacetic Acid
LB	Lysogeny broth
rpm	Revolutions per minute
Tris	tris(hydroxymethyl)aminomethane
HCl	Hydrochloric acid
$MgCl_2$	Magnesium chloride
Taq	Thermus aquaticus
NaCl	Sodium chloride
EST	Expressed sequence tag
RPG	Recurrent parent genome
RIL	Recombinant inbred line
RPG	Recurrent parent genome
TE	Tris/EDTA
%	Percentage
^0C	Degree Celsius
NaOCl	Sodium hypochlorite
V	Voltage
DI	Disease incidence
DSI	Disease severity index
FW	Fusarium wilt
FON	Fusarium oxysporum niveum

CHAPTER 1

INTRODUCTION

1.1 Background

Watermelon (*Citrullus lanatus* L) is a vegetable fruit and the largest among the fruits eaten in hot weather (Zhao *et al.*, 2013). It is an economically important vegetable crop, providing source of income for small–scale farmers worldwide, particularly in China that is rated as the highest producing country (FAOSTAT, 2018; Zhang *et al.*, 2016; Nimmakayala *et al.*, 2014). It is cherished for its sweet-flesh, good source of vitamin A and C, minerals including potassium, iron and calcium, and its possession of high amounts of citrulline and lycopene (its lycopene content is next only to that of tomato) (Reetu and Tomar, 2017; Ren *et al.*, 2012). The fact that high diversity of watermelon are found growing wild in Southern Africa makes many people attributed its origin to the place (Pitrat *et al.*, 1999). World production amounted to 117 million tonnes in the year 2016 and Malaysia, with production of 192,910 tonnes, occupied the 41st position among the producing countries (FAOSTAT, 2018).

Watermelon was reported to have been brought to Peninsular Malaysia in the 14th century through merchandise of the early Indian and Chinese (Salleh, 1986). Though first planted in Kelantan in the 1940s, it gained popularity in Malaysia around 1970s when much sweeter hybdrids were introduced from Taiwan and Japan. Breeding for hybrid watermelon has not been very successful in Malaysia and this has been attributed to lack of genetic resources. There were few choices of parental inbred lines to work with and thus the breeders depend on commercial hybrids released by foreign seed companies (Zainab and Hasnah, 2000). Other challenges militating against successful breeding in watermelon include high humidity and rainfall as well as the outbreak of diseases (Razmunah and Nik, 2016; Salleh, 1986). A number of open-pollinated watermelon varieties that are disease resistant have been developed in Malaysia, these include Super Dragon, Jade Dew and Glamour (Muhammad and Masdek, 2016). Besides being of less vigour, most of these varieties are poor in fruit quality; their flesh is neither dark red in colour nor do they have high sugar content. The emphasis of breeding work on watermelon has therefore shifted to the production of F_1 hybrid varieties and more recently, development of hybrid triploid varieties (seedless). In an effort to produce F_1 hybrid in Malaysia, Zainab and Hasnah (2000), generated four inbred lines (CS-19, BL-14, 6372-4, and CH-8) through pedigree breeding. These inbred lines possessed varying desirable qualities and showed different combining abilities (Bahari *et al.*, 2012).

1.2 Significance of the study

Watermelon is a very popular short-term, non-seasonal fruit in Malaysia. However, most varieties in the country are of low fruit quality. Therefore, there is a need to breed for improved varieties with high yield and good fruit quality. One of the major factors responsible for low yield of watermelon in Malaysia is the outbreak of diseases, mainly, Fusarium wilt. Use of resistant varieties has been found to be the most effective method in controlling the disease in a sustainable manner (Mcgregor, 2013; Park and Cho, 2012). However, there are little varieties that are resistant to Fusarium wilt disease in Malaysia and other ASEAN countries. It is believed that the use of marker-assisted backcross breeding technique would lead to the (timely) development of varieties that are disease resistant and high yielding. This will lead to an increase in production of watermelon for local consumption as well as increase source of more foreign reserves through export. Also, the identification of the polymorphic simple sequence repeat (SSR) markers linked with the disease resistance will add to the pool of knowledge about the genetic base of watermelon in Malaysia.

1.3 Problem Statement

Watermelon contributes about twenty percent of the total fruit exports of Malaysia and it is therefore classified under major fruits by the Ministry of Agriculture and Agro-Based Industry (MOA), Malaysia. In spite of its contribution to the export earning of the country, its production still depends on hybrid seeds imported from other countries. The country spends about RM 10 million annually to import about 1.5 tonnes of seeds needed to meet up its production (Bahari *et al.,* 2012; Mahmood, 2006). However, it has been observed that the imported seeds do not produce high yield in the local environments and are susceptible to Fusarium wilt disease. This soil-borne disease caused by the pathogen *Fusarium oxysporum* f. sp. *niveum* (FON) is recorded to be one of the important diseases of watermelon. It is widespread worldwide except in Antarctica (Everts and Himmelstein, 2015; Egel and Martyn, 2013; Zhou *et al.,* 2010). The pathogen can survive for a long time in the soil and new races continously evolve; these make the control of the disease challenging (Lin *et al.,* 2009). So far, there is little information on the availability of Fusarium wilt resistant variety in Malaysia and this has led to a reduction in production and yield loss of the crop. It is believed that the use of improved varieties will lead to increase yield and subsequently, more income for the local farmers and availability of high quality variety of watermelon for domestic consumption.

1.4 Research objectives

The main objective of this study was to develop a variety of watermelon that is resistant to Fusarium wilt disease and high yielding through marker-assisted backcross breeding using SSR markers.

The specific objectives were to:

1. Identify the polymorphic SSR markers between inbred lines CS-19 and BL-14 for foreground and background selections.
2. Introgress Fusarium wilt resistance gene from CS-19 resistant line into the inbred line BL-14 through marker-assisted backcrossing method.
3. Quantify the genome recovery of the recurrent parent (BL-14) in marker-assisted backcross population

REFERENCES

Abdel, C. G., & Bamerni, K. A. (2011). Effect of pre-planting land flooding durations on growth, yield and anatomical parameters of three Watermelon [*Citrullus lanatus* (Thunb.) Matsum.] Cultivars. *American Journal of Experimental Agriculture*, 1(4), 187- 213.

Adjoumani, K., Bony, S. B., Koffi, G. K., Kouonon, L. C., Brou, F. K. & Sie, R. (2016). Genetic evaluation of seed traits from intraspecific crossing of genetically distinct watermelon varieties. *African Crop Science Journal*, 24(2), 143-154.

Allard, R. W. (1999). Principles of plant breeding. 2nd edn. John Wiley & Sons, New York. 229pp.

Akhtar, S., Bhat, M. A., Wani, S. A., Bhat, K. A., Chalkoo, S., Mir, M. R. & Wani, S. A. (2010). Marker assisted selection in rice. *Journal of Phytology*, 2(10), 66-81.

Alam, M. S., Begum, S. N., Islam, M. M., Moniruzzaman, M. & Patwary, M. A. K. (2012). Marker-assisted foreground selection for identification of salt tolerant rice genotypes. *The Agriculturists*, *10*(2), 1-8.

Amarawathi, Y., Singh, R., Singh, A. K., Singh, V. P., Mohapatra, T., Sharma, T. R. *et al*, (2008). Mapping of quantitative trait loci for basmati quality traits in rice (*Oryza sativa* L.). *Molecular Breeding*, 21(1), 49-65.

Arif, I. A., Bakir, M. A., Khan, H. A., Al Farhan, A. H., Al Homaidan, A. A., Bahkali, A. H., Al Sadoon, M. & Shobrak, M. (2010). A Brief Review of Molecular Techniques to Assess Plant Diversity. *International Journal of Molecular Sciences*, 11, 2079-2096.

Ashraf, M., Akram, N. A., & Foolad, M. R. (2012). Marker-assisted selection in plant breeding for salinity tolerance. *Plant Salt Tolerance: Methods and Protocols*, 305-333.

Babu, R., Nair, S. K., Prasanna, B. M., & Gupta, H. S. (2004). Integrating marker-assisted selection in crop breeding—prospects and challenges. *Current Science*, 87(5), 607-619.

Bahari, M., Rafii, M. Y., Saleh, G. B., & Latif, M. A. (2012). Combining ability analysis in complete diallel cross of watermelon (*Citrullus lanatus* (Thunb.) Matsum. & Nakai). *The Scientific World Journal*, 2012. 6 pp.

Barabaschi, D., Tondelli, A., Desiderio, F., Volante, A., Vaccino, P., Valè, G., & Cattivelli, L. (2016). Next generation breeding. *Plant Science*, *242*, 3-13.

Basavaraj, S. H., Singh, V. K., Singh, A., Singh, A., Singh, A., Anand, D.,Yadav S., Ellur, R.K., Singh, D., Krishnan, S.G., Nagarajan, M., Mohapatra,T., Prabhu, K.V & Singh, A.K. (2010). Marker-assisted improvement of bacterial blight resistance in parental lines of Pusa RH10, a superfine grain aromatic rice hybrid. *Molecular breeding*, 26(2), 293-305.

Ben-Ari, G.& Lavi, U. (2012). Marker-assisted selection in plant breeding. In *Plant Biotechnology and Agriculture*, Pp. 163-184. Academic Press.

Ben-Yephet, Y., & Shtienberg, D. (1997). Effects of the host, the pathogen, the environment and their interactions, on Fusarium wilt in carnation. *Phytoparasitica*, *25*(3), 207-216.

Bhat, R. G., & Subbarao, K. V. (1999). Host range specificity in *Verticillium dahliae. Phytopathology*, 89(12), 1218-1225.

Bhering, L. L., Brasil Pereira Pinto, C. A., Gandolfi Benites, F. R., Leite, M. E., & Lopes da Silva, F. (2009). Seleção assistida por marcadores para teor de matéria seca e açúcares redutores em tubérculos de batata. *Ciência Rural*, 39(1), 38-44.

Bie, Z., Nawaz, M. A., Huang, Y., Lee, J. M., and Colla, G. (2017). "Introduction of vegetable grafting," 1–21, in Colla *et al*., (eds) Vegetable Grafting, Principles and Practices, Wallingford: CABI Publishing.

Bjørnstad, Å., Patil, V., Tekauz, A., Marøy, A. G., Skinnes, H., Jensen, A., Magnus, H. & MacKey, J. (2002). Resistance to scald (Rhynchosporium secalis) in barley (Hordeum vulgare) studied by near-isogenic lines: I. Markers and differential isolates. *Phytopathology*, *92*(7), 710-720.

Blair, M. W., Fregene, M. A., Beebe, S. E., & Ceballos, H. (2007). Marker-assisted selection in common beans and cassava. *Marker-assisted selection: Current Status and Future Perspectives in Crops, Livestock, Forestry and Fish*, 81-115.

Bo, K., Ma, Z., Chen, J. & Weng, Y. (2015). Molecular mapping reveals structural rearrangements and quantitative trait loci underlying traits with local adaptation in semi-wild Xishuangbanna cucumber (*Cucumis sativus* L. var. *xishuangbannanesis* Qi et Yuan). *Theor Appl. Genet*, 128(1), 25-39.

Bonnett, D. G., Rebetzke, G. J., & Spielmeyer, W. (2005). Strategies for efficient implementation of molecular markers in wheat breeding. *Molecular Breeding*, *15*(1), 75-85.

Boyhan, G., Norton, J. D., Jacobsen, B. J., & Abrahams, B. R. (1992). Evaluation of watermelon and related germplasm for resistance to zucchini yellow mosaic virus. *HortScience*, 27(11), 1173-1173.

Branham, S. E., Levi, A., Farnham, M. W., & Wechter, W. P. (2017). A GBS-SNP-based linkage map and quantitative trait loci (QTL) associated with resistance to Fusarium oxysporum f. sp. niveum race 2 identified in *Citrullus lanatus* var. *citroides*. *Theoretical and applied genetics*, *130*(2), 319-330.

Breseghello, F., & Coelho, A. S. G. (2013). Traditional and modern plant breeding methods with examples in rice (*Oryza sativa* L.). *Journal of Agricultural and Food Chemistry*, 61(35), 8277-8286.

Brown, J. & Caligari, P.D.S. (2013). Genetics and plant breeding. 60- 95.In Brown & Calgari (edn) *An Introduction to Plant Breeding.*Willey- Blackwell Publisher, 2nd edition, pp.296.

Bruton, B. D., & Damicone, J. P. (1999). Fusarium wilt of watermelon: Impact of race 2 of *Fusarium oxysporum* f. sp. *niveum* on watermelon production in Texas and Oklahoma. Subtrop. *Plant Science*, 51, 4-9.

Caixeta, E.T, Oliveira, A.C.B de, Brito, G.G. de & Sakuyama, N.S. (2009). Tipos de Marcadores Moleculares. In: Marcadores Moleculares (Borém A and Caixeta ET, eds.). UFV, Viçosa, 11-94.

Castro, A. J., Capettini, F., Corey, A. E., Filichkina, T., Hayes, P. M., Kleinhofs, A., Kudrna, D., Richardson, K., Sandoval-Islas, S., Rossi, C. & Vivar, H. (2003).Mapping and pyramiding of qualitative and quantitative resistance to stripe rust in barley. Theorl Appl Genet, 107(5), 922-930.

Cirulli, M. (1972). Variaton of pathogenicity in *fusarium oxysporum* FSP *niveum* and resistance in Watermelon cultivars. in: Actas III Congr. Un. Fitopatol. Mediterr. Oeiras. 491-500.

Cohen, R., Tyutyunik, J., Fallik, E., Oka, Y., Tadmor, Y., & Edelstein, M. (2014). Phytopathological evaluation of exotic watermelon germplasm as a basis for rootstock breeding. *Scientia Horticulturae*, 165, 203-210.

Collard, B. C., & Mackill, D. J. (2008). Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 363(1491), 557-572.

Cota, L. G., Moreira, P. A., Menezes, E. V., Gomes, A. S., Ericsson, A. R. O., Oliveira, D. A. & Melo Jr, A. F. (2012). Transferability and characterization of simple sequence repeat markers from Anacardium occidentale to A. humile (Anacardiaceae). *Genetics and Molecular Research*, *11*(4), 4609-4616.

Crall, J. (1981). Fifty years of watermelon breeding at ARC Leesburg. In Proc. *Florida. State Horticultural. Society* .Vol. 94, pp. 156-158.

Cuc, L. M., Huyen, L. T., Hien, P. T., Hang, V. T., Dam, N. Q., Mui, P. T., Quang, V.D., Ismail, A. M. & Ham, L. H. (2012). Application of marker assisted backcrossing to introgress the submergence tolerance QTL *SUB1* into the Vietnam elite rice variety-AS996. *American Journal of Plant Sciences*, 3(04), 528 - 536.

Decoux, G., & Hospital, F. (2002). Popmin: A program for the numerical optimization of population sizes in marker-assisted backcross programs. *Journal of Heredity*, 93(5), 383-384.

Dekkers, J. C. (2004). Commercial application of marker-and gene-assisted selection in livestock: Strategies and lessons 1 2. Journal of animal science, 82(13_suppl), E313-328.Delannay, I. Y., & Staub, J. E. (2010). Use of molecular markers aids in the development of diverse inbred backcross lines in Beit Alpha cucumber (*Cucumis sativus* L.). *Euphytica*, 175(1), 65-78.

Dhingani, R. M., Umrania, V. V., Tomar, R. S., Parakhia, M. V., & Golakiya, B. (2015). Introduction to QTL mapping in plants. *Ann. Plant Sci*, *4*, 1072-1079.

Divya, B., Robin, S., Rabindran, R., Senthil, S., Raveendran, M. & Joel, A. J. (2014). Marker assisted backcross breeding approach to improve blast resistance in Indian rice (Oryza sativa) variety ADT43. *Euphytica*, 200(1), 61-77.

Doyle, J. J., Doyle, J. L. & Hortoriun, L. B. (1990). Isolation of Plant DNA from Fresh Tissue. *Focus* 12, 13-15.

Dreher, K., Khairallah, M., Ribaut, J. M., & Morris, M. (2003). Money matters (I): costs of field and laboratory procedures associated with conventional and marker-assisted maize breeding at CIMMYT. *Molecular Breeding*, 11(3), 221-234.

Dwivedi, S. L., Crouch, J. H., Mackill, D. J., Xu, Y., Blair, M. W., Ragot, M., Upadhyaya, H. D. & Ortiz, R. (2007). The molecularization of public sector crop breeding: progress, problems, and prospects. *Advances in Agronomy*, 95, 163-318.

Eathington, S. R., Crosbie, T. M., Edwards, M. D., Reiter, R. S., & Bull, J. K. (2007). Molecular markers in a commercial breeding program. *Crop Science*, 47(Supplement_3), S-154.

Egel, D. S., & Martyn, R. D. (2013). Fusarium wilt of watermelon and other cucurbits. *The Plant Health Instructor*, 10, 1094.

Ellul, P., C. Lelivelt, M. Naval, F. Noguera, S. Sanchez, A. Atarés…… & R. Dirks. (2007). Watermelon, p. 129-165. In: R. Davey (ed.). Transgenic crops. Springer, Berlin.

Elmstrom, G. W., & Hopkins, D. L. (1981). Resistance of watermelon cultivars to fusarium wilt. *Plant Disease*, 65(10), 825-827.

Everts, K. L., Egel, D. S., Langston, D., & Zhou, X. G. (2014). Chemical management of Fusarium wilt of watermelon. *Crop Protection*, 66, 114-119.

Everts, K. L., & Himmelstein, J. C. (2015). Fusarium wilt of watermelon: Towards sustainable management of a re-emerging plant disease. *Crop Protection*, 73, 93-99.

FAOSTAT data.Food and Agriculture Organization of the United Nations. (2018). List of Countries and their Production of watermelon in 2013.

Food and Agriculture Organization of the United Nations, Statistics Division (FAOSTAT). 2018. Retrieved 10 February 2018.

Farooq, S., & Azam, F. (2002). Molecular markers in plant breeding-I: Concepts and characterization. *PakistanJjournal of Biological Sciences*, 5 (10), 1135-1140.

Fehr, W.R., 1993. Principles of Cultivar Development, Theory and Technique, Vol. 1, 536 pp. Macmillan Publishing Company.

Feng, D., Ling, W. H., & Duan, R. D. (2010). Lycopene suppresses LPS-induced NO and IL-6 production by inhibiting the activation of ERK, p38MAPK, and NF-κB in macrophages. *Inflammation Research*, 59(2), 115-121.

Filippi, M. C., & Prabhu, A. S. (2001). Phenotypic virulence analysis of *Pyricularia grisea* isolates from Brazilian upland rice cultivars. *Pesquisa Agropecuária Brasileira*, 36(1), 27-35

Francia, E., Tacconi, G., Crosatti, C., D. Barabaschi, D. Bulgarelli, E. Dall'Aglio & G. Vale`. (2005). Marker assisted selection in crop plants. *Plant Cell, Tissue and Organ Culture,* 82: 317–342.

Frisch, M., & Melchinger, A. E. (2005). Selection theory for marker-assisted backcrossing. *Genetics*, 170(2), 909–917.

Frisch, M., & Melchinger, A. E. (2001). Marker-assisted backcrossing for simultaneous introgression of two genes. *Crop Science*, 41(6), 1716-1725.

Frisch, M., Bohn, M., & Melchinger, A. E. (1999a). Comparison of selection strategies for marker-assisted backcrossing of a gene. *Crop Science*, 39(5), 1295-1301.

Frisch, M., Bohn, M., & Melchinger, A. A. (1999b). Minimum sample size and optimal positioning of flanking markers in marker-assisted backcrossing for transfer of a target gene. *Crop Science*, 39(4), 967-975.

Gama, R. N., Santos, C. A. F., Dias, R. D. C. S., & Souza, F. F. (2013). Molecular characterization of watermelon cultivars using microsatellite markers. *Horticultura Brasileira*, 31(4), 522-527.

Gama, R. N. C. S., Santos, C. A. F., Dias, R. C. S., Alves, J. C. S. F., & Nogueira, T. O. (2015a). Microsatellite markers linked to the locus of the watermelon fruit stripe pattern. *Genetics and Molecular Research*, 14(1), 269-276.

Gama, R. N. C. S, Santos, C. A. F., de Cassia Souza Dias, R., de Souza, R. R. C., & de Queiróz, M. A. (2015b). Microsatellite markers linked to powdery mildew resistance locus in watermelon. *Australian Journal of Crop Science*, 9 (1), 92-97.

Gao, P., Liu, S., Zhu, Q. L., & Luan, F. S. (2015). Marker-assisted selection of Fusarium wilt-resistant and gynoecious melon (*Cucumis melo* L.). *Genetics and Molecular Research*, 14(4), 16255-16264.

Gardes, M., & Bruns, T. D. (1993). ITS primers with enhanced specificity for basidiomycetes-application to the identification of mycorrhizae and rusts. *Molecular Ecology*, *2*(2), 113-118.

Gbotto, A. A., Koffi, K. K., Bi, N. D. F., Bi, S. T. D., Tro, H. H., Baudoin, J. P., & Bi, I. A. Z. (2016). Morphological diversity in oleaginous watermelon (Citrullus mucosospermus) from the Nangui Abrogoua University germplasm collection. *African Journal of Biotechnology*, *15*(21), 917-929.

Ghislain, M., Spooner, D. M., Rodriguez, F., Villamón, F., Nunez, J., Vásquez, C., Waugh, R. & Boniabale, M. (2004). Selection of highly informative and user-friendly microsatellites (SSRs) for genotyping of cultivated potato. *Theoretical and Applied Genetics*, 108(5), 881-890.

Giovannucci, E., Rimm, E. B., Liu, Y., Stampfer, M. J. & Willett, W. C. (2002). A prospective study of tomato products, lycopene, and prostate cancer risk. *Journal of the National Cancer Institute*, 94(5), 391-398

Gordon, V. S. & Staub, J. E. (2014). Backcross introgression of plastomic factors controlling chilling tolerance into elite cucumber (*Cucumis sativus* L.) germplasm: early generation recovery of recurrent parent phenotype. *Euphytica*, 195(2), 217-234.

Gordon, T. R. & Martyn, R. D. (1997). The evolutionary biology of Fusarium oxysporum. *Annual Review of Phytopathology*, *35*(1), 111-128.

Gouda, P. K., Saikumar, S., Varma, C. M., Nagesh, K., Thippeswamy, S., Shenoy, V., Ramesha, M. S. & Shashidhar, H. E. (2013). Marker-assisted breeding of *Pi-1* and *Piz-5* genes imparting resistance to rice blast in PRR 78, restorer line of Pusa RH-10 B asmati rice hybrid. *Plant Breeding*, 132(1), 61-69.

Guerra-Sanz, J. M. (2002). Citrullus simple sequence repeats markers from sequence databases. *Molecular Ecology Notes*, 2(3), 223-225.

Gunner, N., & Wehner, T. C. (2003). Gene list for watermelon. *Cucurbit Genetics Cooperative Report*, 26: 76-92.

Guo, S., Xu, Y., Zhang, H., Gong, G., Huang, S., Yi, H., Wu, M., Zheng, Y.& Fei, Z. (2010). Latest advances in watermelon genomics. *Acta horticulturae*, (871), 599-606.

Guo, S., Zhang, J., Sun, H., Salse, J., Lucas, W. J., Zhang, H., Zheng, Y., Mao, L., Ren, Y., Wang Z., Min, J., Guo, X., Murat, F., Ham, B.K., Zhang, Z., Gao, S., Huang, M., Xu, Y., Zhong, S., Bombarely, A., Mueller, L.A., Zhao, H., He, H., Zhang, Y., Zhang, Z., Huang, S., Tan, T., Pang, E., Lin, K., Hu, Q., Kuang, H., Ni, P., Wang, B., Liu, J., Kou, Q., Hou, W., Zou, X., Jiang, J., Gong, G., Klee, K., Schoof, H., Huang, Y., Hu, X., Dong, S., Liang. D., Wang, J., Wu, K., Xia, Y., Zhao, X., Zheng, Z., Xing, M., Liang, X., Huang, B., Lv, T., Wang, J., Yin, Y., Yi, H., Li, R., Wu, M., Levi, A., Zhang, X., Giovannoni, J.J., Wang, J., Li, Y., Fei, Z. & Xu, Y. (2013). The draft genome of watermelon (*Citrullus lanatus*) and resequencing of 20 diverse accessions. *Nature Genetics*, *45*(1), 51-58.

Guo, H., Mendrikahy, J. N., Xie, L., Deng, J., Lu, Z., Wu, J., Li, X., Shahid, M.Q. & Liu, X. (2017). Transcriptome analysis of neo-tetraploid rice reveals specific differential gene expressions associated with fertility and heterosis. *Scientific Reports*, *7*, 40139. Pp. 12.

GuoYou, Y., Ogbonnaya, F., & Ginkel, M. V. (2010). Marker-assisted recurrent backcrossing in cultivar development. In Singh, R.K *et al.* (eds) *Molecular Plant Breeding: Principle, Method and Application*, 295-319.

Gusmini, G., Wehner, T. C., Joobeur, T., Dean, R. A., & Levi, A. (2004). Protocol for DNA extraction from watermelon leaves for SSR marker studies. *Cucurbit Genetics Cooperative Report*, 27, 25-29.

Hall, C.V. (2004). Watermelons as food in the 22nd century. In: P. Nath, P.B. Gaddagimath, and O.P. Dutta (eds.), *Food security and vegetables: a global perspective*. Prem Nath Agric. Sci. Foundation, Bangalore, India. 135–148.

Hanci, F. & Gökçe, A. F. (2016). Molecular characterization of Turkish onion germplasm using SSR markers. *Czech Journal of Genetics and Plant Breeding*, *52*(2), 71-76.

Harris, K. R., Wechter, W. P., & Levi, A. (2009). Isolation, sequence analysis, and linkage mapping of nucleotide binding site–leucine-rich repeat disease resistance gene analogs in watermelon. *Journal of the American Society for Horticultural Science*, 134(6), 649-657.

Hasan, M. M., Rafii, M. Y., Ismail, M. R., Mahmood, M., Rahim, H. A., Alam, M. A., Ashkani, S., Abdul Malek, M., & Latif, M. A. (2015). Marker-assisted backcrossing: a useful method for rice improvement. *Biotechnology & Biotechnological Equipment*, *29*(2), 237-254.

Hasan, N., Rafii, M. Y., Abdul, H. R., Nusaibah, S. A., Mazlan, N., & Abdullah, S. (2017). Genetic analysis and identification of SSR markers associated with rice blast disease in a BC_2F_1 backcross population. *Genetics and molecular research: GMR*, *16*(1), Pp.11.

Hashizume, T., Shimamoto, I., Harushima, Y., Yui, M., Sato, T., Imai, T., & Hirai, M. (1996). Construction of a linkage map for watermelon (*Citrullus lanatus*(Thunb.) Matsum & Nakai) using random amplified polymorphic DNA (RAPD). *Euphytica*, 90(3), 265-273.

Hawkins, L. K., Dane, F., Kubisiak, T. L., Rhodes, B. B., & Jarret, R. L. (2001). Linkage mapping in a watermelon population segregating for fusarium wilt resistance. *Journal of the American Society for Horticultural Science*, 126(3), 344-350.

He, J., Zhao, X., Laroche, A., Lu, Z. X., Liu, H., & Li, Z. (2014). Genotyping-by-sequencing (GBS), an ultimate marker-assisted selection (MAS) tool to accelerate plant breeding. *Frontiers in Plant Science*, 5, 484. Pp. 8.

Henderson, W. R., Jenkins, S. F., & Rawlings, J. O. (1970). The Inheritance of Fusarium wilt resistance in watermelon, *Citrullus lanatus* (Thunb.) Mansf. *Journal of the American Society of Horticultural Science*, 95, 276-82.

Hirabayashi, H., Sato, H., Nonoue, Y., Kuno-Takemoto, Y., Takeuchi, Y., Kato, H., Nemoto, H., Ogawa, T., Yano, M., Imbe, T., & Ando, I. (2010). Development of introgression lines derived from *Oryza rufipogon* and *O. glumaepatula* in the genetic background of japonica cultivated rice (*O. sativa* L.) and evaluation of resistance to rice blast. *Breeding Science*, *60*(5), 604-612.

Hochholdinger, F & Baldauf, J.A. (2018). Heterosis in plants. *Current Biology* 28(18). 1089-1092. Doi.10.1016/j.cub.2018.06.041

Holland, J. B. (2004). Implementation of molecular markers for quantitative traits in breeding programs—challenges and opportunities. In "New Directions for a Diverse Planet". Proceedings for the 4th International Crop Science Congress. Regional Institute, Gosford, Australia, www. cropscience. org. au/icsc2004.

Hong, M. Y., Hartig, N., Kaufman, K., Hooshmand, S., Figueroa, A., & Kern, M. (2015). Watermelon consumption improves inflammation and antioxidant capacity in rats fed an atherogenic diet. *Nutrition Research*, *35*(3), 251-258.

Hopkins, D. L., Levi, A. & Pitrat, M. (2008). Progress in the development of Crimson Sweet-type watermelon breeding lines with resistance to *Acidovorax avenae* subsp. *citrull*i. Cucurbitaceae 2008, Proceedings of the IXth EUCARPIA meeting on genetics and breeding of Cucurbitaceae (Pitrat M, ed), INRA, Avignon (France), May 21-24th, 2008. 6pp.

Hospital, F. (2005). Selection in backcross programmes. *Philosophical Transactions: Biological Sciences*, (360), 1503-1511.

Hospital, F. (2003). Marker-assisted breeding. In: H.J. Newbury, editor. *Plant molecular breeding*. Oxford and Boca Raton: Blackwell Publishing and CRC Press. Pp. 30-59.

Hospital, F., & Charcosset, A. (1997). Marker-assisted introgression of quantitative trait loci. *Genetics* 147(3), 1469-1485.

Huang, D., Zhang, Y., Jin, M., Li, H., Song, Z., Wang, Y., & Chen, J. (2014). Characterization and high cross-species transferability of microsatellite markers from the floral transcriptome of *Aspidistra saxicola* (Asparagaceae). *Molecular Ecology Resources*, 14(3), 569-577.

Jarret, R. L., Merrick, L. C., Holms, T., Evans, J., & Aradhya, M. (1997). Simple sequence repeats in watermelon (*Citrullus lanatus* (Thunb.) Matsum. & Nakai). *Genome*, 40(4), 433-441.

Jeong, H. S., Jang, S., Han, K., Kwon, J. K., & Kang, B. C. (2015). Marker-assisted backcross breeding for development of pepper varieties (*Capsicum annuum*) containing capsinoids. *Molecular breeding*, 35(12), 226. Pp. 10.

Jiang, G. L. (2013). Plant marker-assisted breeding and conventional breeding: challenges and perspectives. *Adv Crop Sci Tech*, 1(3), e106.

Jiang, G. L. (2015). Molecular marker-assisted breeding: a plant breeder's review. In *Advances in Plant Breeding Strategies: breeding, biotechnology and molecular tools*, 431-472. Springer, Cham.

Johnston-Monje, D., Loewen, S., & Lazarovits, G. (2017). Mycobiomes of tomato plants with vine decline. *Canadian journal of plant pathology*, *39*(2), 184-200.

Joobeur, T., Gusmini, G., Zhang, X., Levi, A., Xu, Y., Wehner, T. C., Oliver, M. & Dean, R. A. (2006). Construction of a watermelon BAC library and identification of SSRs anchored to melon or *Arabidopsis* genomes. *Theoretical and Applied Genetics*, 112(8), 1553-1562.

Joobeur, T., King, J. J., Nolin, S. J., Thomas, C. E., & Dean, R. A. (2004). The fusarium wilt resistance locus Fom-2 of melon contains a single resistance gene with complex features. *The Plant Journal*, 39(3), 283-297.

Joshi, M., Srivastava, R., Sharma, A. K., & Prakash, A. (2013). Isolation and characterization of Fusarium oxysporum, a wilt causing fungus, for its pathogenic and non-pathogenic nature in tomato (*Solanum lycopersicum*). *Journal of Applied and Natural Science*, *5*(1), 108-117.

Kalia, R. K., Rai, M. K., Kalia, S., Singh, R. & Dhawan, A. K. (2011). Microsatellite markers: an overview of the recent progress in plants. *Euphytica*, 177(3), 309-334.

Keinath, A. P. & DuBose, V. B. (2004). Evaluation of fungicides for prevention and management of powdery mildew on watermelon. *Crop Protection*, 23(1), 35-42.

Keinath, A. P., Hassell, R. L., Everts, K. L. & Zhou, X. G. (2010). Cover crops of hybrid common vetch reduce Fusarium wilt of seedless watermelon in the eastern United States. *Plant Health Progress*. Online publication.

Keinath, A. P., & Hassell, R. L. (2014). Control of Fusarium wilt of watermelon by grafting onto bottlegourd or interspecific hybrid squash despite colonization of rootstocks by Fusarium. *Plant disease*, 98(2), 255-266.

Kim, C. H., Park, M. K., Kim, S. K., & Cho, Y. H. (2014). Antioxidant capacity and anti-inflammatory activity of lycopene in watermelon. *International Journal of Food Science & Technology*, *49*(9), 2083-2091.

Kim, J., Kim, D. S., Lee, E. S., Ahn, Y. K., Chae, W. B., & Lee, S. S. (2017). The Construction of a Chinese Cabbage Marker-assisted Backcrossing System Using High-throughput Genotyping Technology. Horticultural Science and Technology 35(2):232-242.

Kiruthika, S. & Padmanabha, B. V. (2018). Analysis of Hybrid Purity in Watermelon using Microsatellite marker in comparison with field GOT .*International Research Journal of Engineering and Technology 5(*4), 761-763.

Kishine, M., Tsutsumi, K., & Kitta, K. (2017). A set of tetra-nucleotide core motif SSR markers for efficient identification of potato (Solanum tuberosum) cultivars. *Breeding Science*, *67*(5), 544-547.

Kleczewski, N. M. & Egel, D. S. (2011). A diagnostic guide for Fusarium wilt of watermelon. *Plant Health Progress*. Pp.8

Koech, R. & Langat, P. (2018). Improving irrigation water use efficiency: A Review of advances, challenges and opportunities in the Australian context. *Water*, 10(1771), Pp. 17.

Koike, S. T., Gladders, P., & Paulus, A. (2006). Vegetable diseases: A colour handbook. CRC Press, Texas, USA. 320pp.

Konstantinov, K., Babic, M., & Drinic, S. M. (2012). Conventional and molecular plant breeding: Benefit and risks in seed and plant quality improvement. In Third International Scientific Symposium" Agrosym 2012", Jahorina, Bosnia and Herzegovina, 15-17 November, 2012. Book of Proceedings (pp. 46-54).

Kordrostami, M., & Rahimi, M. (2015). Molecular markers in plants: concepts and applications. *G3M*, *13*, 4024-4031.

Kumar, V., Rajvanshi, S. K. & Yadav, R.K. (2014) Potential Application of Molecular Markers in Improvement of Vegetable Crops. *International Journal of Advanced Biotechnology and Research* (IJBR). 5(40), 690-707.

Kwon, Y. S., Oh, Y. H., Yi, S. I., Kim, H. Y., An, J. M., Yang, S. G., Ok, S.H. & Shin, J. S. (2010). Informative SSR markers for commercial variety discrimination in watermelon (*Citrullus lanatus*). *Genes & Genomics*, 32(2), 115-122.

Lambel, S., Lanini, B., Vivoda, E., Fauve, J., Wechter, W. P., Harris-Shultz, K. R. & Levi, A. (2014). A major QTL associated with Fusarium oxysporum race 1 resistance identified in genetic populations derived from closely related watermelon lines using selective genotyping and genotyping-by-sequencing for SNP discovery. *Theoretical and Applied Genetics*, 127(10), 2105-2115.

Lang, N. T., Ha, P. T. T., Tru, P. C., Toan, T. B., Buu, B. C., & Cho, Y. C. (2015). Breeding for heat tolerance rice based on marker-assisted backcrosing in Vietnam. *Plant Breeding and Biotechnology*, 3(3), 274-281.

Lateef, D. D. (2015). DNA marker technologies in plants and applications for crop improvements. *Journal of Biosciences and Medicines*, *3*(05), 7-18.

Lau, W. C. P., Rafii, M. Y., Ismail, M. R., Puteh, A., Latif, M. A., Asfaliza, R., & Miah, G. (2017). Development of advanced fragrant rice lines from MR269× Basmati 370 through marker-assisted backcrossing. *Euphytica*, 213(1), 11, pp. 15.

Lembright, H. W. (1990). Soil fumigation: principles and application technology. *Journal of Nematology*, 22(4S), 632-644.

Leslie, J. F., & Summerell, B. A. (2006). *The Fusarium laboratory manual*. Balckwell Publishing, Victoria, Australia. Pp 388.

Levi, A., Thomas, C. E., Keinath, A. P., & Wehner, T. C. (2001a). Genetic diversity among watermelon (*Citrullus lanatus* and *Citrullus colocynthis*) accessions. *Genetic Resources and Crop Evolution*, 48(6), 559-566.

Levi, A., Thomas, C. E., Zhang, X., Joobeur, T., Dean, R. A., Wehner, T. C., & Carle, B. R. (2001b). A genetic linkage map for watermelon based on randomly amplified polymorphic DNA markers. *Journal of the American Society for Horticultural Science*, 126(6), 730-737.

Levi, A., Thomas, C. E., Wehner, T. C., & Zhang, X. (2001c). Low genetic diversity indicates the need to broaden the genetic base of cultivated watermelon. *HortScience*, 36(6), 1096-1101.

Levi, A., Thomas, C., Joobeur, T., Zhang, X., & Davis, A. (2002). A genetic linkage map for watermelon derived from a testcross population *Citrullus lanatus* var. *citroides*× *C. lanatus* var. *lanatus*)× *Citrullus colocynthis*. *Theoretical and Applied Genetics*, 105(4), 555-563.

Levi, A., Davis, A., Hernandez, A., Wechter, P., Thimmapuram, J., Trebitsh, T., Tadmor, Y., Katzir, N., Portnoy, V. & King, S. (2006). Genes expressed during the development and ripening of watermelon fruit. *Plant Cell Reports*, 25 (11). 1233- 1245.

Levi, A., Thies, J. A., Wechter, W. P., Harrison, H. F., Simmons, A. M., Reddy, U. K., Nimmakayala, P. & Fei, Z. (2013). High frequency oligonucleotides: targeting active gene (HFO-TAG) markers revealed wide genetic diversity among *Citrullus* spp. accessions useful for enhancing disease or pest resistance in watermelon cultivars. *Genetic Resources and Crop Evolution*, 60(2), 427-440.

Lin, R.M. (2013). Productivity and Efficiency of Watermelon Farms in Malaysia. *Acta Hortic*. 975, 593-600.

Lin, Y. H., Chen, K. S., Chang, J. Y., Wan, Y. L., Hsu, C. C., Huang, J. W. & Chang, P. F. L. (2010). Development of the molecular methods for rapid detection and differentiation of *Fusarium oxysporum* and *F. oxysporum* f. sp. *niveum* in Taiwan. *New Biotechnology*, 27(4), 409-418.

Lin, Y. H., Chen, K. S., Liou, T. D., Huang, J. W. & Chang, P. F. L. (2009). Development of a molecular method for rapid differentiation of watermelon lines resistant to *Fusarium oxysporum* f. sp. *niveum*. *Botanical Studies*, 50(3), 273-280.

Liu, X., Han, F., Kong, C., Fang, Z., Yang, L., Zhang, Y., Zhuang, M., Liu, Y., Li, Z. & Lv, H. (2017). Rapid Introgression of the Fusarium Wilt Resistance Gene into an Elite Cabbage Line through the Combined Application of a Microspore Culture, Genome Background Analysis, and Disease Resistance-Specific Marker Assisted Foreground Selection. *Frontiers in Plant Science*, *8*(354), pp. 11.

Liu, F., Hu, Z., Liu, W., Li, J., Wang, W., Liang, Z., Wang, F. & Sun, X. (2016). Distribution, function and evolution characterization of microsatellite in Sargassum thunbergii (Fucales, Phaeophyta) transcriptome and their application in marker development. *Scientific Reports*, 6(18947), pp.9.

Lu, G., Guo, S., Zhang, H., Geng, L., Martyn, R. D., & Xu, Y. (2014). Colonization of Fusarium Wilt-Resistant and Susceptible Watermelon Roots by a Green-Fluorescent-Protein-tagged Isolate of *Fusarium oxysporum* f. sp. *niveum*. *Journal of Phytopathology*, 162(4), 228-237.

MacKill, D. J. (2006). Breeding for resistance to abiotic stresses in rice: the value of quantitative trait loci. In Lamkey, K.R. and Lee,M (edn) *Plant Breeding*: The Arnel R. Hallauer International Symposium (pp. 201-212). Ames, Iowa, USA: Blackwell Publishing.

Mackill, D. J. & Ni, J. J. (2001). Molecular mapping and marker-assisted selection for major-gene traits in rice. *Rice genetics* IV, 137-151.

Mahmood, W.W. (2006). Developing Malaysian seed industry: Prospects and challenges. *Economic and Technology Management Review*, 1(1), 51-59.

Maisuria, H. J., Patel, R. M. & Suthar, K. P. (2017). Validation of Molecular Markers Linked to Fusarium Wilt Resistance in Chickpea Genotypes. *International Journal of Pure and Applied Bioscience*, 5(1), 254-260.

Mammadov, J., Aggarwal, R., Buyyarapu, R. & Kumpatla, S. (2012). SNP markers and their impact on plant breeding. *International Journal of Plant Genomics*, pp.11.

Mariod, A.A., Ahmed, Y. M., Matthäus, B., Khaleel, G., Siddig, A., Gabra, A. M. & Abdelwahab, S. I. (2009). A comparative study of the properties of six Sudanese cucurbit seeds and seed oils. *Journal of the American Oil Chemists' Society*, 86(12), 1181-1188

Martyn, R. D. (1985). An aggressive race of *Fusarium oxysporum* f. sp. *niveum* new to the United States. *Plant Disease*, 69(1007), 493-495.

Martyn, R. D. (1987). *Fusarium oxysporum* f. sp. *niveum* race 2: A highly aggressive race new to the United States. *Plant Disease*, 71(3), 233-236.

Martyn, R. D. (2012). Fusarium wilt of watermelon: a historical review. In Cucurbitaceae 2012. Proceedings of the Xth EUCARPIA Meeting on Genetics and Breeding of Cucurbitaceae, Antalya, Turkey, 15-18 October, 2012. University of Cukurova, Ziraat Fakultesi, p. 136-156.

Martyn, R. D. (2014). Fusarium wilt of watermelon: 120 years of research. *Horticultural Reviews*, 42, 349-442

Martyn, R. D. & Hartz, T. K. (1986). Use of soil solarization to control Fusarium wilt of watermelon. *Plant Disease*, 70(8), 762-766.

Martyn, R. D., & McLaughlin, R. J. (1983). Effects of inoculum concentration on the apparent resistance of watermelons to *Fusarium oxysporum* f. sp. *niveum*. *Plant Disease*, 67(5), 493-495.

Martyn, R. D., & Netzer, D. (1991). Resistance to races 0, 1, and 2 of Fusarium wilt of watermelon in Citrullus sp. PI-296341-FR. *HortScience*, 26(4),429-432.

Martyn, R. D., & Bruton, B. D. (1989). An initial survey of the United States for races of *Fusarium oxysporum* f. sp. *niveum*. *HortScience*, 24(4), 696-698.

Mason, A.S. (2015) SSR Genotyping. In: Batley J (ed) *Plant Genotyping*. Springer, New York, NY, pp 77-89.

Maynard, D. N. (2001). Watermelons: characteristics, production, and marketing. ASHS Press, Alexandria, USA. Pp. 227.

Maynard, D. N., & Hopkins, D. L. (1999). Watermelon fruit disorders. *HortTechnology*, 9(2), 155-161.

McGregor, C. (2013). Field trial for Fusarium wilt race 2 resistance in watermelon. Cover letter. 7pp. Accessed as https://watermelon.ag/wp content/uploads/2015/06/McGregor_NWA_2013-Report.pdf on September, 7th, 2017.

Melese, L. (2018). Marker Assisted Selection in Comparison to Conventional Plant Breeding: Review Article. *Agricultural Research & Technology*: Open Access J.; 14(2): 555914, pp. 10.

Meru, G. & McGregor, C. (2016). Genotyping by sequencing for SNP discovery and genetic mapping of resistance to race 1 of *Fusarium oxysporum* in watermelon. *Scientia Horticulturae*, 209, 31-40.

Miah, G., Rafii, M. Y., Ismail, M. R., Puteh, A. B., Rahim, H. A., Islam, K. N. & Latif, M. A. (2013). A review of microsatellite markers and their applications in rice breeding programs to improve blast disease resistance. *International Journal of Molecular Sciences*, 14(11), 22499-22528.

Miah, G., Rafii, M. Y., Ismail, M. R., Puteh, A. B., Rahim, H. A. & Latif, M. A. (2015). Recurrent parent genome recovery analysis in a marker-assisted backcrossing program of rice (*Oryza sativa* L.). *Comptes Rendus Biologies*, 338(2), 83-94.

Michail, S. H., Rehim, A., Tarabeih, A. M. & Aly, M. A. (2002). Effect of Fusarium seed-borne infection levels on watermelon wilt incidence. *Acta Phytopathologica et Entomologica Hungarica*, 37(4), 347-351.

Moges, A. D., Admassu, B., Belew, D., Yesuf, M., Njuguna, J., Kyalo, M., & Ghimire, S. R. (2016). Development of microsatellite markers and analysis of genetic diversity and population structure of *Colletotrichum gloeosporioides* from Ethiopia. *PloS one*, *11*(3), e0151257. Pp. 18.

Mohr, H.C. (1986). Watermelon breeding. In: MJ Bassett, (eds.) *Breeding Vegetable Crops*. Pp 37–66. Avi Publishing, Inc. Westport, CT.

Mondal, U., Khanom, M. S. R., Hassan, L., & Begum, S. N. (2013). Foreground selection through SSRs markers for the development of salt tolerant rice variety. *Journal of the Bangladesh Agricultural University*, *11*(1), 67-72.

Morris, M., Dreher, K., Ribaut, J. M., & Khairallah, M. (2003). Money matters (II): costs of maize inbred line conversion schemes at CIMMYT using conventional and marker-assisted selection. *Molecular Breeding*, 11(3), 235-247.

Mrema, E. & Maerere, A. P. (2018). Growth and yield performance of watermelon during dry and wet seasons under tropical conditions. *International Journal of Vegetable Science*, *24*(5), 483-489.

Muhammad, R. M. & Masdek, N. R. N. M. (2016). Overview of Melon Industry in Malaysia. *Selangor: Malaysian Agricultural Research and Development Institute (MARDI)*.

Nadeem, M. A., Nawaz, M. A., Shahid, M. Q., Doğan, Y., Comertpay, G., Yıldız, M., Hatipoglu, R., Ahmad, F., Alsaleh, A., Labhane, N., Özkan, H., Chung, G. & Baloch, S.F. (2018). DNA molecular markers in plant breeding: current status and recent advancements in genomic selection and genome editing. *Biotechnology & Biotechnological Equipment*, *32*(2), 261-285.

Navot, N., Sarfatti, M. & Zamir, D. (1990). Linkage relationships of genes affecting bitterness and flesh color in watermelon. *Journal of Heredity*, 81(2), 162-165.

Nawaz, M. A., Shireen, F., Huang, Y., Bie, Z., Waqar, A. & Saleem, B. A. (2017). Perspectives of vegetable grafting in Pakistan: current status, challenges and opportunities. *International Journal of Agriculture and Biology*, *19*(5), 1165-1174.

Neeraja, C. N., Maghirang-Rodriguez, R., Pamplona, A., Heuer, S., Collard, B. C. Y., Septiningsih, E. M. & Mackill, D. J. (2007). A marker-assisted backcross approach for developing submergence-tolerant rice cultivars. *Theoretical and Applied Genetics*, 115(6), 767-776.

Neophytou, C., Torutaeva, E., Winter, S., Meimberg, H., Hasenauer, H., & Curto, M. (2018). Analysis of microsatellite loci in tree of heaven (Ailanthus altissima (Mill.) Swingle) using SSR-GBS. *Tree Genetics & Genomes*, *14*(82), pp. 12.

Netzer, D., & Dishon, I. (1973). Screening for resistance and physiological specialization of *Fusarium oxysporum* in watermelon and muskmelon. (Abstr. 941) Second International Congress on Plant Pathology. Minneapolis, Mnn. No. 941.

Netzer, D. (1976). Physiological races and soil population level of Fusarium wilt of watermelon. *Phytoparasitica*, 4 (2), 131-136.

Netzer, D., & Weintall, C. (1980). Inheritance of resistance in watermelon to race 1 of *Fusarium oxysporum* f. sp. *niveum*. *Plant Disease*, 64, 853-854.

Nicolai, M., Cantet, M., Lefebvre, V., Sage-Palloix, A. M., & Palloix, A. (2013). Genotyping a large collection of pepper (Capsicum spp.) with SSR loci brings new evidence for the wild origin of cultivated *C. annuum* and the structuring of genetic diversity by human selection of cultivar types. *Genetic Resources and Crop Evolution*, 60(8), 2375-2390.

Nieves Capote, Ana María Pastrana, Ana Aguado and Paloma Sánchez-Torres (2012). Molecular Tools for Detection of Plant Pathogenic Fungi and Fungicide Resistance. *Plant Pathology*, Intech Open, 151-202.

Nimmakayala, P., Abburi, V. L., Bhandary, A., Abburi, L., Vajja, V. G., Reddy, R., Malkaram, S., Venkatramana, P., Wijeratene, A., Tomason, Y. R., Levi, A., Wehner, T.C & Reddy, U.K. (2014a). Use of VeraCode 384-plex assays for watermelon diversity analysis and integrated genetic map of watermelon with single nucleotide polymorphisms and simple sequence repeats. *Molecular Breeding*, 34(2), 537-548.

Nik Rozana, N. M. M., Suntharalingam, C. & Othman, M. F. (2017). Competitiveness of Malaysia's fruits in the global market: Revealed comparative advantage analysis. *Malays. J. Math. Sci*, *11*, 143-157.

Nybom, H. (2004). Comparison of different nuclear DNA markers for estimating intraspecific genetic diversity in plants. *Molecular Ecology*, 13(5), 1143-1155.

Oliveira, E. J., Pádua, J. G., Zucchi, M. I., Vencovsky, R., & Vieira, M. L. C. (2006). Origin, evolution and genome distribution of microsatellites. *Genetics and Molecular Biology*, 29(2), 294-307.

Okungbowa, F.I. & Shittu, H. O. (2012). Fusarium wilts: an overview. *Environmental Research Journal*, *6*(2). 83-102.

Osei, M. K., Prempeh, R., Adjebeng-Danquah, J., Opoku, J. A., Danquah, A., Danquah, E., Blay, E. & Adu-Dapaah, H. (2018). Marker-Assisted Selection (MAS): A Fast-Track Tool in Tomato Breeding. In *Recent Advances in Tomato Breeding and Production*. IntechOpen. 93-113.

Oumouloud, A., Arnedo-Andres, M. S., Gonzalez-Torres, R., & Alvarez, J. M. (2008). Development of molecular markers linked to the *Fom-1* locus for resistance to Fusarium race 2 in melon. *Euphytica*, 164(2), 347-356.

Paeris, G. K. (1949). Watermelon breeding. *Economic Botany*, 3(2), 193-212.

Palti, J. & Cohen, Y. (1980). Downy mildew of cucurbits (*Pseudoperonospora cubensis*): the fungus and its hosts, distribution, epidemiology and control. *Phytoparasitica*, 8(2), 109-147.

Panigrahi, J., Mishra, R. R., Sahu, A. R., Rath, S. C., & Kole, C. R. (2013). Marker-assisted breeding for stress resistance in crop plants. In Rout, G., Das, A. (Eds) *Molecular Stress Physiology of Plants*. Springer, India. pp. 387-426.

Paris, H. S. (2015). Origin and emergence of the sweet dessert watermelon, *Citrullus lanatus*. *Annals of botany*, 116(2), 133-148.

Paris, H. S., Daunay, M. C., & Janick, J. (2013). Medieval iconography of watermelons in Mediterranean Europe. *Annals of botany*, *112*(5), 867-879.

Park, G., Kim, J., Jin, B., Yang, H. B., Park, S. W., Kang, S. C., Chung, S.M. & Park, Y. (2018). Genome-Wide Sequence Variation in Watermelon Inbred Lines and Its Implication for Marker-Assisted Breeding. *Horticultural Science & Technology*, 36(2), 280-291.

Park, Y., & Cho, S. (2012). Watermelon production and breeding in South Korea. *Israel Journal of Plant Sciences*, 60(4), 415-423.

Peng, J. H., Fahima, T., Röder, M. S., Li, Y. C., Grama, A., & Nevo, E. (2000). Microsatellite high-density mapping of the stripe rust resistance gene *YrH52* region on chromosome 1B and evaluation of its marker-assisted selection in the F_2 generation in wild emmer wheat. *The New Phytologist*, 146(1), 141-154.

Perpina, G., Esteras, C., Gibon, Y., Monforte, A. J., & Picó, B. (2016). A new genomic library of melon introgression lines in a cantaloupe genetic background for dissecting desirable agronomical traits. *BMC Plant Biology*, 16(1), 154.

Persley, D. and Horlock, C. (2003). Management of virus diseases and bacterial leaf blotch of melons. VX99037,Final report to Horticulture Australia Ltd, Queensland Department of Primary Industries, Indooroopilly, Qld. In Persley *et al*., (edn): *Integrated Viral Disease Management in Vegetable Crops*, 156pp.

Phan, N. T. & Sim, S. C. (2017). Genomic Tools and Their Implications for Vegetable Breeding. *Horticultural Science and Technology*, 35(2), 149-164.

Phumichai, C., Phumichai, T., & Wongkaew, A. (2015). Novel chloroplast microsatellite (cpSSR) markers for genetic diversity assessment of cultivated and wild Hevea rubber. *Plant Molecular Biology Reporter*, *33*(5), 1486-1498.

Pitrat, M., Chauvet, M., & Foury, C. (1999). Diversity, history and production of cultivated cucurbits. ISHS *Acta Horticulturae,492*, 21-28.

Prothro, J., Sandlin, K., Abdel-Haleem, H., Bachlava, E., White, V., Knapp, S. & McGregor, C. (2012). Main and epistatic quantitative trait loci associated with seed size in watermelon. *Journal of the American Society for Horticultural Science*, 137(6), 452-457.

Ragimekula, N., Varadarajula, N. N., Mallapuram, S. P., Gangimeni, G., Reddy, R. K. & Kondreddy, H. R. (2013). Marker assisted selection in disease resistance breeding. *Journal of Plant Breeding and Genetics*, 1(2), 90-109.

Ragot, M., Lee, M., & Guimaraes, E. (2007). Marker-assisted selection in maize: current status, potential, limitations and perspectives from the private and public sectors. *Marker-Assisted Selection, Current Status and Future Perspectives in Crops, Livestock, Forestry and Fish*, 117-150.

Rai, N., Bellundagi, A., Kumar, P. K., Kalasapura Thimmappa, R., Rani, S., Sinha, N., Krishna, H., Jain, N., Singh, G. P., Singh, P. K., Chand, S., Prabhu, K. V. & Chand, S. (2018). Marker-assisted backcross breeding for improvement of drought tolerance in bread wheat (*Triticum aestivum* L. em Thell). *Plant Breeding*, *137*(4), 514-526.

Reddy, U. K., Nimmakayala, P., Levi, A., Abburi, V. L., Saminathan, T., Tomason, Y. R., Vajja, G., Reddy, R., Abburi, L., Wehner, T.C., Ronin, Y., & Karol, A. (2014). High-resolution genetic map for understanding the effect of genome-wide recombination rate on nucleotide diversity in watermelon. G3: *Genes, Genomes, Genetics*, 4(11), 2219-2230.

Reddy, V. R. P. (2017). New concepts in plant breeding and genetics. *Adv Plants Agric Res*, 7(1):241–242.

Reetu, V. & Tomar, M. (2017). Watermelon: A Valuable Horticultural Crop with Nutritional Benefits. *Popular Kheti*, 5(2). 5-9.

Ren, Y., Jiao, D., Gong, G., Zhang, H., Guo, S., Zhang, J. & Xu, Y. (2015). Genetic analysis and chromosome mapping of resistance to *Fusarium oxysporum* f. sp. *niveum* (FON) race 1 and race 2 in watermelon (*Citrullus lanatus* L.). *Molecular Breeding*, 35(9), 183.

Ren, Y., McGregor, C., Zhang, Y., Gong, G., Zhang, H., Guo, S., Sun, H., Cai, W., Zhang, J., & Xu, Y. (2014). An integrated genetic map based on four mapping populations and quantitative trait loci associated with economically important traits in watermelon (*Citrullus lanatus*). *BMC Plant Biology*, 14(330, pp 11.

Ren, Y., Zhao, H., Kou, Q., Jiang, J., Guo, S., Zhang, H., Hou, W., Zou, X., Sun, H., Gong, G., Levi, A. & Xu, Y. (2012). A high resolution genetic map anchoring scaffolds of the sequenced watermelon genome. *PLoS One*, 7(1), e29453. Pp.10.

Ribaut, J. M., Banziger, M., Betran, J., Jiang, C., Edmeades, G. O., Dreher, K.& Hoisington, D. (2002). Use of molecular markers in plant breeding: drought tolerance improvement in tropical maize. In Kang, M.S. (edn) *Quantitative Genetics, Genomics, and Plant Breeding*. Pp 85-99.

Robinson, J. (2005). Desertification and disarray: the threats to plant genetic resources of southern Darfur, western Sudan. *Plant Genetic Resources*, 3(1), 3-11.

Robinson, R.W. & Decker-Walters, D.S. (1997). *Cucurbits*. CABI International, New York. N.Y: 226pp.

Saha, D., Rana, R. S., Chakraborty, S., Datta, S., Kumar, A. A., Chakraborty, A. K. & Karmakar, P. G. (2017). Development of a set of SSR markers for genetic polymorphism detection and interspecific hybrid jute breeding. *The Crop Journal*, *5*(5), 416-429.

Sakiyama, N. S., Ramos, H. C. C., Caixeta, E. T. & Pereira, M. G. (2014). Plant breeding with marker-assisted selection in Brazil. *Crop Breeding and Applied Biotechnology*, *14*(1), 54-60.

Salleh, M.M. & Yusof, M. R. (2006). Tropical fruits and vegetables in Malaysia: Production and impact on health. Paper presented at Fruits and vegetable for health workshop. 15- 16, August, 2006, Seoul, Korea.

Salleh, H. (1986). Constraint and challenges in melon breeding in Peninsular Malaysia. In: Proceeding of the Plant and Animal Breeding Workshop, 7- 9th October, MARDI, Serdang, Selngor, Malaysia.

Sambrook, J. & Russell, D. W. (2006). The condensed protocols from molecular cloning: a laboratory manual, CSHL Press, New York. Pp 800.

Sandlin, K., Prothro, J., Heesacker, A., Khalilian, N., Okashah, R., Xiang, W., Bachlava, E., Caldwell, D.G., Taylor, C.A., Seymour, D.K., White, V., Chan, E.,Tolla, G., White, C., Safran, D.,Graham, E., Knapp, S. & McGregor, C. & White, V. (2012). Comparative mapping in watermelon [*Citrullus lanatus* (Thunb.) Matsum. et Nakai]. *Theoretical and Applied Genetics*, *125*(8), 1603-1618.

Santillán-Mendoza, R., Fernández-Pavía, S. P., O'Donnell, K., Ploetz, R. C., Ortega-Arreola, R., Vázquez-Marrufo, G., Benitez-Malvido, J., Montero-Castro, J.C., Soto-Plancarte, A & Rodríguez-Alvarado, G. (2018). A novel disease of big-leaf mahogany caused by two Fusarium species in Mexico. *Plant Disease*, *102*(10), 1965-1972.

Santos, M. H. D., Rodrigues, R., Gonçalves, L. S. A., Sudré, C. P. & Pereira, M. G. (2012). Agrobiodiversity in Cucurbita spp. landraces collected in Rio de Janeiro assessed by molecular markers. *Crop Breeding and Applied Biotechnology*, *12*(2), 96-103.

Sarhan, A. R. T., Barna, B., & Kiraly, Z. (1982). Effect of nitrogen nutrition on Fusarium wilt of tomato plants. *Annals of Applied Biology*, *101*(2), 245-250.

Sarria, E. (2017). Global challenges for the future of watermelon breeding. *Acta Horticulturae*, (*1151*) 5-8.

Semagn, K., Bjørnstad, Å. & Ndjiondjop, M. N. (2006). Progress and prospects of marker assisted backcrossing as a tool in crop breeding programs. *African Journal of Biotechnology*, 5(25). 2588-2603.

Schreuder, W., Lamprecht, S. C. & Holz, G. (2000). Race determination and vegetative compatibility grouping of *Fusarium oxysporum* f. sp. *melonis* from South Africa. *Plant Disease*, 84(3), 231-234.

Servin, B. & Hospital, F. (2002). Optimal positioning of markers to control genetic background in marker-assisted backcrossing. *Journal of Heredity*, 93(3), 214-217.

Sidhu, A. S., & Brar, J. S. (1985). Genetic divergence and hybrid performance in watermelon. *Indian Journal of Agricultural Sciences* 55(7):459-461.

Slater, A. T., Cogan, N. O. & Forster, J. W. (2013). Cost analysis of the application of marker-assisted selection in potato breeding. *Molecular breeding*, *32*(2), 299-310.

Sim, S. C., Robbins, M. D., Wijeratne, S., Wang, H., Yang, W. & Francis, D. M. (2015). Association analysis for bacterial spot resistance in a directionally selected complex breeding population of tomato. *Phytopathology*, 105(11), 1437-1445.

Singh, D., Sinha, B., Rai, V. P., Singh, M. N., Singh, D. K., Kumar, R. & Singh, A. K. (2016). Genetics of Fusarium Wilt (F. udum) Resistance in Pigeonpea (*Cajanus cajan*) and Efficacy of Associated SSR Markers. *Plant Pathology Journal*, 32(1), 1-7.

Singh, Y. (2011). Molecular approaches to assess genetic divergence in rice. *GERF Bulletin of Biosciences*, 2, 41-48.

Singh, R. K., Jena, S. N., Khan, S., Yadav, S., Banarjee, N., Raghuvanshi, S., Bhardwaj, V., Dattamajumder, S. K., Kapur, R., Solomon, S., Swapna, M., Strivastava, S. & Tyagi, A.K. (2013). Development, cross-species/genera transferability of novel EST-SSR markers and their utility in revealing population structure and genetic diversity in sugarcane. *Gene*, 524(2), 309-329.

Singh, V. K., Singh, B. D., Kumar, A., Maurya, S., Krishnan, S. G., Vinod, K. K., Singh, M. P., Ellur, R.K.,Bhowmick, P. K.& Singh, A. K. (2018). Marker-Assisted Introgression of Saltol QTL Enhances Seedling Stage Salt Tolerance in the Rice Variety "Pusa Basmati 1". *International journal of genomics*, *2018*. Pp. 12.

Smith, E. F. (1899). Wilt disease of cotton, watermelon and cowpea (*Neocosmospora nov.* gen.). US. Dept. Agriculture. Division of. Vegetable. Physiology. Pathology. *Bulletin*, (17), 1-54.

Smith, R. J., Uddin, J. M., Gillies, M. H., Moller, P. & Clurey, K. (2016). Evaluating the performance of automated bay irrigation. *Irrigation Science*, *34*(3), 175-185.

Song, R., Gusmini, G., Wehner, T. C., Lebeda, A. & Paris, H. S. (2004). A summary of eleven preliminary studies of greenhouse and field testing methods for resistance to gummy stem blight in watermelon. In *Progress in Cucurbit Genetics and Breeding Research*. 301-305.

Sousaraei, N., Ramshini, H., Lotfi, M. & Sharzei, A. (2018). Marker assisted backcrossing for introgression of Fusarium wilt resistance gene into melon. *Euphytica*, 214(7), pp.7.

Stoskopf, N. C. T., Tomes, D.T., & Christie, B. R (1993). *Plant breeding: theory and practice*, 1st edition. Westview Press, California, USA. Pp. 531.

Suh, J. P., Roh, J. H., Cho, Y. C., Han, S. S., Kim, Y. G., & Jena, K. K. (2009). The *Pi40* gene for durable resistance to rice blast and molecular analysis of Pi40-advanced backcross breeding lines. *Phytopathology*, 99(3), 243-250.

Sundaram, R. M., Vishnupriya, M. R., Biradar, S. K., Laha, G. S., Reddy, G. A., Rani, N. S., Sarma, N.P. & Sonti, R. V. (2008). Marker assisted introgression of bacterial blight resistance in Samba Mahsuri, an elite indica rice variety. *Euphytica*, 160(3), 411-422.

Sundaray, J. K., Rasal, K. D., Chakrapani, V., Swain, P., Kumar, D., Ninawe, A. S., Samiran, N. & Jayasankar, P. (2016). Simple sequence repeats (SSRs) markers in fish genomic research and their acceleration via next-generation sequencing and computational approaches. *Aquaculture International*, *24*(4), 1089-1102.

Suvanprakorn, K. & Norton, J. D. (1980). Inheritance of resistance to race 2 anthracnose in watermelon. *Journal of the American Society for Horticultural Science*, 105(6), 862-865.

Tabiri, B., Agbenorhevi, J. K., Wireko-Manu, F. D. & Ompouma, E. I. (2016). Watermelon seeds as food: Nutrient composition, phytochemicals and antioxidant activity. *International Journal of Nutrition and Food Sciences*, 5(2), 139-144.

Takeuchi, Y., Ebitani, T., Yamamoto, T., Sato, H., Ohta, H., Hirabayashi, H., Kato, H., Ando, I., Nemoto, H., Imbe, T. & Yano, M. (2006). Development of isogenic lines of rice cultivar Koshihikari with early and late heading by marker-assisted selection. *Breeding Science*, 56(4), 405-413.

Tanksley, S. D., Young, N. D., Paterson, A. H. & Bonierbale, M. W. (1989). RFLP mapping in plant breeding: new tools for an old science. *Nature Biotechnology*, 7(3), 257-264.

Tanweer, F. A., Rafii, M. Y., Sijam, K., Rahim, H. A., Ahmed, F., Ashkani, S., & Latif, M. A. (2015). Introgression of blast resistance genes (putative *Pi-b* and *Pi-kh*) into elite rice cultivar MR219 through marker-assisted selection. *Front. Plant. Sci*, 6(1002), Pp. 11.

Thulaja,N.R.(2005).Watermelon.http://eresources.nlb.gov.sg/infopedia/articles/SIP_209_2005-01-06.html www. Accessed online on 18th November, 2016.

Tian, F., Li, D. J., Fu, Q., Zhu, Z. F., Fu, Y. C., Wang, X. K., & Sun, C. Q. (2006). Construction of introgression lines carrying wild rice (*Oryza rufipogon* Griff.) segments in cultivated rice (*Oryza sativa* L.) background and characterization of introgressed segments associated with yield-related traits. *Theoretical and Applied Genetics*, *112*(3), 570-580.

Tibihika, P. D., Curto, M., Dornstauder-Schrammel, E., Winter, S., Alemayehu, E., Waidbacher, H., & Meimberg, H. (2018). Application of microsatellite genotyping by sequencing (SSR-GBS) to measure genetic diversity of the East African Oreochromis niloticus. *Conservation Genetics*, 1-16.

Tran-Nguyen, L. T. T., Condé, B. D., Smith, S. H., & Ulyatt, L. I. (2013). Outbreak of Fusarium wilt in seedless watermelon seedlings in the Northern Territory, Australia. *Australasian Plant Disease Notes*, *8*(1), 5-8.

Tuberosa, R., Salvi, S., Sanguineti, M. C., Maccaferri, M., Giuliani, S. & Landi, P. (2003). Searching for quantitative trait loci controlling root traits in maize: a critical appraisal. *Plants and Soil*, 255(1), 35-54.

Usman, M. G., Rafii, M. Y., Martini, M. Y., Yusuff, O. A., Ismail, M. R. & Miah, G. (2018). Introgression of heat shock protein (Hsp70 and sHsp) genes into the Malaysian elite chilli variety Kulai (*Capsicum annuum* L.) through the application of marker-assisted backcrossing (MAB). *Cell Stress and Chaperones*, 23(2), 223-234.

Van Berloo, R. (2008). GGT 2.0: versatile software for visualization and analysis of genetic data. *Journal of Heredity*, 99(2), 232-236.

Varshney, R. K., Graner, A., & Sorrells, M. E. (2005). Genic microsatellite markers in plants: features and applications. *Trends in Biotechnology*, 23(1), 48-55.

Varshney, R. K., Nayak, S. N., Jayashree, B., Eshwar, K., Upadhyaya, H. D., & Hoisington, D. A. (2007). Development of cost-effective SNP assays for chickpea genome analysis and breeding. SAT eJournal 3(1), 1-3.

Varshney, R. K., Mohan, S. M., Gaur, P. M., Chamarthi, S. K., Singh, V. K., Srinivasan, S., Swapna, M., Sharma, M,. Singh, S., Kaur, L. & Pande, S (2014). Marker-assisted backcrossing to introgress resistance to Fusarium wilt race 1 and Ascochyta blight in C 214, an elite cultivar of chickpea. *The Plant Genome*, *7*(1). pp 11.

Vieira, M. L. C., Santini, L., Diniz, A. L. & Munhoz, C. D. F. (2016). Microsatellite markers: what they mean and why they are so useful. *Genetics and Molecular Biology*, *39*(3), 312-328.

Vignal, A., Milan, D., SanCristobal, M., & Eggen, A. (2002). A review on SNP and other types of molecular markers and their use in animal genetics. *Genetics Selection Evolution*, 34(3), 275-305.

Visscher, P. M., Haley, C. S. & Thompson, R. (1996). Marker-assisted introgression in backcross breeding programs. *Genetics*, 144(4), 1923-1932.

Wang, Y. H., Thomas, C. E. & Dean, R. A. (2000). Genetic mapping of a fusarium wilt resistance gene (*Fom-2*) in melon (Cucumis melo L.). *Molecular Breeding*, 6(4), 379-389.

Wang, B. & Chee, P. W. (2010). Application of advanced backcross QTL analysis in crop improvement. *Journal of Plant Breeding and Crop Science*, *2*(8), 221-232.

Wang, P., Li, Q., Hu, J. & Su, Y. (2015). Comparative analysis of genetic diversity among Chinese watermelon germplasm using SSR and SRAP markers, and implications for future genetic improvement. *Turkish Journal of Agriculture and Forestry*, 39(2), 322-331.

Wechter, W. P., Whitehead, M. P., Thomas, C. E. & Dean, R. A. (1995). Identification of a randomly amplified polymorphic DNA marker linked to the *Fom 2* fusarium wilt resistance gene in muskmelon MR-1. *Phytopathology*, 85(10), 1245-1249.

Wechter, W. P., Kousik, C., McMillan, M., & Levi, A. (2012). Identification of Resistance to *Fusarium oxysporum* f. sp. *niveum* Race 2 in *Citrullus lanatus* var. *citroides* plant introductions. *HortScience*, 47(3), 334-338.

Wehner, T.C. (2008). Watermelon. In: J Prohens, F Nuez, eds. *Handbook of plant breeding, vegetables I*. New York: Springer, 381–418.

Weising, K., Nybom, H., Pfenninger, M., Wolff, K. & Kahl, G. (2005). *DNA Fingerprinting in Plants: Principles, Methods and Applications*. CRC Press. New York. Pp. 472.

White, T. J., Bruns, T., Lee, S. J. W. T. & Taylor, J. L. (1990). Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *PCR Protocols: A Guide to Methods and Applications*, 18(1), 315-322.

Wu, H. S., Gao, Z. Q., Zhou, X. D., Shi, X., Wang, M. Y., Shang, X. X., Liu, Y.D, Gu, L. & Wang, W. Z. (2013). Microbial dynamics and natural remediation patterns of Fusarium-infested watermelon soil under 3-yr of continuous fallow condition. *Soil Use and Management*, 29(2), 220-229.

Xiao, G., Liu, J., Xiao, L., Wu, D. & Luo, H. (2000). Studies and utilization of resistance to Fusarium wilt in watermelon introduced from bottle gourd. *Journal of Hunan Agricultural University*, 26(2), 90-92.

Xu, Y., Kang, D., Shi, Z., Shen, H. & Wehner, T. (2004). Inheritance of resistance to zucchini yellow mosaic virus and watermelon mosaic virus in watermelon. *Journal of Heredity*, 95(6), 498-502.

Xu, Y., Ouyang, X., Zhang, H., Kang, G., Wang, Y., & Chen, H. (1999). Identification of a RAPD marker linked to fusarium wilt resistant gene in wild watermelon germplasm (*Citrullus lanatus* var. *citroides*). *Acta botanica sinica*, 41(9), 952-955.

Xu, Y., Zhang, H. Y., Kang, G. B., Wang, Y. J., & Chen, H. (2000). Studies of molecular marker-assisted-selection for resistance to Fusarium wilt in watermelon (*Citrullus lanatus*) breeding. *Acta genetica Sinica*, *27*(2), 151-157.

Yang, S., Fresnedo-Ramírez, J., Wang, M., Cote, L., Schweitzer, P., Barba, P., Takacs, E.M.,Clark, M., Luby, J., Manns, D.C., Sacks, G., Mansfield, A.K., Londo, J., Fennell, A., Gadoury, D., Reisch, B., Cadle-Davidson, L. & Sun, Q. (2016). A next-generation marker genotyping platform (AmpSeq) in heterozygous crops: a case study for marker-assisted selection in grapevine. *Horticulture research*, 3 (16002), pp. 12.

Ye, G. & Smith, K. F. (2008). Marker-assisted gene pyramiding for inbred line development: Basic principles and practical guidelines. *Int J Plant Breed*, *2*(1), 1-10.

Yetısır, H., Sari, N., & Yücel, S. (2003). Rootstock resistance to Fusarium wilt and effect on watermelon fruit yield and quality. *Phytoparasitica*, 31(2), 163-169.

Yildiz, M., Cuevas, H. E., Sensoy, S., Erdinc, C., & Baloch, F. S. (2015). Transferability of cucurbita SSR markers for genetic diversity assessment of Turkish bottle gourd (Lagenaria siceraria) genetic resources. *Biochemical Systematics and Ecology*, *59*, 45-53.

Yohannes, T., Abraha, T., Kiambi, D., Folkertsma, R., Hash, C. T., Ngugi, K., Mutitu, E., Abraha, N., Weldetsion, M., Mugoya, C., Masiga, C.W. & Villiers, S. (2015). Marker-assisted introgression improves Striga resistance in an eritrean farmer-preferred sorghum variety. *Field Crops Research*, 173, 22-29.

Young, N. D., & Tanksley, S. D. (1989a). RFLP analysis of the size of chromosomal segments retained around the Tm-2 locus of tomato during backcross breeding. *Theoretical and Applied Genetics*, 77(3), 353-359.

Young, N. D., & Tanksley, S. D. (1989b). Restriction fragment length polymorphism maps and the concept of graphical genotypes. *Theoretical and Applied Genetics*, 77(1), 95-101.

Yuge, L. I., Aijiao, X. U., Wei, D. O. N. G., Zhi, L. I., & Guoshen, L. I. (2016). Genetic Analysis of a Dwarf Vine and Small Fruit Watermelon Mutant. *Horticultural Plant Journal*, 2(4), 224-228.

Zainab, R.S. & Hasnah. K.A.K. (2000). Breeding for hybrid watermelon, local assessments of the parental lines. Proceeding of the Fourth National Congress on Genetics, 26-28 September, 2000, Genting Highlands, Pahang.

Zainab, R.S., Zaharah, A. & Bahagia. G.M. (2002). Efficiency of combining abilities of selected parents under different environments. Paper presented at Horticulture research center technical meeting, Mardi, 27-29 August 2002, Port Dickson.

Zane, L., Bargelloni, L. & Patarnello, T. (2002). Strategies for microsatellite isolation: a review. *MolecularEecology*, 11(1), 1-16.

Zhao, W. E., Lv, P. & Gu, H. (2013). Studies on carotenoids in watermelon flesh. *Agricultural Sciences*, *4*(7A), 13-20.

Zhang, H., Fan, J., Guo, S., Ren, Y., Gong, G., Zhang, J., Weng, Y., Davis, A. & Xu, Y. (2016). Genetic diversity, population structure, and formation of a core collection of 1197 *Citrullus* accessions. *HortScience*, 51(1), 23-29.

Zhang, N., Xu, B. H., Bi, Y. F., Lou, Q. F., Chen, J. F., Qian, C. T., Zhang, Y.B. & Yi, H. P. (2017). Development of a muskmelon cultivar with improved resistance to gummy stem blight and desired agronomic traits using gene pyramiding. *Czech Journal of Genetics and Plant Breeding*, *53*(1), 23-29.

Zhang, S. P., Miao, H., Yang, Y. H., Xie, B. Y., Wang, Y., & Gu, X. F. (2014). A major quantitative trait locus conferring resistance to fusarium wilt was detected in cucumber by using recombinant inbred lines. *Molecular Breeding*, 34(4), 1805-1815.

Zhang, Y., Zhang, H. Y., Guo, S. G., Ren, Y., Zhang, J., Geng, L. H., ... & Yong, X. (2013). Developments of molecular markers tightly linked to Fon-1 for resistance to *Fusarium oxysporum* f. sp. *niveum* race 1 in watermelon. *Scientia Agricultura Sinica*, 46, 2085-2093.

Zhang, Z., Zhang, J., Wang, Y. & Zheng, X. (2005). Molecular detection of Fusarium oxysporum f. sp. niveum and Mycosphaerella melonis in infected plant tissues and soil. *FEMS Microbiology Letters*, *249*(1), 39-47.

Zhang, R., Xu, Y., Yi, K., Zhang, H., Liu, L., Gong, G. & Levi, A. (2004). A genetic linkage map for watermelon derived from recombinant inbred lines. *Journal of the American Society for Horticultural Science*, 129(2), 237-243.

Zhang, X. P., Rhodes, B. B., Baird, W. V., Skorupska, H. T., & Bridges, W. C. (1996). Development of genic male-sterile watermelon lines with delayed-green seedling marker. *HortScience*, 31(1), 123-126.

Zhou, X. G., & Everts, K. L. (2003). Races and inoculum density of *Fusarium oxysporum* f. sp. *niveum* in commercial watermelon fields in Maryland and Delaware. *Plant Disease*, 87(6), 692-698.

Zhou, X. G., & Everts, K. L. (2004). Quantification of root and stem colonization of watermelon by *Fusarium oxysporum* f. sp. *niveum* and its use in evaluating resistance. *Phytopathology*, 94(8), 832-841.

Zhou, X. G., Everts, K. L., & Bruton, B. D. (2010). Race 3, a new and highly virulent race of *Fusarium oxysporum* f. sp. *niveum* causing Fusarium wilt in watermelon. *Plant Disease*, 94(1), 92-98.

Zhu, H., Song, P., Koo, D. H., Guo, L., Li, Y., Sun, S., Weng, Y. & Yang, L. (2016). Genome wide characterization of simple sequence repeats in watermelon genome and their application in comparative mapping and genetic diversity analysis. *BMC Genomics*, 17(1), 557.

Zohary, D., Hopf, M. & Weiss, E. (2012). Domestication of Plants in the Old World: The origin and spread of domesticated plants in Southwest Asia, Europe, and the Mediterranean Basin. Oxford University Press, Oxford. Pp. 243.

Zou X-H, Zhang H-Y, Li S, Geng L-H, Gong G-Y, Ren Y, Xu Y (2011). Inheritance of resistance to race 2 of *Fusarium oxysporum* f. sp. *niveum* in watermelon wild germplasm PI296341-FR (*Citrullus lanatus* var. *citriodes)*. *Acta Horticulturae Sinica* 9, 1699-1706.

BIODATA OF STUDENT

Kazeem Kolapo was born on the 12th October 1974 in Ede, Osun State, Nigeria. On completing his primary and secondary education, he was admitted to University of Ibadan, Ibadan, Nigeria where he had his B.Sc Agriculture (Agronomy) and M.Sc Forest Resources Management (Forest Biology and Silviculture) in the years 2001 and 2005 respectively.

He worked briefly as an agricultural extension officer with the Osun State Government bewtween 2006 and 2009 before taking up a lecturing job in the Department of Agronomy, Osun State University, Osogbo, Nigeria from year 2009 till date.

Kazeem was awarded Nigeria's government sponsored Tertiary Education Trust Fund (TETFUND) to pursue his PhD. He started the programme in 2015 at the Institute of Tropical Agriculture and Food Security, Universiti Putra Malaysia under the supervision of Prof Dr. Mohd Rafii Yusop.

He is happily married to Mrs Idayat Idowu and the marriage is blessed with promising children.

LIST OF PUBLICATIONS

Kazeem K. Olalekan, Mohd Y. Rafii, Azrul M. Salleh, Mahmud TM. Mohamed, Khairulmazmi Ahmad, Azizah Misran,Tanweer F. Abro, Yusuff Oladosu, Ibrahim W. Arolu, Chukwu Samuel, Magaji Usman. (2019). Analysis of Recurrent Parent Genome Recovery in Marker-Assisted Backcross Breeding Program in Watermelon. *International Journal of Scientific & Technology Research*. 8(08): 945-955.

Olalekan Kazeem Kolapo, M. K. A. Wahab, Md. Aktar Hossain, Adegeye O. Adebola and Nor Aini Ab. Shukor. (2014). Effects of *Albizia saman* (Jacq. Mull) leaf mulch on vegetative growth of maize (*Zea mays* L.) and soil chemical properties through biomass transfer. *Res. on Crops* **15** (4): 768-774.

Olalekan K.K, Rafii ,M.Y, M.S. Azrul, Mahmud T.M, Khairulmasmi A , Azizah Misran , Ibrahim .W.A and Magaji Usman. Identification of simple sequence repeat markers associated with wilt resistance in inbred lines of watermelon in Malaysia. (Submitted to Scientia horticulturae, IF. 1.76, Q1)

UNIVERSITI PUTRA MALAYSIA

STATUS CONFIRMATION FOR THESIS / PROJECT REPORT AND COPYRIGHT

ACADEMIC SESSION : Second Semester 2018/2019

TITLE OF THESIS / PROJECT REPORT :

DEVELOPMENT OF FUSARIUM WILT RESISTANT AND HIGH YIELDING WATERMELON (*Citrullus lanatus* L.) VARIETY THROUGH MARKER-ASSISTED BACKCROSS BREEDING

NAME OF STUDENT : OLALEKAN KAZEEM KOLAPO

I acknowledge that the copyright and other intellectual property in the thesis/project report belonged to Universiti Putra Malaysia and I agree to allow this thesis/project report to be placed at the library under the following terms:

1. This thesis/project report is the property of Universiti Putra Malaysia.
2. The library of Universiti Putra Malaysia has the right to make copies for educational purposes only.
3. The library of Universiti Putra Malaysia is allowed to make copies of this thesis for academic exchange.

I declare that this thesis is classified as :

*Please tick (√)

☐	**CONFIDENTIAL**	(Contain confidential information under Official Secret Act 1972).
☐	**RESTRICTED**	(Contains restricted information as specified by the organization/institution where research was done).
☐	**OPEN ACCESS**	I agree that my thesis/project report to be published as hard copy or online open access.

This thesis is submitted for :

☐ **PATENT** Embargo from _____ (date) until _____ (date)

Approved by:

_____
(Signature of Student)
New IC No/ Passport No.:

Date :

_____
(Signature of Chairman of Supervisory Committee)
Name:

Date :

[Note : If the thesis is CONFIDENTIAL or RESTRICTED, please attach with the letter from the organization/institution with period and reasons for confidentially or restricted.]