



***GENETICS AND COMBINING ABILITY OF CORN (*Zea mays* L.)
GENOTYPES FOR FORAGE UTILIZATION***

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FP 2019 52



**GENETICS AND COMBINING ABILITY OF CORN (*Zea mays* L.)
GENOTYPES FOR FORAGE UTILIZATION**

By

MAIZURA BINTI ABU SIN

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

June 2019

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DEDICATION

To Family Members:

My Beloved Parents

Abu Sin bin Md Din

Samsiah bte Rebin

Siblings

Noraini Abu Sin, Norashikin Abu Sin, Eyuddin Abu Sin, Ibrahim

Abu Sin, Nohanida Abu Sin, Hairul Azuan Abu Sin

Nieces and Nephews

Nur Nadia Nor Khairul Azha, Huraiyah Nabillah Zaaday,

Akmal Hisyam Nor Khairul Azha, Muhammad Zulhilmi

Zaaday, Huraiyah Rasyiqah Zaaday, Muhammad Haziq

Zaaday, Huraiyah Az-Zahra Zaaday, Muhammad Hazim

Zaaday, Harraz Naufal Hairul Azuan and Muhammad Uwais

Al-Qarni Abdul Fattah, and

Husband

Mohd Zakwan bin Zamri

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

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June 2019

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Studies were conducted to evaluate agronomic and nutritive quality performance of forage corn inbred lines obtained from the International Wheat and Maize Improvement Center (CIMMYT), with the objectives to reveal genetic variation among these genotypes using simple sequence repeat (SSR) DNA markers, to investigate and select potential parental inbred lines from different heterotic groups based on genetic diversity revealed by agronomic and molecular characteristics towards hybrid variety production, and to determine their heterosis and combining ability, and performance of hybrids produced for forage utilization. In the first study, genetic diversity and relationships among 30 corn inbred lines comprising of 28 introductions from the International Wheat and Maize Improvement Center (CIMMYT), one from Indonesia and a locally developed one, were evaluated using 100 simple sequence repeat (SSR) markers. A total of 550 alleles were detected on 100 loci from the 30 inbred lines. Results showed that allelic richness per locus was in the range of 2 to 13 loci, with an average of 5.50 alleles. From these, the effective alleles (N_e) per locus was estimated at 3.75 alleles, indicating that those alleles were effective in showing diversity among the inbred lines. Although allelic richness among the inbred lines was high, estimate of observed heterozygosity (H_o) was found to be low for each inbred line, with an average of 0.017. This indicates that the inbred lines have reached homozygosity at almost all loci amplified. Polymorphic information content (PIC) values among the 100 loci ranged from 0.178 to 0.874, with mean value of 0.624, showing that the SSR markers used were informative and able to assess genetic diversity among the inbred lines. Four heterotic groups were formed from the dendrogram constructed using Unweighted Pair Group with Arithmetic Averages (UPGMA) method within a similarity index of 0.350. In the second study, 19 diverse homozygous inbred lines representing 28 inbred lines from the first study were evaluated under optimum conditions,

and were found to show significant differences in performance of the traits among them, indicating that the lines varied in many aspects, and these differences could be exploited for specific purposes in breeding programs. Genetic distances among the inbred lines based on phenotypic and molecular characteristics were used to identify major heterotic groups and have revealed the presence of high level of genetic diversity among the inbred lines studied. Selection of the parental inbred lines among the genetically diverse ones for making crosses was conducted based on their performance for important forage traits. In the third study, six parental inbred lines were selected and crossed in a half-diallel arrangement to produce 15 single-cross hybrids. Fifteen single-cross hybrids and their parental inbred lines were evaluated in a randomized complete block design (RCBD) with three replications at two different environments, for agronomic and forage nutritive quality performances. All hybrids showed superiority over their parental inbred lines for biomass traits studied, indicating the existence of a substantial amount of heterosis in the hybrids. Among the hybrids produced, HF10, HF3, HF15, HF1 HF13 and HF11 revealed forage yield, forage yield components and forage nutritive quality performance better than the check varieties (BTL1 and Pool26) in the two environments studied. Moreover, these hybrids exhibited consistently high mid-parent and better-parent heterosis for the traits studied, indicating the accumulation of favorable genes inherited from their parental inbred lines. Mid-parent and better-parent heterosis estimates revealed from the evaluations were positive for all traits except acid detergent fiber (ADF), neutral detergent fiber (NDF), days to tasseling and days to silking, where the lower magnitudes of these traits were superior, indicating earliness. The combining ability analysis reveals the presence of significant general combining ability (GCA) for all traits except dry leaf yield, dry ear yield and ADF, and the presence of significant specific combining ability (SCA) for all traits except NDF, days to silking and days to tasseling from the combined data of the two environments. This indicates that there were significant additive and non-additive gene actions involved in the genetic control of the traits measured from the combined data of the two environments. Inbred line CML428 was identified as the best general combiner among the parental inbred lines and performed consistently, with significant GCA estimates for fresh plant yield, dry plant yield, fresh stem yield, dry stem yield, plant height and ear height, and was therefore identified as the superior one possessing high accumulation of favorable additive genes. In addition, high negative estimates of GCA were found contributing to early days to flowering of the progeny. Among the crosses, HF9 (CML331 x CML498), HF6 (CML331 x CML383), HF11 (CML383 x CML491) and HF10 (CML383 x CML428) were identified as the best combinations giving favorable positive SCA estimates for forage yield and yield related traits at each environment and pooled environments. In general, fresh and dry matter yields exhibited low narrow-sense heritability although having high broad-sense heritability, indicating the preponderance of non-additive gene actions in the inheritance of the yield traits measured. Based on genetic similarities among the parental inbred lines, when data were taken from amplifications of microsatellite markers with more than 30% polymorphic bands, CML491 and CML498 were found to reveal the highest genetic similarity (0.410), while CML383 and CML428 were found to exhibit the lowest genetic similarity (0.149). The low genetic similarity could indicate diverse genetic background among the inbred lines, due to prior selection applied on the parental inbred lines from different heterotic groups. The combination of CML383 x CML428 (HF10) was identified among

those with high yield and good nutritive quality performance. In addition, this combination was one of the best, with favorable positive SCA estimates for forage yield and yield related traits at each environment and pooled environments. There were significant positive relationships between genetic similarities of parental inbred lines based on 100 microsatellite markers used and mid-parent heterosis for fresh plant yield, and between genetic similarities of parental inbred lines based on microsatellite markers with more than 30% polymorphic bands and mid-parent heterosis for fresh plant yield in Field 10 and also when data of the two environments were combined. This reveals the effectiveness of the markers used in this study for prediction of performance of hybrids produced for forage utilization. The performance of these superior hybrids was consistent across environments, and therefore these hybrids should be considered for further testing in multi-locational trials to reveal their potential, before their release as new forage corn hybrid varieties in the future.

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

**GENETIK DAN KEUPAYAAN BERGABUNG GENOTIP JAGUNG
(*Zea mays* L.) UNTUK KEGUNAAN FORAJ**

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Beberapa kajian telah dijalankan untuk menilai prestasi agronomi dan kualiti nutrisi titisan-titisan inbred jagung foraj yang diperolehi daripada *International Wheat and Maize Improvement Center* (CIMMYT), dengan objektif untuk mempamerkan variasi genetik dalam kalangan genotip-genotip ini melalui penanda DNA jujukan mudah berulang (SSR), untuk mengkaji dan memilih titisan inbred induk yang berpotensi dari kumpulan heterotik yang berbeza berdasarkan kepelbagaian genetik menggunakan ciri agronomi dan molekul ke arah pengeluaran varieti hibrid, dan menentukan heterosis dan keupayaan bergabung antaranya, dan prestasi hibrid yang dihasilkan untuk kegunaan foraj. Dalam kajian yang pertama, kepelbagaian genetik dan hubungan di kalangan 30 titisan inbred jagung yang terdiri daripada 28 yang diperkenalkan dari *International Wheat and Maize Improvement Center* (CIMMYT), satu dari Indonesia dan satu inbred tempatan yang dibangunkan, telah dikaji dengan menggunakan 100 penanda mikrosatelit DNA (SSR). Sejumlah 550 alel telah dikesan pada 100 lokus dalam 30 titisan inbred tersebut. Keputusan menunjukkan kekayaan alel untuk setiap lokus adalah pada julat 2 hingga 13 lokus, dengan purata 5.50 alel. Dari ini, alel yang efektif (N_e) setiap lokus adalah dalam anggaran 3.75 alel, menunjukkan bahawa alel beketaan adalah efektif dalam mempamerkan kepelbagaian di kalangan titisan-titisan inbred tersebut. Walaupun kekayaan alel antara titisan inbred adalah tinggi, anggaran heterozigositi diperolehi (H_o) didapati rendah bagi setiap titisan inbred, dengan purata 0.017. Ini menunjukkan bahawa titisan-titisan inbred tersebut telah mencapai homozigositi hampir di semua lokus yang diampifikasi. Nilai kandungan maklumat polimorfik (PIC) di kalangan 100 lokus ber julat dari 0.178 hingga 0.874, dengan nilai purata 0.624, menunjukkan bahawa penanda SSR yang digunakan adalah penanda yang bermaklumat dan boleh mengakses kepelbagaian genetik antara titisan-titisan inbred. Empat kumpulan heterotik

telah dihasilkan daripada dendrogram yang dibina menggunakan kaedah Kumpulan Pasangan Tak Berpemberat dengan Purata Aritmatik (UPGMA) di dalam indeks persamaan 0.350. Dalam kajian kedua, 19 titisan inbred yang pelbagai dan homozigot mewakili 28 titisan inbred dari kajian pertama telah dinilai di dalam keadaan yang optimum, dan didapati menunjukkan perbezaan ketara titisan-titisan tersebut dalam prestasi ciri-ciri yang diukur. Ini memberi gambaran bahawa titisaan-titisan tersebut berbeza dalam pelbagai aspek, dan perbezaan ini boleh dieksploitasi untuk tujuan khusus dalam program pembiakbakaan. Jarak genetik di kalangan titisan-titisan inbred ini untuk ciri-ciri fenotip dan ciri-ciri molekul telah digunakan untuk mengenal pasti kumpulan heterotik utama dan telah menunjukkan kehadiran kepelbagaian genetik yang tinggi antara titisan-titisan inbred yang dikaji. Pemilihan titisan inbred induk di kalangan yang berkepelbagaian tinggi untuk menghasilkan kacukan telah dibuat berdasarkan prestasi untuk sifat-sifat penting foraj. Dalam kajian yang ketiga, enam titisan inbred induk telah dipilih dan dikacukkan di dalam susunan separuh-diallel untuk menghasilkan 15 hibrid kacukan tunggal. Lima belas hibrid kacukan tunggal berkenaan bersama-sama dengan enam titisan inbred tersebut kemudiannya telah dinilai di dalam RCB dengan tiga replikasi di dua persekitaran yang berbeza untuk prestasi agronomi dan kualiti nutrisi forajnya. Kesemua hibrid menunjukkan keunggulan dibandingkan titisan inbred induknya untuk ciri-ciri biomas yang diukur, menunjukkan wujudnya heterosis yang ketara pada hibrid-hibrid ini. Antara hibrid yang dihasilkan, HF10, HF3, HF15, HF1 HF13 dan HF11 telah mendedahkan prestasi hasil foraj, komponen hasil foraj dan kualiti foraj yang lebih baik daripada varieti-varieti kawalan (BTL1 dan Pool26) di kedua-dua persekitaran yang dikaji. Tambahan lagi, hibrid-hybrid ini mempamerkan heterosis induk-pertengahan dan heterosis induk-terbaik yang konsisten tinggi untuk ciri-ciri yang dikaji, yang menunjukkan terjadinya pengumpulan gen yang diperlukan diwarisi dari induk titisan inbrednya. Anggaran heterosis berdasarkan nilai pertengahan induk dan nilai induk terbaik yang diperolehi dari penilaian ini adalah positif untuk semua ciri-ciri kecuali kandungan 'asid detergent fiber' (ADF), 'neutral detergent fiber' (NDF), hari pentaselan dan hari perambutan, di mana magnitud yang lebih rendah bagi sifat-sifat ini adalah yang unggul dan menunjukkan sifat awal. Analisis keupayaan bergabung mendedahkan wujudnya keupayaan bergabung am (GCA) yang bererti bagi semua ciri kecuali hasil daun kering, hasil tongkol kering dan ADF, dan wujudnya keupayaan bergabung khusus (SCA) yang bererti bagi semua ciri kecuali NDF, hari pentaselan dan hari perambutan, dari data gabungan kedua-dua persekitaran. Ini menunjukkan terdapatnya tindakan gen additif dan tindakan gen bukan-additif yang ketara dalam kawalan genetik ciri-ciri yang diukur pada data gabungan dari kedua-dua persekitaran. Titisan inbred CML428 telah dikenalpasti sebagai penggabung am yang terbaik di kalangan titisan inbred induk, dan menunjukkan prestasi yang konsisten dengan anggaran GCA yang ketara untuk hasil pokok segar, hasil pokok kering, hasil batang segar, hasil batang kering, ketinggian pokok dan ketinggian tongkol, dan dengan itu dikenalpasti sebagai yang unggul, dan memperolehi banyak pengumpulan alel additif yang diinginkan. Tambahan lagi, anggaran GCA negatif bermagnitud tinggi, didapati telah menyumbang kepada awalnya hari berbunga pada progeni. Antara kacukan, HF9 (CML331 x CML498), HF6 (CML331 x CML383), HF11 (CML383 x CML491) dan HF10 (CML383 x CML428) telah dikenalpasti sebagai gabungan yang terbaik, dengan anggaran SCA positif yang diperlukan untuk ciri-ciri hasil foraj dan komponen-komponen berkaitan hasil foraj di setiap

persekitaran dan apabila data dari yang persekitaran digabungkan. Secara amnya, hasil bahan segar dan hasil bahan kering mempamerkan kebolehwarisan sempit yang rendah walaupun mempunyai kebolehwarisan luas yang tinggi, menunjukkan bahawa ada dominasi tindakan gen bukan-aditif dalam pewarisan ciri-ciri hasil yang diukur. Berdasarkan persamaan genetik antara induk -titisan-titisan inbred, apabila data diambil dari penanda mikrosatelit yang menunjukkan lebih daripada 30% jujukan polimorfik, CML491 dan CML498 mendedahkan persamaan genetik tertinggi (0.410), manakala CML383 dan CML428 mempamerkan persamaan genetik yang paling rendah (0.149). Persamaan genetik yang rendah yang dipamerkan menunjukkan latar belakang genetik yang luas antara titisan inbred, kerana pemilihan awal yang telah dilakukan ke atas induk titisan inbred tersebut yang diperolehi dari kumpulan heterotik yang berbeza. Gabungan antara titisan inbred CML383 x CML428 (HF10) telah dikenalpasti sebagai gabungan yang mempunyai hasil yang tinggi dan mempunyai prestasi kualiti nutrisi foraj yang baik. Di samping itu, kombinasi ini juga adalah salah satu daripada gabungan terbaik, dengan anggaran SCA positif yang diinginkan, bagi ciri-ciri hasil foraj dan ciri berkaitan hasil foraj pada setiap persekitaran dan bila data dari persekitaran digabungkan. Terdapat hubungan positif yang ketara antara persamaan genetik induk titisan inbred berdasarkan 100 penanda mikrosatelit yang digunakan dengan heterosis berdasarkan nilai pertengahan-induk untuk hasil pokok segar, dan di antara persamaan genetik antara induk titisan inbred berdasarkan penanda mikrosatelit dengan lebih daripada 30 % jujukan polimorfik dan heterosis berdasarkan nilai pertengahan-induk untuk hasil pokok segar di Ladang 10 dan juga apabila data dari dua persekitaran digabungkan. Ini mendedahkan keberkesanan penanda yang digunakan dalam kajian ini untuk meramal prestasi hibrid yang dihasilkan untuk kegunaan foraj. Prestasi hibrid ini adalah konsisten pada semua persekitaran, oleh itu hibrid-hibrid yang unggul ini perlu dipertimbangkan untuk diuji selanjutnya dalam pengujian pelbagai lokasi bagi mempamerkan potensinya, sebelum diisytiharkan sebagai potensi penggunaannya dalam ujian multi-lokasi berskala besar sebelum ia didaftarkan sebagai varieti hibrid jagung foraj baru akan datang.

ACKNOWLEDGEMENTS

All praises and thanks to The Almighty Allah for His mercy and bounteous blessings in enabling me to complete this study.

My deepest gratitude and appreciation go to Professor Dr. Ghizan bin Saleh, my main supervisor and chairman of my supervisory committee for the guidance, supportive criticism, valuable advice and knowledge, and support in accomplishing this study as well as other aspects during the completion of this study at Universiti Putra Malaysia. His patience, support, useful comments and sacrifices will always be remembered. I would also like to show my sincere appreciation and thanks to the former committee members, Associate Professor Dr. Nur Ashikin Psyquay Abdullah and Associate Professor Dr. Mohd Ridzwan A. Halim, for their respectful guidance, advice, constructive comments and encouragements during the period of this research study. Their great help and valuable ideas are always appreciated. My sincere appreciation and gratitude also go to Dr. Pedram Kashiani for his time spent, constructive ideas, encouragements and advice through the course of this study. Also, to the present new committee members, Professor Dr. Loh Teck Chwen and Professor Dr. Mahmud Tengku Muda Mohamed, thanks for the support.

My sincere gratitude and appreciation also go to various institutions and individuals who have assisted me and contributed to the completion of this study. Special thanks go to the Ministry of Science, Technology and Innovation, Malaysia (MOSTI) for the financial support of the research under the grant from the Agro-Biotechnology Institute of Malaysia initiative (Project No. 10-05-ABI-AB035) obtained by Professor Dr. Ghizan bin Saleh. Thanks and appreciations go to Universiti Putra Malaysia (UPM) for providing me the financial support under the Special Graduate Research Allowance (S-GRA), and Ministry of Higher Education (MOHE) for the financial support under the sponsorship of MyBrain15. Thanks to the International Maize and Wheat Improvement Center (CIMMYT), Mexico for supplying seeds of the corn inbred lines.

I would also like to express my deepest appreciations and thanks to the staff members of the Faculty of Agriculture, UPM, in particular all the staff members at Field 2 and Field 10 including Mr. Zainee Mohd Luis, Mr. Adnan Abdul Karim, Mr. Mohd Shahril Ab. Rahman, Mrs Siti Nadirah Dasar and Mr. Khalid Ismail. Also, to the Science Officers of Department of Crop Science, Faculty of Agriculture, Mr. Mohd Norhaizan Saliudin, Mr. Mohd. Khoiri Kandar, Mr. Helmy Hamisan and Mr. Muhammad Bin Yaacob, for their kind assistance and providing equipments for the laboratory work. I would also like to express my thanks to my colleagues, to mention some, Mrs. Nazatul Shima Naharuddin, Mrs. Nor Fadzillah Mohd Fazdil, Mr. Neyaz Mustafa Rashid, the research assistants and the undergraduate students that were involved in this study. My special thanks and gratitude also go to my dearest and lovely friends, Mrs Anis Syahirah Mohktar, Mr. Mohd Akmal Mohd Raffi, Ms Siti Mahsuri Talib, Ms Nurulhasanah

Ishak, Ms Ilyana Che Hasan, Ms Kasmaliza Mohd Razali and members of Postgraduate Room 4 for their kind friendship and moral support through the past years.

Finally, yet importantly, I am very much thankful and grateful to express my love and respects to my beloved father, Abu Sin bin Md Din and my lovely mother, Samsiah bte Rebin for their understanding, moral support and sacrifices, and endless love. My deep gratitude goes to the family members; sisters and brothers, nieces and nephews and husband for their love and support. Thank you for this endless love and understanding. May Allah bless you with His love. In Shaa Allah.



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

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LIST OF ABBREVIATIONS

ADF	Acid detergent fiber
ADL	Acid detergent lignin
ADS	Acid detergent solution
AFLP	Amplified fragment length polymorphism
ANOVA	Analysis of variance
BME	Beta mercaptoethanol
bp	Base pair
BPH	Better-parent heterosis
CIMMYT	International Maize and Wheat Improvement Center
CP	Crude protein
CTAB	Cetyltrimethylammonium bromide
CV	Coefficient of variation
DM	Dry matter
DMI	Dry matter index
DNMRT	Duncan's New Multiple Range Test
DVS	Department of Veterinary Services
EDTA	Ethylenediamine tetra-acetic acid
GML	Ground magnesium limestone
GWG	Green World Genetics
GT	Genotype-trait
MAB	Marker assisted breeding
MT	Metric tonnes
MOA	Ministry of Agriculture
MMAS	Molecular marker assisted selection
MPH	Mid-parent heterosis
NDF	Neutral detergent fiber
NIRS	Near infrared reflectance spectroscopy
PCA	Principal component analysis
PCoA	Principal coordinate analysis
PCR	Polymerase chain reaction
PIC	Polymorphic information content
PKC	Palm kernel cake
POME	Palm oil mill effluent
PPF	Palm press fiber
RAPD	Random amplified polymorphic DNA
RCBD	Randomized complete block design
RCF	Relative centrifugal force
RFLP	Restriction fragment length polymorphism
SAS	Statistical analysis system
SBE	Spent bleaching earth
SD	Standard deviation
SE	Standard error
SSR	Simple sequence repeat
SVD	Singular value decomposition
TBE	Tris-borate-EDTA buffer
TE	Tris-EDTA buffer
TFNet	Tropical Fruit Network
UPM	Universiti Putra Malaysia

CHAPTER 1

INTRODUCTION

Corn is one of the world's most important food crops besides rice and wheat (FAOSTAT, 2017). The diverse use of corn as human food, animal feed, forage and bio-fuel has led to its production in great amount. There are many types of cultivated corn, among commonly grown are flint corn, dent corn, flour corn, popcorn and sweet corn. Corn is mostly planted for the grains but the plant biomass is also harvested for forage used as feed to the ruminants. Presently, there is an increasing demand for corn plants for use as forage in the form of silage. Corn when used as forage offers a high-quality feed for dairy cattle (Michalet-Doreau and Philippeau, 1999). It is also widely used as an energy and roughage source for beef cattle (Mosanto, 2010). This is because of its high digestibility, energy, nutritive quality and palatability (Craig, 2010).

Corn has been widely planted with a total world production of 1,134.7 million MT harvested from 197.2 million ha, as reported by FAOSTAT (2018). The United States is the leading corn producer (371 million MT of total corn production), with 4.0 million MT harvested for forage utilization in 2017 (FAOSTAT, 2018). In Malaysia, corn production was mainly for sweet corn and occupied approximately 10 000 ha of land, with a total production of 64 900 MT in 2016. Corn is mainly grown in the states of Perak, Johor, Pahang and Kelantan (MOA, 2016). Recently, the Malaysian government has aimed to allocate 20,000 hectares of land for grain corn production, with early trials grown in Terengganu states. This effort was taken by the government in order to reduce the county's dependence on importation, especially from Argentina and Brazil which worth RM3.3 billion annually (USDA, 2015). In addition, this effort explains that corn will be grown widely in Malaysia not only for sweet corn for human consumption but also for animal feed.

Malaysia utilizes more than three million tonnes of animal feed materials every year, including the available agriculture by-products. Feed contributes to a large proportion of the cost of production in livestock industry. The livestock industry is dependent on imported feedstuffs ranging from cereal grains, vegetable and animal protein such as soybean meal, corn gluten meal, fish meal, meat and bone meals, mineral sources and various micro-ingredients including vitamins, minerals and other additives used to improve feed efficiency and growth (Loh, 2003). However, the ruminant industry depends primarily on locally available native pastures and supplemented with crop residues and agro-agricultural by-products such as rice-bran, copra cake, palm kernel cake (PKC), oil palm fronds, palm oil mill effluent (POME), spent bleaching earth (SBE), palm press fiber (PPF), rice straw, rice bran and rice husk (Wan Zahari and Wong, 2009). Livestock production in the country is mainly in the hands of smallholders who are largely dependent on forages for their feed resources (Mohamed, 2007; Mohamed *et al.*, 2013). Feeding methods that are usually practiced in Malaysia are 'cut and carry' and grazing system. These methods are extended and

traditionally practiced using grasses such as *Brachiaria decumbens*, *Brachiaria humidicola*, *Panicum maximum*, *Pennisetum purpureum* and *Setaria sphacelata* (Wan Zahari and Wong, 2009). Yet, high quality feed is insufficient for adequate nutrients required for body weight increment and milk production to support ruminants. Grasses have low protein content (6% to 13%), digestibility and energy concentration (Alimon and Hair-Bejo, 1996). Apart from highly digestible forages, productive performance can be greatly improved by supplementing with protein sources, concentrate or combination of both. Thus, the use of grasses needs extra supplementary feeds to increase the nutritional values of the feed for ruminant consumptions.

Conventionally, sweet corn is the main type of corn grown in Malaysia. Sweet corn plants are also used to make silage as a by-product after the cobs are harvested. This sweet corn silage production is mainly conducted in the state of Terengganu, amounting to 120 tonnes per year. Since the introduction of the sweet corn stover ensilage program in 1996, an estimated amount of 400 tonnes has been produced to feed the farmers' cattle. The Department of Veterinary Services (DVS) in Malaysia undertakes silage making as a form of fodder conservation since the 1960s. Unfortunately, there has not been any breeding program specifically dedicated to developing corn varieties suitable for this purpose. To date, there is lack of corn varieties specifically bred for forage production. Improvement of hybrid varieties from combinations of inbred lines with wide genetic background would be effective if the traits are selected from those which have small environmental biases. Determination of genetic backgrounds based on phenotypic and genetic diversity is important for conserving, evaluating and utilizing genetic resources, in order to understand the pre-breeding and breeding potential of germplasm, so that uniqueness and distinctness of genotypes could be realized (Franco *et al.*, 2001). Moreover, studies on genetic diversity and relationships among plant materials are important in crop development programs including corn hybrid breeding. Knowledge on genetic variability among corn germplasm can provide information to estimate degree of inheritance, variation and level of heterosis needed in a breeding program. This requires evaluation and selection of promising corn inbred lines for use in hybrid production. Those hybrids should meet the requirements for direct use as forage. Therefore, the objectives of the present study were:

- i. To investigate genetic variation among 30 corn inbred lines for forage traits using simple sequence repeat (SSR) markers, and subsequently place them into heterotic groups,
- ii. To evaluate yield and nutritive quality performance of these forage corn inbred lines obtained from various sources, and select potential ones based on their genetic variations from molecular and agronomic characterizations of important forage traits,
- iii. To evaluate general combining ability and specific combining ability among six selected inbred lines for forage traits, towards hybrid production, and
- iv. To evaluate performance of 15 corn hybrids, and estimate heterosis, heritability and genetic components for forage traits measured on them.

REFERENCES

- Abadi, J.M., Khorasani, S.K., Sar, B.S., Movafeg, S., and Golbashy, M. (2011). Estimation of combining ability and gene effects in forage maize (*Zea mays* L.) using line x tester crosses. *Journal of Plant Physiology and Breeding* 1(1): 63 - 73.
- Abdullah, N., Yusop, M.R., Ithnin, M., Saleh, G., and Latif, M.A. (2011). Genetic variability of oil palm parental genotypes and performance of its' progenies as revealed by molecular markers and quantitative traits. *Comptes Rendus Biologies* 334: 290 - 299.
- Abou-Deif, M.H. (2007). Estimation of gene effects on some agronomic characters in five hybrids and six populations of maize (*Zea mays* L.). *World Journal of Agricultural Science* 3(1): 86 - 90.
- Abuali, A.I., Abdelmulla, A.A., Khalafalla, M.M., Idris, A.E., and Osman, A.M. (2012). Combining ability and heterosis for yield components in maize (*Zea mays* L.). *Australian Journal of Basic and Applied Sciences* 6(10): 36 - 41.
- Aci, M.M., Revilla, P., Morsli, A., Djemel, A., Belalia, N., Kadri, Y., et al. (2013). Genetic diversity in Algerian maize (*Zea mays* L.) landraces using SSR markers. *Maydica* 58: 304-310.
- Acquaah, G. (2012). *Principles of plant genetics and breeding* (2nd ed.). Oxford: Wiley-Blackwell.
- Ahsan, M. (1999). Performance of six maize (*Zea mays* L.) inbred lines and their all possible as well as reciprocal cross combinations. *Pakistan Journal of Biology Sciences* 2(1): 222 - 224.
- Ajmone-Marsan, P., Castiglioni, P., Fusari, F., Kuiper, M., and Motto, M. (1998). Genetic diversity and its relationship to hybrid performance in maize as revealed by RFLP and AFLP markers. *Theoretical Applied Genetics* 96: 219 - 227.
- Akkaya, M.S., Bhagwat, A.A., and Cregan, P.B. (1992). Length polymorphism of simple sequence repeat DNA in soybean. *Genetics* 132: 1131 - 1139.
- Aldrich, S.R., Scott, W.O., and Leng, E.R. (1978). *Modern corn production* (3rd ed.). United States: A & L Production.

- Ali, E.S., and Saleh, G. (2003). Response of two cycles of phenotypic mass selection and heritability on two tropical sweet corn (*Zea mays* L. *saccharata*) populations. *Asian Journal of Plant Sciences* 2(1): 65 - 70.
- Alika, J.E. (1994). Diallel analysis of ear morphological characters in maize (*Zea mays* L.). *Indian Journal of Genetics* 54(1): 22 - 26.
- Alimon, A.R., and Hair-Bejo, M. (1996). *Feeding systems based on oil palm by-products in Malaysia*. Paper presented at the Proceeding 1st International Symposium on the Intergration of Livestock to Oil Palm Production, Kuala Lumpur, Malaysia.
- Allard, R.W. (1960). *Principles of plant breeding*. New York: John Wiley & Sons, Inc.
- Allen, M.S., Coors, J.G., and G.W., R. (2003). Corn silage. In D. R. Buxton, M. R.E., and J. H. Harrison (Eds.), *Silage Science and Technology* (pp. 547 - 608). ASA, CSSA, SSSA, Madison: American Society of Agronomy, Inc.
- Amiruzzaman, M., Islam, M.A., Hasan, L., Kadir, M., and Rohman, M.M. (2013). Heterosis and combining ability in a diallel among elite inbred lines of maize (*Zea mays* L.). *Emirates Journal of Food & Agriculture* 25(2): 132 - 137.
- Anderson, E., and Cutler, H. (1942). Races of *Zea mays*: I. Their recognition and classification. *Annals of the Missouri Botanical Garden* 21: 69 - 88.
- Anderson, J.A., Churchill, G.A., Autrique, J.E., Tanksley, S.D., and Sorrells, M.E. (1993). Optimizing parental selection for genetic linkage maps. *Genome* 36(1): 181-186.
- Andorf, C.M., Lawrence, C.J., Harper, L.C., Schaeffer, M.L., Campbell, D.A., and Sen, T.Z. (2010). The locus lookup tool at MaizeGDB: Identification of genomic regions in maize by integrating sequence information with physical and genetic maps. *Bioinformatics* 26: 434 - 436.
- Anonymous. (1998). *Application of DNA Based Marker Mutations for Improvement of Cereals and other Sexually Reproduced Crop Plants*. Vienna: INTERNATIONAL ATOMIC ENERGY AGENCY.
- Argillier, O., Barriere, Y., and Hebert, Y. (1995a). Genetic variation and selection criterion for digestibility traits for forage. *Euphytica* 82: 175 - 184.

- Argillier, O., Hebert, Y., and Barriere, Y. (1995b). Relationships between biomass yield, grain production, lodging susceptibility and feeding value in silage maize. *Maydica* 40: 125 - 126.
- Bal, M.A., Shaver, R.D., Shinnors, K.J., Coors, J.G., Lauer, J., Straub, R.J., et al. (2000). Stage of maturity, processing, and hybrid effects on ruminal in situ disappearance of whole-plant corn silage. *Animal Feed Science and Technology* 86(1 - 2): 83 - 94. doi:10.1016/S0377-8401(00)00163-2
- Ball, D.M., Collins, M., Lacefield, G.D., Martin, N.P., Mertens, D.A., Olson, K.E., et al. (2001). *Understanding forage quality*. Park Ridge, IL: American Farm Bureau Federation Publication 1-01.
- Barata, C., and Carena, M.J. (2006). Classification of North Dakota maize inbred lines into heterotic groups based on molecular and testcross data. *Euphytica* 151: 339 - 349.
- Baretta, D., Nardino, M., Konflanz, V.A., Carvalho, I.R., Busanello, C., de Oliveira, A.C., et al. (2016). Partial diallel analysis between maize inbred lines. *Jaboticabal* 44(1): 71 - 82.
- Barrett, B.A., and Kidwell, K.K. (1998). AFLP-based genetic diversity assessment among wheat cultivar from the Pacific Northwest. *Crop Science* 38: 1261 - 1271.
- Barrett, B.A., Kidwell, K.K., and Fox, P.N. (1998). Comparison of AFLP and pedigree-based genetic diversity assessment methods using wheat cultivars from the Pacific Northwest. *Crop Science* 38: 1271 - 1278.
- Barrière, Y., Alber, D., Dolstra, O., Lapierre, C., Motto, M., Ordas, A., et al. (2005). Past and prospects of forage maize breeding in Europe: I. The grass cell wall as a basis of genetic variation and future improvements in feeding value. *Maydica* 50: 259 - 274.
- Bartlett, M.S. (1937). *Properties of sufficiency and statistical tests*. Paper presented at the Royal Society of London Series A, London.
- Bassetti, H.J., and Westgate, M.E. (1993). Water deficit affects receptivity of maize silks. *Crop Science* 33: 279 - 282.
- Bates, G. (1998). Corn silage. *The University of Tennessee Agriculture Extension Service* 9: 1 - 8.

- Baynes, R.A., and Brawn, R.I. (1973). Influence of cytoplasmic effects on some agronomic characters in corn. *Canadian Journal of Plant Science* 53: 101 - 104.
- Beadle, G.W. (1939). Teosinte and the origin of maize. *Journal of Heredity* 30: 245 - 247.
- Beadle, G.W. (1980). The ancestry of corn. *Scientific American* 242(1): 112 - 119.
- Beaumont, M.A., Barratt, E.M., Gottelli, D., Kitchener, A.C., Daniels, M.J., Pritchard, J.K., *et al.* (2001). Genetic diversity and introgression in the Scottish wildcat. *Molecular Ecology* 10(2): 319 - 336.
- Beck, D.L., Vasal, S.K., and Crossa, J. (1991). Heterosis and combining ability among subtropical and temperate intermediate-maturity maize germplasm. *Crop Science* 31: 68 - 73.
- Begna, S.H., Hamilton, R.I., Dwyer, L.M., Stewart, D.W., and Smith, D.L. (2000). Variability among maize hybrids differing in canopy architecture for above-ground dry matter and grain yield. *Maydica* 45: 135 - 141.
- Benchimol, L.L., De Souza, C.L.J., Garcia, A.A.F., Kono, P.M.S., Mangolin, C.A., Barbosa, A.M.M., *et al.* (2000). Genetic diversity in tropical maize inbred lines: heterotic group assignment and hybrid determined by RFLP markers. *Plant Breeding* 119: 491 - 496.
- Bennetzen, J.L., and Hake, S.C. (2009). *Handbook of maize: Genetics and genomics*. California: Springer.
- Bernardo, R., Murigneux, A., Maisinneuve, J.P., Johnsson, C., and Karaman, Z. (1997). RFLP-based estimates of parental contribution to F2- and BC1-derived maize inbreds. *Theoretical Applied Genetics* 94: 652 - 656.
- Bertoia, L.M., and Aulicino, M.B. (2014). Maize forage aptitude: Combining ability of inbred lines and stability of hybrids. *The Crop Journal* 2(6): 407 - 418.
- Beyene, Y., Botha, A.M., and Myburg, A.A. (2005). A comparative study of molecular and morphological methods of describing genetic relationships in traditional Ethiopian Highland maize. *African Journal of Biotechnology* 4(7): 586 - 595.
- Bhatnagar, S., Betrán, F.J., and Rooney, L.W. (2004). Combining abilities of quality protein maize inbreds. *Crop Science* 44: 1997 - 2005.

- Bisen, A., Khare, D., Nair, P., and Tripathi, N. (2014). SSR analysis of 38 genotypes of soybean (*Glycine max* (L.) Merr.) genetic diversity in India. *Physiology and Molecular Biology of Plants* 21(1): 109 - 115. doi:10.1007/s12298-014-0269-8
- Bispo, N.B., Tessele, C., and Neto, J.F.B. (2009). Phenotypic and molecular characterization of hybrids released from 1980 to 2000. *Ciência Rural* 39(7): 1960 - 1966.
- Block, E.L., Muller, D., Griel Jr, L.C., and Garwood, D.L. (1981). Brown midrib-3 corn silage and heat extruded soybeans for early lactating dairy cows. *Journal of Dairy Science* 64: 1813 - 1825.
- Boonlertnirun, K., Srinives, P., Sarithniran, P., and Jompuk, C. (2012). Genetic distance and heterotic pattern among single hybrids within waxy maize (*Zea mays* L.). *SABRAO Journal of Breeding and Genetics* 44(2): 382 - 397.
- Boppenmaier, J., Melchinger, A.E., Brunklaus-Jung, E., Geiger, H.H., and Herrmann, R.G. (1991). Genetic diversity for RFLPs in European maize inbreds: I. Relation to performance of flint x dent crosses for forage traits. *Crop Science* 32(4): 895 - 902.
- Botstein, D., White, R.L., Skolnick, M., and Davis, R.W. (1980). Construction of genetic linkage map in man using restricted fragment length polymorphism. *American Journal of Human Genetics* 23: 314 - 331.
- Branco, C., Vieira, E., Malone, G., Kopp, M., Malone, E., Bernandes, A., et al. (2007). IRAP and REMAP assessments of genetic similarity in rice. *Journal of Applied Genetics* 48: 107 - 113.
- Brandolini, A. (1970). Maize. In O. H. Frankel and E. Benner (Eds.), *Genetic resources in plants: Their exploration and conservation* (pp. 273 - 309). Oxford: Blackwell Scientific Publications.
- Brewbaker, J.L. (2003). The corn plant *Corn production in the tropics: The Hawaii experience* (pp. 13 - 19). University of Hawaii at Manoa: College of Tropical Agriculture and Human Resources.
- Brown, A.H.D. (1989). The case for core collection. In A. H. D. Brown, O. H. Frankel, D. R. Marshall, and J. T. Williams (Eds.), *The use of plant genetic resources* (pp. 136 - 156). Cambridge: Cambridge University Press.
- Brown, M.B., and Forsythe, A.B. (1974). Robust tests for the equality of variances. *Journal of American Statistical Association* 69: 364 - 367.

- Buckler, E.S., and Holtsford, T.P. (1996). Zea systematics: Ribosomal ITS evidence. *Molecular Biology and Evolution* 13: 612 - 622.
- Burnham, C.R. (1947). Maize genetics. *Cooperation Newsletter* 21: 36.
- Burnham, C.R., and Brink, R.A. (1932). Linkage relations of a second brown midrib gene (*bm2*) in maize. *Journal of the American Society of Agronomy* 24: 960 - 963.
- Buxton, D.R., Redfearn, D.D., Jung, H.G., and Mertens, D.A. (2006). *Improving forage quality-related characteristics of corn*. Paper presented at the Informational Conference with Dairy and Forage Industries, US Dairy Forage Research Center, USA.
- Carpici, E.B., and Çelik, N. (2010). Determining possible relations between yield and yield related components in forage maize (*Zea mays* L.) by correlation and path analyses. *Notulae Botanicae Horti Agrobotanici Cluj-Napoca* 38(3): 280 - 285.
- Chen, Y., Zhou, D., and Zhang, Y. (2004). Temporal and spatial variations of chemical constituent in maize. *Ying Yong Sheng Tai Xue Bao* 15(9): 1589 - 1593.
- Chiari, Y., Orozco-terWengel, P., Vences, M., Vieites, D.R., Sarovy, A., Randrianirina, J.E., *et al.* (2006). Genetic identification of units for conservation in tomato frogs, genus *Dyscophus*. *Conservation Genetics* 7(4): 473 - 482.
- Chin, F.Y. (2001). *Silage production and techniques in Malaysia*. Paper presented at the 7th Meeting of the Regional Working Group on Grazing and Feed Resources.
- Choukan, R. (1999). General and specific combining ability of ten maize inbred lines for different traits in diallel cross. *Seed Plant* 15: 280 - 295.
- CIMMYT Global Maize Program. (2015). CIMMYT Maize Lines (CMLs) - Pedigree and Characterization Data. Retrieved 01 October 2015, from Dataverse Network CIMMYT <http://hdl.handle.net/11529/10246>
- Clerc, V.L., Bazante, F., Baril, C., Guiard, J., and Zhang, D. (2005). Assessing temporal changes in genetic diversity of maize varieties using microsatellite markers. *Theoretical Applied Genetics* 110: 294 - 302. doi:10.1007/200122-004-1834-2

- Collard, B.C.Y., Jahufer, M.Z.Z., Brouwer, J.B., and Pang, E.C.K. (2005). An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: The basic concepts. *Euphytica* 142(1): 169 - 196.
- Cömertpay, G., Baloch, F.S., Kilian, B., Ülger, A.C., and Özkan, H. (2012). Diversity assessment of Turkish maize landraces based on fluorescent labeled SSR markers. *Plant Molecular Biology Reporter* 30: 261 - 274.
- Coors, J.G. (1996). *Findings of the Wisconsin corn silage symposium*. Paper presented at the Cornell Nutrition Conference for Feed Manufacturers, Rochester, NY.
- Coors, J.G., Carter, P.R., and Hunter, R.B. (1994). Silage corn. In A. R. Hallauer (Ed.), *Specialty Corns* (pp. 305 - 340). Boca Raton: CRC Press.
- Cornelious, B.K., and Sneller, C.H. (2002). Yield and molecular diversity of soybean lines derived from crosses of northern and southern elite parents. *Crop Science* 42: 642 - 647.
- Cox, T.S., Murphy, J.P., and Rodgers, D.M. (1986). Changes in genetic diversity in the red winter wheat regions of the United States. *Proceeding of National Academy Sciences* 83: 5583 - 5586.
- Craig, D.L. (2010). *Current and future genetics in corn silage*. Paper presented at the Proceeding of California Alfalfa & Forage Symposium and Corn/Cereal Silage Mini-Symposium, Visalia, California.
- Crow, J.F. (1948). Alternative hypotheses of hybrid vigor. *Genetics* 33: 477 - 487.
- Crow, J.F. (1998). Perspective: Anecdotal, historical and critical commentaries on genetics. *Genetics* 148: 923 - 928.
- Dado, R.G. (1999). Nutritional benefits of specialty maize grain hybrids in dairy diets. *Journal of Animal Science* 77: 197-207.
- Dandolini, T.S., Scapim, C.A., Júnior, A.T.d.A., Mangolin, C.A., Machado, M.d.F.P.d.S., Mott, A.d.S., et al. (2008). Genetic divergence in popcorn lines detected by microsatellite markers. *Crop Breeding and Applied Biotechnology* 8: 313 - 320.
- Darwin, C.R. (1876). *The effects of cross and self fertilization in the vegetable kingdom*. London: John Murray, Albemarle Street.

- Davenport, C.B. (1908). Degeneration, albinism and inbreeding. *Science* 28(718): 454 - 455.
- de Souza Neto, I.L., Bath Pinto, R.J., Scapim, C.A., Jobim, C.C., Torre Figueiredo, A.S., and Bignotto, L.S. (2015). Diallel analysis and inbreeding depression of hybrid forage corn for agronomic traits and chemical quality. *Plant Breeding* 74(1): 42 - 49. doi:10.1590/1678-4499.0315
- de Souza, S.G.H., Carpentieri-Pípolo, V., de Fátima Ruas, C., Carvalho, V.d.P., Ruas, P.M., and Gerage, A.C. (2008). Comparative analysis of genetic diversity among the maize inbred lines (*Zea mays* L.) obtained by RAPD and SSR markers. *Brazilian Archive of Biology and Technology* 51(1). doi:10.1590/S1516-89132008000100022
- Dereeper, A., Guignon, V., Blanc, G., Audic, S., Buffet, S., Chevenet, F., *et al.* (2008). Phylogeny.fr: robust phylogenetic analysis for the non-specialist. *Nucleic Acids Research* 36: W465 - W469. doi:10.1093/nar/gkn180
- Dhillon, B.S., Singh, A.K., Lather, B.P.S., and Srinivasan, G. (2004). *Plant breeding: Advances in hybrid breeding methodology* (J. K. Jain and M. C. Kharkwal Eds., 10.1007/978-94-007-1040-5_18). New Delhi: Springer Netherland.
- Di Rienzo, A., Peterson, A.C., Garza, J.C., Valdes, A.M., Slatkin, M., and Freimer, N.B. (1994). Mutational processes of simple-sequence repeat loci in human populations. *Proceeding of the National Academy of Sciences of the United States of America* 91: 3166 - 3170.
- Dias, P.M.B., Julier, B., Sampoux, J.-P., Barre, P., and Dall'Agnol, M. (2008). Genetic diversity in red clover (*Trifolium pratense* L.) revealed by morphological and microsatellite (SSR) markers. *Euphytica* 160: 189 - 205.
- Dice, L.R. (1945). Measures of the amount of ecologic association between species. *Ecology* 26: 297 - 302.
- Dixon, W.J., and Massey, F.J. (1969). *Introduction to statistical analysis*. New York: McGraw-Hill.
- Doebley, J. (2003). The morphology of maize and teosinte2016(8 March). Retrieved from <http://teosinte.wisc.edu/morphology.html>
- Doebley, J. (2004). The genetics of maize evolution. *Annual Review of Genetics* 38: 37 - 59.

- Doebley, J.F. (1990). Molecular evidence for gene flow among *Zea* species. *BioScience* 40: 443 - 448.
- Dubreuil, P., and Charcosset, A. (1998). Genetic diversity within and among maize populations: a comparison between isozyme and nuclear RFLP loci. *Theoretical Applied Genetics* 96: 577 - 587.
- Dubreuil, P., Dufour, P., Krejci, E., Causse, M., de Vienne, D., Gallais, A., *et al.* (1996). Organization of RFLP diversity among inbred lines of maize representing the most significant heterotic groups. *Crop Science* 36: 790 - 799.
- Duvick, D.N. (1977). Genetic rates of gain in hybrid maize yields during the past 40 years. *Maydica* 22: 187 - 196.
- Duvick, D.N. (1999a). Commercial strategies for exploitation of heterosis. In J. G. Coors and S. Pandey (Eds.), *The genetics and exploitation of heterosis in crops* (pp. 295 - 304). Madison, Wisconsin: American Society of Agronomy.
- Duvick, D.N. (1999b). Heterosis: Feeding people and protecting natural resources. In J. G. Coors and S. Pandey (Eds.), *The genetics and exploitation of heterosis in crops* (pp. 19 - 29). Madison: American Society of Agronomy.
- Duvick, D.N. (2001). Biotechnology in the 1930s: the development of hybrid maize. *Nature Reviews Genetics* 2: 69 - 74. doi:10.1038/35047587
- Dwayne, R.B. (1996). Quality-related characteristics of forage as influenced by plant environment and agronomic factors. *Animal Feed Science Technology* 59: 37 - 49.
- East, E.M. (1908). Inbreeding in corn. *Connecticut Agricultural Experiments Station*: 419 - 428.
- Ellneskog-Staam, P., Henry Loaisiga, C., and Merker, A. (2007). Chromosome C-banding of the teosinte *Zea nicaraguensis* and comparison to other *Zea* species. *Hereditas* 144: 96 - 101.
- Emerson, R.A., Beadle, G.W., and Fraser, A.C. (1935). A summary of linkage studies in maize. *Agriculture Experiment Station Memoir* 180: 1 - 83.

- Enoki, H., Sato, H., and Koinuma, K. (2002). SSR analysis of genetic diversity among maize inbred lines adapted to cold regions of Japan. *Theoretical Applied Genetics* 104: 1270 - 1277.
- Esau, K. (1977). The leaf: Variations in structure *Anatomy of seed plants* (Second ed., pp. 351 - 374). New York: John Wiley & Sons, Inc.
- Falconer, D.S., and Mackay, T.F.C. (1996). *Introduction to quantitative genetics* (4th ed.). Harlow: Benjamin Cummings.
- FAOSTAT. (2017). Crop production. FAOSTAT Retrieved 9 March 2016 <http://faostat3.fao.org/browse/Q/QC/E>
- FAOSTAT. (2018). Statistical Database of Food and Agriculture Organization of the United Nations. Retrieved 22th January 2018 <http://faostat3.fao.org/>
- Farnham, D.E., Benson, G.O., and Pearce, R.B. (2003). Corn perspective and culture. In P. J. White and L. A. Johnson (Eds.), *Corn: Chemistry and technology* (Second ed., pp. 1 - 33). Minnesota: American Association of Cereal Chemists, Inc. St. Paul.
- Fedoroff, N. (2000). Transposons and genome evolution in plants. *Proceeding of National Academy Sciences* 97: 7002 - 7007.
- Felsenstein, J. (1989). PHYLIP - Phylogeny Inference Package (Version 3.2). *Cladistics* 5: 164 - 166.
- Ferraretto, L., and Shaver, R. (2012). *What's new with corn silage for dairy cattle?* Paper presented at the Tri-State Dairy Nutrition Conference, Fort Wayne, Ind.
- Franco, J., Crossa, J., Ribaut, J.M., Betran, J., Warburton, M.L., and Khairallah, M. (2001). A method for combining molecular markers and phenotypic attributes for classifying plant genotypes. *Theoretical Applied Genetics* 103: 944 - 952.
- Fransen, S.C. (2004). Yield components and quality of silage corn in the Pacific Northwest. In S. Bittman and C. G. Kowalenko (Eds.), *Agassiz. Advanced silage corn management: Pacific Field Corn Association*.
- Fufa, H., Baenziger, P.S., Beecher, B.S., Dweikat, I., Graybosch, R.A., and Eskridge, K.M. (2005). Comparison of phenotypic and molecular marker-based classifications of hard red winter wheat cultivars. *Euphytica* 145: 133 - 146.

- Gabriel, L.C., Maximo, B.L., and Ruggero, B. (2009). Heterosis and heterotic patterns among maize landraces for forage. *Crop Breeding and Applied Biotechnology* 9: 229 - 238.
- Garcia, A.A.F., Benchimol, L.L., Barbosa, A.M.M., Geraldi, I.O., Souza Jr., C.L., and de Souza, A.P. (2004). Comparison of RAPD, RFLP, AFLP and SSR markers for diversity studies in tropical maize inbred lines. *Genetics and Molecular Biology* 27(4): 579 - 588.
- Gardner, C.O. (1963). Estimation of genetic parameters in cross-pollinated plants and their implications in plant breeding. In W. D. Hanson and H. F. Robinson (Eds.), *Statistical Genetics and Plant Breeding* (pp. 225 - 252). Washington, D. C: NAS-NRC Publication.
- Gauthier, P., Gouesnard, B., Dallard, J., Redaelli, R., Rebourg, C., Charcosset, A., et al. (2002). RFLP diversity and relationships among traditional European maize populations. *Theoretical Applied Genetics* 105: 91 - 99.
- Geiger, H.H., Melchinger, A.E., Seitz, G., and Schmidt, G.A. (1986). *Methods of predicting three-way crosses from single crosses between flint and dent inbred lines in forage maize (Zea mays L.)*. Paper presented at the Proceeding 6th Meeting EUCARPIA Sect Biomet. Plant Breed., Birmingham.
- Gerber, S., Mariette, S., Streiff, R., Bodénès, C., and Kremer, A. (2000). Comparison of microsatellites and amplified fragment length polymorphism markers for parentage analysis. *Molecular Ecology* 9: 1037 - 1048.
- Gibbon, B.C., and Larkins, B.A. (2005). Molecular genetic approaches to developing quality protein maize. *Trends in Genetics* 21: 227 - 233.
- Glaszmann, J.C., Grivet, L., Courtois, B., Noyer, J.L., Luce, C., Jacquot, M., et al. (2003). Asian rice. In P. Hamon, M. Seguin, X. Perrier, and J. C. Glaszmann (Eds.), *Genetic diversity of cultivated tropical plants* (pp. 77 - 98). Enfield: Science Publishers and CIRAD.
- Goodman, M.M., and Brown, W.L. (1988). Races of corn. In G. F. Sprague and J. W. Dudley (Eds.), *Corn and corn improvement* (pp. 33 - 79). Madison: American Society of Agronomy, Inc.
- Gouesnard, B., Dallard, J., Panouille, A., and Boyat, A. (1997). Classification of French maize populations based on morphological traits. *Agronomie* 17: 491 - 498.

- Graham, G.I., Wolff, D.W., and Stuber, C.W. (1997). Characterization of a yield quantitative trait locus on chromosome five of maize by fine mapping. *Crop Science* 37: 1601 - 1610. doi:10.2135/cropsci1997.0011183X003700050033x
- Graham, K.M., and Yap, T.C. (1972). *Chinta, a new tropical sweet corn*. Kuala Lumpur: Faculty of Agriculture, University Malaya.
- Griffing, B. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences* 9(4): 463 - 493.
- Guerrero, C.G., Robles, M.A.G., Ortega, J.G.L., Castillo, I.O., Vázquez, C.V., Carrillo, M.G., *et al.* (2014). Combining ability and heterosis in corn breeding lines to forage and grain. *American Journal of Plant Sciences* 5: 845 - 856.
- Gungula, D.T., Togun, A.O., and Kling, J.G. (2005). The influence of N rates on maize leaf number and senescence in Nigeria. *World Journal of Agricultural Science* 1(1): 1 - 5.
- Guyader, J., Baron, V.S., and Beauchemin, K.A. (2018). Corn Forage Yield and Quality for Silage in Short Growing Season Areas of the Canadian Prairies. *Agronomy* 8(9): 164.
- Guzman, P.S., and Lamkey, K.R. (2000). Effective population size and genetic variability in the BSI maize population. *Crop Science* 40: 338 - 346.
- Hadado, T.T., Rau, D., Bitocchi, E., and Papa, R. (2010). Adaptation and diversity along an altitudinal gradient in Ethiopian barley (*Hordeum vulgare* L.) landraces revealed by molecular analysis. *BMC Plant Biology* 10(121): 1 - 20. doi:10.1186/1471-2229-10-121
- Hahn, V., Blankenhorn, K., Schwall, M., and Melchinger, A.E. (1995). Genetic diversity revealed with RAPD markers and comparison with RFLP and pedigree data. *Maydica* 40: 299 - 310.
- Hake, S., and Walbot, V. (1980). The genome of *Zea mays*, its organization and homology to related grasses. *Chromosoma* 79: 251 - 270.
- Hall, A.J., Vilella, F., Trapani, N., and Chimenti, C. (1982). The effects of water stress and genotype on the dynamics of pollen-shedding and silking in maize. *Field Crops Research* 5: 349 - 363.

- Hallauer, A.R., and Carena, M.J. (2009). Maize breeding. In M. J. Carena (Ed.), *Handbook of plant breeding: Cereals*. New York: Springer.
- Hallauer, A.R., Carena, M.J., and Filho, J.B.M. (2010). *Quantitative genetics in maize breeding* (6th ed.). Iowa: Springer.
- Hallauer, A.R., Carena, M.J., and Miranda, F.J.B. (1981). *Quantitative genetics in maize breeding* (2nd ed.). Ames: Iowa State University Press.
- Hallauer, A.R., and Miranda, F.J.B. (1988). *Quantitative genetics in maize breeding*. Ames, Iowa: Iowa State University Press.
- Hamza, H., Elbekkay, M., Ben Abederrahim, M.A., and Ali, A.F. (2011). Molecular and morphological analyses of date palm (*Phoenix dactylifera* L.) subpopulations in southern Tunisia. *Spanish Journal of Agricultural Research* 9: 484 - 493.
- Hancock, J.F. (2012). Agricultural origins and crop evolution. In J. F. Hancock (Ed.), *Plant Evolution and the Origin of Crop Species* (2nd ed.). Oxfordshire: CABI Publishing.
- Hansen, L.A., Bagget, J.R., and Rowe, K.E. (1977). Quantitative genetic analysis of ten characteristics in sweet corn (*Zea mays* L.). *Journal of American Society of Horticultural Sciences* 102: 158 - 162.
- Haq, Q.M.I., Hussain, T., and Kumar, A. (2016). Molecular markers: A tool to identify hidden science with especial emphasis on agricultural crops. *International Journal of Biology Research* 1(5): 50 - 59.
- Hayes, H.K., Immer, F.R., and Hayes, D.C.S. (1955). *Methods of plant breeding*. New York: McGraw Hill.
- Henry, R.J. (1997). *Practical applications of plant molecular biology*. London: Chapman and Hall.
- Heuzé, V., Tran, G., Edouard, N., and F., L. (2017, June 21, 2017). Maize green forage. Retrieved from <https://www.feedipedia.org/node/358>
- Hill, J., Becker, H.C., and Tigerstedt, P.M.A. (1998). *Quantitative and ecological aspects of plant breeding*. London: Chapman and Hall.
- Hinen, M.S.J. (2006). *The big 6 - Focus on the 6 keys to quality corn silage*. Paper presented at the Mid-South Ruminant Nutrition Conference.

- Hoisington, D., Khairallah, M., and González-Léon, D. (2005). *Laboratory protocols: CIMMYT applied molecular genetics laboratory* (3rd ed.). Mexico: D.F: CIMMYT.
- Hussain, M.R., and Aziz, K. (1998). Study of combing ability in maize line × tester hybridization. *Pakistan Journal of Biological Science* 1: 196 - 198.
- Idris, D.M., Lassim, M.M., and Hashim, N. (1982). *Tanaman bijian*. Selangor: Percetakan Dewan Bahasa dan Pustaka.
- Inglett, G.E. (1970). *Corn: Culture, processing, products. Major feed and food crops in agriculture and food series*. Connecticut: The Avi Publishing Company, Inc.
- Izhar, T., and Chankraborty, M. (2013). Combining ability and heterosis for grain yield and its components in maize inbreds over environments (*Zea mays* L.). *African Journal of Agricultural Research* 8(25): 3276 - 3280.
- Jain, S., Porter, L.D., Kumar, A., Mir, R.R., Eigenbrode, S.D., and McPhee, K.E. (2014). Molecular and phenotypic characterization of variation related to pea enation mosaic virus resistance in lentil (*Lens culinaris* Medik.). *Canadian Journal of Plant Science* 94: 1333 - 1344.
- Johnson, A.N.A. (2007). Size matters: Toward understanding the natural history of genome *Darwinian detectives : Revealing the natural history of genes and genomes: Revealing the natural history of genes and genomes* (pp. 169). England: Oxford University Press.
- Jones, C.J., Edwards, K.J., Castaglione, S., Winfield, M.O., Sala, F., Wiel, C.v.d., et al. (1997a). Reproducibility testing of RAPD, AFLP and SSR markers in plants by a network of European laboratories. *Molecular Breeding* 3: 381 – 390.
- Jones, C.J., Edwards, K.J., Castiglione, S., and Winfield, M.O. (1997b). Reproducibility testing of RAPD, AFLP and SSR markers in plants by a network of European laboratories. *Molecular Breeding* 3(5): 381 - 390.
- Jones, D.F. (1918). The effects of inbreeding and crossbreeding upon development. *Connecticut Agricultural Experiments Station* 107: 100.
- Jorgenson, L.R. (1931). Brown midrib in maize and its lineage relations. *Journal of the American Society of Agronomy* 23: 549 - 557.

- Kanagarasu, S., Nallathambi, G., Ganesan, K., Kannan, S., Shobhana, V., and Senthil, N. (2013). Determination of genetic polymorphism among indigenous and exotic maize inbreds using microsatellite markers. *African Journal of Biotechnology* 12: 5723 - 5728.
- Kantety, R.V., Zeng, X., Bennetzen, J.L., and Zehr, B.E. (1995). Assessment of genetic diversity in dent and popcorn (*Zea mays* L.) inbred lines using inter-simple sequence repeat (ISSR) amplification. *Molecular Breeding* 1: 365 - 373.
- Kapoor, R. (2017). Genetic variability and association studies in maize (*Zea mays* L.) for green fodder yield and quality trait. *Forage Research* 43(1): 67-69.
- Kashiani, P., Saleh, G., and Abdullah, N.A.P. (2008). *Performance, heritability and correlation studies on nine advanced sweet corn inbred lines*. Paper presented at the 10th Symposium of Malaysian Society of Applied Biology, Malaysia.
- Kashiani, P., Saleh, G., Abdullah, N.A.P., and Abdullah, S.N. (2010). Variation and genetic studies on selected sweet corn inbred lines. *Asian Journal of Crop Science* 2(2): 78 - 84.
- Kashiani, P., Saleh, G., Abdullah, N.A.P., and Maizura, A.S. (2014). Evaluation of genetic variation and relationship among tropical sweet corn inbred lines using agronomic traits. *Maydica* 59(3): 275 - 282.
- Kashiani, P., Saleh, G., Panandam, J.M., Abdullah, N.A.P., and Selamat, A. (2012a). Dermacation of informative chromosomes in tropical sweet corn inbred lines using microsatellite DNA markers. *Genetics and Molecular Biology* 35: 614 - 621.
- Kashiani, P., Saleh, G., Panandam, J.M., Abdullah, N.A.P., and Selamat, A. (2012b). Molecular characterization of tropical sweet corn inbred lines using microsatellite markers. *Maydica* 57: 154 - 163.
- Kearsey, M.J., and Pooni, H.S. (1998). *The genetical analysis of quantitative traits*. England: Stanley Thornes (Publishers) Ltd.
- Kempthorne, O., and Curnow, R.N. (1961). The partial diallel cross. *Biometrics* 17(2): 229 - 250.
- Khan, S.A., Ahmad, H., Khan, A., Saeed, M., Khan, S.M., and Ahmad, B. (2009). Using line x tester analysis for earliness and plant height traits in

sunflower (*Helianthus annuus* L.). *Recent Research in Science and Technology* 1: 202 – 206.

Kiang, L.C. (1987). *Country Reports: Production and research: Malaysia*. Paper presented at the Proceeding of Second Asian Regional Maize Workshop, Jakarta and East Java, Indonesia.

Kimura, M., and Crow, J.F. (1964). The number of alleles that can be maintained in a finite population. *Genetics* 49: 725 - 738.

Kirkpatrick, K.M. (2008). *The evaluation of maize genotypes for potential use in cellulosic ethanol production*. (Master of Science), Iowa State University, Ames, Iowa. (1453905)

Konak, C., Unay, A., Serter, E., and Basal, H. (1999). Estimation of combining ability effects, heterosis and heterobeltiosis by line x tester method in maize. *Turkish Journal of Field Crops* 4: 1 - 9.

Koundinya, V. (2009). Corn stover. Retrieved from <https://www.agmrc.org/renewable-energy/corn-stover>

Kuehn, C.S., Linn, J.G., Johnson, D.G., Jung, H.G., and Endres, M. (1999). Effects of feeding silages from corn hybrids selected for leafiness or grain to lactating dairy cows. *Journal of Dairy Science* 82: 2746 - 2755.

Kumar Srivas, S., and Singh, U.P. (2004). Genetic variability, character association and path analysis of yield and its component traits in forage maize (*Zea mays* L.). *Range Management and Agroforestry* 25(2): 149 - 153.

Lanza, L.L.B., de Souza Jr., C.L., Ottoboni, L.M.M., Vieira, M.L.C., and de Souza, A.P. (1997). Genetic distance of inbred lines and prediction of maize single-cross performance using RAPD markers. *Theoretical Applied Genetics* 94: 1023 - 1030.

Lauer, J. (1995). Corn germplasm for silage uses. *Field Crops* 28: 4 - 5.

Lechtenberg, V.L., Muller, L.D., Bauman, L.F., Rhykerd, C.L., and Barnes, R.F. (1972). Laboratory and in vitro evaluation of inbred and F2 populations of brown midrib mutants of *Zea mays* L. *Agronomic Journal* 64: 657 - 660.

- Lee, C.D., Herbek, J.H., Lacefield, G., and Smith, R. (2005). Producing corn for silage, 1 - 8. Retrieved from <http://www2.ca.uky.edu/agcomm/pubs/agr/agr79/agr79.pdf>
- Lee, E.A., and Tracy, W.F. (2009). Modern Maize Breeding. In J. L. Bennetzen and S. Hake (Eds.), *Handbook of Maize*. New York: Springer.
- Lee, M., Godshalk, E.B., Lamkey, K.R., and Woodman, W.W. (1989). Association of restriction fragment length polymorphisms among maize inbreds with agronomic performance of their crosses. *Crop Science* 29: 1067 - 1071.
- Legesse, B.W., Myburg, A.A., Pixley, K.V., and Botha, A.M. (2006). Genetic diversity of African maize inbred lines revealed by SSR markers. *Hereditas* 18: 415 - 423.
- Lenaric, A., B., Svenson, K.L., Churchill, G.A., and Valdar, W. (2012). A general bayesian approach to analyzing diallel. *Genetics* 190: 413 - 435.
- Leng, R.A. (2002). *Requirements for protein meals for ruminant meat production in developing countries*. Paper presented at the FAO Animal Production and Health, Bangkok.
- Levene, H. (1949). On a matching problem arising in genetics. *The Annals of Mathematical Statistics* 20: 91 - 94.
- Levene, H. (1960). Robust tests for equality of variances. In P. A. Olkin (Ed.), *Contributions to probability and statistics* (pp. 278 - 292). CA: Stanford University Press.
- Lewontin, R.C. (1972). Testing the theory of natural selection. *Nature* 236: 181 - 182.
- Li, M., Guo, X., Zhang, M., Wang, X., Zhang, G., Tian, Y., *et al.* (2010). Mapping QTLs for grain yield and yield components under high and low phosphorus treatments in maize (*Zea mays* L.). *Plant Science* 178: 454-462.
- Li, M.S., Li, X.H., Salvi, S., Tuberosa, R., Yuan, L.X., Rotondo, F., *et al.* (2006). Genetic relationships among CIMMYT subtropical QPM and Chinese maize inbred lines based on SSRs. *Maydica* 51: 543 - 549.

- Li, Y., Du, J., Wang, T., Shi, Y., Song, Y., and Jia, J. (2002). Genetic diversity and relationships among Chinese maize inbred lines revealed by SSR markers. *Maydica* 47: 93 - 101.
- Li, Y.L., LV, D.B., Wang, Y.Z., Chen, S.J., and Tang, J.H. (2004). Study on the genetic diversity of popcorn inbreds and their germplasm relationship with normal corn inbreds using SSR markers. *Maydica* 49: 327 - 333.
- Liu, K., and Muse, S.V. (2005). PowerMarker: Integrated analysis environment for genetic marker data. *Bioinformatics* 21(9): 2128 - 2129.
- Liu, R., Vitte, C., Ma, J., Mahama, A.A., Dhliwayo, T., Lee, M., et al. (2007). A GeneTrek analysis of the maize genome. *Proceeding of National Academy Sciences* 104: 11844 - 11849.
- Livini, C., Anjmore-Marsan, P., Melchinger, A.E., Messmer, M.M., and Motto, M. (1992). Genetic diversity of maize inbred lines within and among heterotic groups revealed by RFLPs. *Theoretical Applied Genetics* 103: 613 - 617.
- Llaurado, M., and Moreno-Gonzalez, J. (1993). Classification of Northern Spanish populations of maize by methods of numeral taxonomy. I. Morphological traits. *Maydica* 38: 115 - 121.
- Loh, T.C. (2003). *Livestock production and the feed industry in Malaysia*. Paper presented at the Expert Consultation and Workshop, Bangkok.
- Lombard, V., Baril, C.P., Dubreuil, P., Blouet, F., and Zhang, D. (2000). Genetic relationships and fingerprinting of rapeseed cultivars by AFLP: Consequences for varietal registration. *Crop Science* 40: 1417-1425.
- Lubberstedt, T., Melchinger, A.E., Dußle, C., Vuylsteke, M., and Kuiper, M. (2000). Relationships among early European maize inbreds: IV. Genetic diversity revealed with AFLP markers and comparison with RFLP, RAPD, and pedigree data. *Crop Science* 40(3): 783 - 791.
- Lukas, F.K., and Donald, M.W. (2002). Inbreeding effects in wild populations. *Trends in Ecology and Evolution* 17: 230 - 241.
- Lukoschek, V., Waycott, M., and Keogh, J.S. (2008). Relative information content of polymorphic microsatellites and mitochondrial DNA for inferring dispersal and population genetics structure in the olive sea snake, *Aipysurus laevis*. *Molecular Ecology* 17: 3062 - 3077.

- MaizeSequence. (2010). *Zea mays* assembly and gene annotation. Retrieved from http://ensembl.gramene.org/Zea_mays/Info/Annotation/
- Makumbi, D., Betrán, J.F., Bänziger, M., and Ribaut, J.M. (2011). Combining ability, heterosis and genetic diversity in tropical maize (*Zea mays* L.) under stress and non-stress conditions. *Euphytica* 180: 143 - 162.
- Malook, S., Ali, Q., Ahsan, M., Mumtaz, A., and Sajjad, M. (2014). An overview of conventional breeding for drought tolerance in *Zea mays*. *Nature and Science* 12: 7 - 22.
- Mangelsdorf, P.C. (1974). *Corn - Its origin, evolution and improvement*. New York: The Bellknap Press.
- Manly, B.F.J. (1997). *Randomization, bootstrap and Monte Carlo methods in biology*. London: Chapman & Hall.
- Mantel, N., and Valand, R.S. (1970). A technique of nonparametric multivariate analysis. *Biometrics* 26: 547 - 558.
- Mantel, N.A. (1967). The detection of disease clustering and a generalized regression approach. *Cancer Research* 27: 209 - 220.
- Marsan, P.A., Castiglioni, P., Fusari, F., Kuiper, M., and Motto, M. (1998). Genetic diversity and its relationship to hybrid performance in maize as revealed by RFLP and AFLP markers. *Theoretical and Applied Genetics* 96(2): 219 - 227.
- Martin, N.P., Mertens, D.R., Hall, M.B., and Lauer, J.G. (2008). *Fiber digestibility and starch content of corn silage*. Paper presented at the Idaho Alfalfa and Forage Conference, U.S. Dairy Forage Research Center, USDA-ARS.
- Mason, L., Mondart, C.L., Jr Chaney, C.R., Martin, P., and Milam, M. (1974). Corn forage as affected by plant population, nitrogen rate and hybrid. *Olivier Soil Bulletin*, p. 23.
- Massey, R., and Horner, J. (2010). Estimating silage value for the crop producer, 1 - 4. Retrieved from University of Missouri Extension website: <https://extension2.missouri.edu/g4591>
- McWhirter, K.S. (1979). Breeding of cross pollinated crops. In R. Knight (Ed.), *Plant Breeding* (pp. 79 - 121). Australia: Australian Vice-Chancellors' Committee.

- Melchinger, A.E. (1993). Use of RFLP markers for analysis of genetic relationship among breeding materials and prediction of hybrid performance. In D. R. Buxton, R. Shibles, R. A. B. Forsberg, B.L. , K. H. Asay, G. M. Paulsen, and R. F. Wilson (Eds.), *International Crop Science I* (pp. 621 - 628). Madison: Crop Science Society of America.
- Melchinger, A.E. (1999). Genetic diversity and heterosis. In J. G. Coors and S. Pandey (Eds.), *The genetics and exploitation of heterosis in crops* (pp. 99 - 118). Madison: CSSA.
- Melchinger, A.E., Boppenmaier, J., Dhillon, B.S., Pollmer, W.G., and Herrmann, R.G. (1992). Genetic diversity for RFLPs in European maize inbreds: II. Relation to performance of hybrids within versus between heterotic groups for forage traits. *Theoretical Applied Genetics* 84: 672 - 681.
- Mertens, D.R. (2002). *Nutritional implications of fiber and carbohydrates characteristics of corn silage and alfalfa hay*. Paper presented at the California Animal Nutrition Conf. Fresno, CA.
- Messmer, M.M., Melchinger, A.E., Boppenmaier, J., Herrmann, R.G., and Brunklaus-Jung, E. (1992). RFLP analyses of early-maturing European maize germplasm: I. Genetic diversity among flint and dent inbred lines. *Theoretical Applied Genetics* 83: 1003 - 1012.
- Michalet-Doreau, B., and Philippeau, C. (1999). Maize silage genotype and ruminant digestion. *Zootehnika* 74(1): 37 - 46.
- Ming, H., Xie, F., Chen, L., Zhao, X., Jojee, L., and Madonna, D. (2010). Comparative analysis of genetic diversity and structure in rice using ILP and SSR markers. *Rice Science* 17(4): 257 - 268.
- Mladenović Drinić, S., Kostadinović, M., Ristić, D., Stevanović, M., Čamdžija, Z., Filipović, M., *et al.* (2012). Correlation of yield and heterosis of maize hybrids and their parental lines with genetic distance based on SSR markers. *Genetika* 44(2): 399 - 408.
- Mohamed, Z., Hosseini, A., and Kamarulzaman, N.H. (2013). Analysis of Malaysian beef industry in Peninsular Malaysia under different importation policies scenarios and rate management systems. *Pertanika Journal of Social Sciences & Humanities* 21(S): 1 - 16.
- Mohamed, Z.A. (2007). The Livestock Industry. In I. S.A., M. A. Fatimah, N. M. Raja Abdullah, B. Kaur, and A. M. Abdullah (Eds.), *50 Years of Malaysian Agriculture: Transformation Issues, Challenges and Direction* (pp. 553 - 584). Selangor, Malaysia: Universiti Putra Malaysia Press.

- Mohammadi, S.A., Prasanna, B.M., and Singh, N.N. (2003). Sequential path model for determining interrelationships among grain yield and related characters in maize. *Crop Science* 43: 1690 - 1697.
- Moreira, V.R., Han, K.J., and McCormick, M. (2008). *Corn silage management*. Paper presented at the Mississippi State University Statewide Dairy Field Day Tylertown, Mississippi.
- Mosanto. (2010). Evaluation of corn silage quality for beef cattle. *Agronomic Spotlight*, 1-2.
- Mufti, M.U., Saleem, M., and Hussain, A. (2002). Diallel analysis of yield and yield components in maize (*Zea mays* L.). *Pakistan Journal of Agricultural Research* 17(1): 22 - 26.
- Mumtaz, A., Zafar, F., Malook, S., and Shehzad, A. (2015). A review on mating design. *Nature and Science* 13(2): 98 - 105.
- Nawar, A., A-Ibrahim, M., and E-Khalil, A.N.M. (1991). The efficiency of three conventional selection indices in corn. *Annals of Agricultural Science Moshtohor* 29: 63 - 75.
- Nei, M. (1972). Genetic distance between populations. *The American Naturalist* 106(949): 283 - 292.
- Nei, M. (1973). Analysis of genetic diversity in subdivided populations *Proceedings of the National Academy of Sciences* 70: 3321 - 3323.
- Nei, M. (1979). Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proceedings of the National Academy of Sciences* 76: 5269 - 5273.
- Nei, M., and Li, W.H. (1979). *Mathematical model for studying genetic variation in terms of restriction endonucleases*. Paper presented at the Proceedings of the National Academy of Sciences, USA.
- Nelson, A.I., and Steinberg, M.P. (1970). Sweet corn. In G. E. Inglett (Ed.), *Corn: Culture, Processing, Product*. Madison: The AVI Publishing Company.
- Nigussie, M., and Saleh, G. (2007). Genetic variability and heritability within sweet corn (*Zea mays* L. *saccharata*) breeding population. *Malaysian Applied Biology Journal* 36: 15 - 20.

- Noel, K. (2009). *Hybrid: The history and science of plant breeding*. Chicago: University of Chicago Press.
- Norziha, A., Rafii, M.Y., Maizura, I., and Saleh, G. (2008). Genetic variation among oil palm parent genotypes and their progenies based on microsatellite markers. *Journal of Oil Palm Research* 20: 533 - 541.
- Oba, M., and Allen, M. (1999). Evaluation and the importance of the digestibility of neutral detergent fiber from forage: Effects on dry matter intake and milk yield in dairy cows. *Journal of Dairy Science* 82: 589 - 596.
- Office of the Gene Technology Regulator. (2008). *The biology of Zea mays L. ssp mays (maize or corn)*. Canberra: Australian Government Office of the Gene Technology Regulator
- Ojo, D.K., Ornikunle, O.A., Oduwaye, M.O., and Ogunbayo, S.A. (2006). Heritability, character correlation and path correlation analysis among six inbred- lines of maize (*Zea mays L.*). *World Journal of Agricultural Science* 2(3): 352 - 358.
- Oliveira, J.P., Chaves, L.J., Duarte, J.B., Brasil, E.M., Ferreira, J.L.T., and Ribeiro, K.O. (2004). Teor de proteína no grão em populações de milho de alta qualidade protéica e seus cruzamentos. [Protein content in grain in populations of high protein quality corn and its crossings]. *Pesquisa Agropecuária Tropical* 34: 45 - 51.
- Onaga, G., Edema, R., and Asea, G. (2012). Tolerance of rice germplasm to iron toxicity stress and the relationship between tolerance, Fe²⁺, P and K content in the leaves and roots. *Archives of Agronomic and Soil Science* 59: 213 - 219.
- Orozco-terWengel, P., Corander, J., and Schlotterer, C. (2011). Genealogical lineage sorting leads to significant, but incorrect Bayesian multilocus inference of population structure. *Molecular Ecology* 20: 1108 - 1121.
- Pajić, Z., Erić, U., Mladenović Drinić, S., J., S., and Filipović, M. (2008). Genetic divergence estimated by RAPD markers and its relationship with hybrid performance in popcorn. *Cereal Research Communications* 38(2): 184 - 192.
- Paliwal, R.L. (2000a). Genetic resources. In R. L. Paliwal, G. Granados, H. R. Lafitte, and A. D. Vlolc (Eds.), *Tropical maize: Improvement and production* (pp. 1 - 3). Rome: Food and Agriculture Organization of the United Nations.

- Paliwal, R.L. (2000b). Introduction to maize and its importance *Tropical maize: Improvement and production* (pp. 1 - 3). Rome: Food and Agriculture Organization of the United Nations.
- Pasev, N., and Trifunovic, V. (1968). Influence of the morphological characters of the parents on the extent of manifestation of heterosis in the F₁ maize generation. *Arh. Poljopr. Nank.* 21(75): 12 - 30.
- Pejic, I., Ajmone-Marsan, P., Morgante, M., Kozumplick, V., Castiglioni, P., Taramino, G., et al. (1998). Comparative analysis of genetic similarity among maize inbred lines detected by RFLPs, RAPDs, SSRs, and AFLPs. *Theoretical Applied Genetics* 97: 1248 - 1255.
- Petrovic, Z. (1998). *Combining abilities and mode of inheritance of yield and yield components in maize (Zea mays L.)*. Novi Sad: Univerzitet u Novom Sadu.
- Phingzhong, G., Gardner, C.O., and Obaidi, M. (1986). Genetic variation and gene effects controlling prolificacy and other traits in maize (*Zea mays* L.). *Acto Genetica Sinica* 13(1): 35 - 42.
- Pinto, R.d.M.C., de Souza Jr., C.L., Carlini-Garcia, L.A., Garcia, A.A.F., and de Souza, A.P. (2003). Comparison between molecular markers and diallel crosses in the assignment of maize lines to heterotic groups. *Maydica* 48: 63 - 73.
- Poehlman, J.M. (1987). *Breeding field crops*. New York: Van Nostrand Reinhold.
- Prasad, M., Varshney, R.K., Roy, J.K., Balyan, H.S., and Gupta, P.K. (2000). The use of microsatellites for detecting DNA polymorphism, genotype identification and genetic diversity in wheat. *Theoretical Applied Genetics* 100: 584 - 592.
- Prasanna, B.M., Vasal, S.K., Kassahun, B., and Singh, N.N. (2001). Quality protein maize. *Current Science* 81: 1308 - 1319.
- Pswarayi, A., and Vivek, B. (2008). Combining ability amongst maize (*Zea mays* L.) germplasm under stress and non-stress conditions and identification of testers. *Euphytica* 162: 353 - 362.
- Purseglove, J.W. (1972). *Tropical Crops: Monocotyledons*. New York: Longman Scientific and Technical

- Qadri, M.I., Agrawal, K.N., and Sanghi, A.K. (1983). Combining ability under two population sizes for ear traits in maize. *Indian Journal of Genetics* 43: 208 - 211.
- Rai, J.N., Singh, H.N., and Saxena, A.K. (1991). Combining ability in relation to heterosis for quantitative characters in sugarcane. *Indian Journal of Genetics* 51: 96 - 101.
- Reid, L.M., Xiang, K., Zhu, X., Baum, B.R., and Molnar, S.J. (2011). Genetic diversity analysis of Canadian maize inbred lines based on pedigree and simple sequence repeat markers. *Canadian Journal of Plant Science* 91: 651 - 661.
- Revilla, P., Malvar, R.A., Carrea, M.E., Soengas, P., and Ordas, A. (2002). Heterotic relationships among European maize inbreds. *Euphytica* 126: 259 - 264.
- Robinson, H.F., Comstock, R.E., and Harvey, P.H. (1949). Estimates of heritability and degree of dominance in corn. *Agronomic Journal* 41: 353 - 359.
- Rohlf, F. (2000). NTSYS-pc: Numerical taxonomy and multivariate analysis system (Version 2.10). Setauket, NY: Exeter Publishing, Ltd.
- Rohlf, F. (2002). NTSYS-pc: Numerical taxonomy system (Version 2.1). Setauket, New York: Exeter Publishing. Ltd.
- Rohlf, F., and Fisher, D. (1968). Test for hierarchical structure in random data sets. *Systematic Zoology* 17: 407 - 412.
- Rojas, B.A., and Sprague, G.F. (1952). A comparison of variance components in corn yield trials: III. General and specific combining ability and their interaction with locations and years. *Agronomy Journal* 44: 462 - 466.
- Roth, G.W., and Heinrichs, A.J. (2001). Corn silage production and management. *Penn State Extension, Agronomy Fact 18*. Retrieved from <http://www.cas.psu.edu>
- Russell, W.A. (1974). *Comparative performance for maize hybrids representing different eras of maize breeding*. Paper presented at the 29th Annual Corn and Sorghum Research Conference, ASTA, Washington, DC.

- Russell, W.A. (1976). Genetic effects and genetic effects X year interactions at three gene loci in sublines of a maize inbred line. *Canadian Journal of Genetics and Cytology* 18: 23 - 33.
- Russell, W.A., and Halauer, A.R. (1980). Corn. In W. R. Fehr and H. H. Hadley (Eds.), *Hybridization of crop plants* (pp. 299 - 312). Madison: American Society of Agronomy and Crop Science Society of America.
- Sa'at, N.H.M., Hussin, F., Ahmad, S., and Saiin, S.S. (2012). Jagung manis hibrid baharu Hibrimas. *Buletin Teknologi MARDI, Bil. 1*, 107 - 110.
- Sadek, S.E., Ahmed, M.A., and Abd El-Ghaney, H.M. (2006). Correlation and path coefficient analysis in five parents inbred lines and their six white maize (*Zea mays* L.) single crosses developed and grown in Egypt. *Journal of Applied Sciences Research* 2(3): 159 - 167.
- Saha, U., Sonon, L., Hancock, D., Hill, N., Stewart, L., Heusner, G., *et al.* (2013). Common terms used in animal feeding and nutrition. *Bulletin* 1367, 1-20. Retrieved from University of Georgia Extension website: https://secure.caes.uga.edu/extension/publications/files/pdf/B%201367_3.PDF
- Saleh, G. (1998). Putra J-58- The hybrid grain maize variety. *Bulletin for the launching of the grain maize variety*.
- Saleh, G. (2003). *Putra GS-2002: The improved sweet corn (Zea mays L.) genotype developed by introgression of exotic germplasm*. Paper presented at the Malaysian Science and Technology Expo, Selangor, Malaysia.
- Saleh, G., Abdullah, D., and Rahim, A.A. (2002a). Effects of location on performance of selected tropical maize hybrids development in Malaysia. *Pertanika Journal of Tropical Agriculture* 25(2): 75 - 86.
- Saleh, G., Abdullah, O., and Anuar, A.R. (2002b). Performance, heterosis and heritability in selected tropical maize single, double and three-way cross hybrids. *Journal of Agriculture Science* 138: 21 - 28.
- Saleh, G.B., Yusop, M.R., and Yap, T.C. (1993). Inbreeding depression and heterosis in sweet corn varieties Manis Madu and Bakti-1. *Pertanika Journal of Tropical Agriculture* 16(3): 209 - 214.
- SAS Institute Inc. (2011). SAS/STAT® user's guide 9.3 (Version 9.3). Cary: SAS Institute Inc.

- Sattler, S.E., Funnell-Harris, D.L., and Pedersen, J.F. (2010). Brown midrib mutations and their importance to the utilization of maize, sorghum, and pearl millet lignocellulosic tissues *Plant Science* 178(3): 229 - 238. doi:<https://doi.org/10.1016/j.plantsci.2010.01.001>
- Satyavathi, C.T., Bhat, K., Bharadwaj, C., Tiwari, S., and Chaudhury, V. (2006). AFLP analysis of genetic diversity in Indian soybean (*Glycine max* L. Merr.) varieties. *Genetic Resources and Crop Evolution* 53: 1069 - 1079. doi:10.1007/s10722-005-2011-4
- Schnable, P.S., Ware, D., Fulton, R.S., Stein, J.C., Wei, F., Pasternak, S., *et al.* (2009). The B73 maize genome: Complexity, diversity, and dynamics. *Science* 326: 1112 - 1115.
- Senior, M.J.L., Murphy, J.P., Goodman, M.M., and Stuber, C.W. (1998). Utility of SSRs for determining genetic similarity and relationships in maize using an agarose gel system. *Crop Science* 38: 1088 - 1098.
- Senior, M.L., and Heun, M. (1993). Mapping maize microsatellites and polymerase-chain-reaction confirmation of the targeted repeats using a CT primer. *Genome* 36: 884 - 889.
- Sharma, J.R. (1988). *Statistical and biometrical techniques in plant breeding*. New Delhi: New Age International (P) Limited Publishers.
- Sharma, J.R. (1998). *Statistical and biometrical techniques in plant breeding*. New Delhi: New Age International (P) Limited Publishers.
- Shenk, J.S., and Westerhaus, M.O. (1994). The application of near infrared reflectance spectroscopy (NIRS) to forage analysis. In G. C. Fahey Jr., M. Collins, D. R. Mertens, and L. E. Moser (Eds.), *Forage quality, evaluation, and utilization*. Madison: ASA, CSSA, and SSSA.
- Shull, G.H. (1908). The composition of a field of maize. *American Breeders Association Reports* 4: 296 - 301.
- Shull, G.H. (1909). A pure line method of corn breeding. *American Breeders Association Reports* 5: 51 - 59.
- Shull, G.H. (1914). Duplicated genes for capsule form in *Bursa bursapastoris* Z. *Induktive Abstammungs und Vererbungslehre* 12: 97 - 149.
- Singh, J., and Chaudhary, L.B. (1979). *Biometrical methods in quantitative genetic analysis*. New Delhi: Kalyani Publishers, Ludhiana.

- Sleper, D.A., and Poehlman, J.M. (2006). Breeding corn (maize) *Breeding field crops* (5th ed., pp. 277 - 296). Iowa: Blackwell Publishing.
- Smith, C.W., Betrán, J., and Runge, E.C.A. (2004). *Corn: Origin, history, technology and production*. New Jersey: John Wiley & Sons Inc.
- Smith, J.S.C. (1984). Genetic variability within U.S. hybrid maize: Multi-variate analysis of isozyme data. *Crop Science* 24: 1041 - 1046.
- Smith, J.S.C., Chin, E.C.L., Shu, H., Smith, O.S., Wall, S.J., Senior, M.L., *et al.* (1997). An evaluation of the utility of SSR loci as molecular markers in maize (*Zea mays* L.): Comparisons with data from RFLPS and pedigree. *Theoretical Applied Genetics* 95(1-2): 163 - 173.
- Smith, J.S.C., Smith, O.S., and Lamkey, K.R. (2005). Maize breeding. *Maydica* 50: 185 - 192.
- Smith, O.S., and Smith, J.S.C. (1992). Measurement of genetic diversity among maize hybrids: A comparison of isozymic, RFLP, pedigree and heterosis data. *Maydica* 37: 53 - 60.
- Snedecor, G.W., and Cochran, W.G. (1989). *Statistical Methods* (Eight ed.). Iowa: Iowa State University Press.
- Sokal, R.R., and Michener, C.D. (1958). A statistical method for evaluating systematic relationships. *University of Kansas Scientific Bulletin* 38 Pt. 2(22): 1409 - 1438.
- Sprague, G.F., and Tatum, L.A. (1942). General vs. specific combining ability in single crosses of corn. *Journal of the American Society of Agronomy* 34: 923 - 932.
- Srdic, J., Nikolic, A., and Pajic, Z. (2008). SSR markers in characterization of sweet corn inbred lines. *Genetika* 40(2): 169-177. doi:10.2298/gensr0802169s
- Sserumaga, J.P., Makumbi, D., Ji, H., Njoroge, K., Muthomi, J.W., Chemining'wa, G.N., *et al.* (2014). Molecular characterization of tropical maize inbred lines using microsatellite DNA markers. *Maydica* 59: 267 - 274.
- Stearns, F.W. (2010). One hundred years of pleiotropy: A retrospective. *Genetics Society of America* 186: 767 - 773.

- Stepansky, A., Kovalski, I., and Perl-Treves, R. (1999). Intraspecific classification of melons (*Cucumis melo* L.) in view of their phenotypic and molecular variation. *Plant Systematics and Evolution* 217: 313 - 332.
- Strable, J., and Scanlon, M.J. (2009). Maize (*Zea mays*): a model organism for basic and applied research in plant biology. *Cold Spring Harbor Protocols* 2. doi:10.1101/pdb.emo132
- Sujiprihati, S., Saleh, G., and Ali, S. (2001). Combining ability of yield and related characters in single cross hybrid. *SABRAO Journal of Breeding and Genetics* 33(2): 111 - 120.
- Swift, M.L. (2001). *Fibre and energy in corn silage*. Retrieved from British Columbia: <https://farmwest.com/node/974>
- Taramino, G., and Tingey, S. (1996). Simple sequence repeats for germplasm analysis and mapping in maize. *Genome* 39(2): 277 - 287.
- Tautz, D. (1989). Hypervariability of simple sequences as a general source for polymorphic DNA markers. *Nucleic Acids Research* 17: 6463 - 6471.
- Tito, C.M., Poggio, L., and Naranjo, C.A. (1991). Cytogenetic studies in the genus *Zea* - 3. DNA content and heterochromatin in species and hybrids. *Theoretical and Applied Genetics* 83: 58 - 64.
- Tollenaar, M., Ahmadzadeh, A., and Lee, E.A. (2004). Crop physiology and metabolism: Physiological basis of heterosis for grain yield in maize. *Crop Science* 44: 2086 - 2094.
- Tollenaar, M., and Wu, J. (1999). Yield improvement in temperate maize is attributable to greater stress tolerance. *Crop Science* 39: 1597 - 1604.
- Troyer, A.F. (1990). A retrospective view of corn genetic resources. *Journal of Heredity* 81: 17 - 24.
- Troyer, A.F. (1999). Background of U.S. hybrid corn. *Crop Science* 39: 621 - 626.
- Troyer, A.F., and Larkins, J.R. (1985). Selection for early flowering in corn: 10 late sunthehtics. *Crop Science* 25: 695 - 697.
- Uddin, M.S., Khatun, F., Ahmed, S., Ali, M.R., and Bagum, S.A. (2006). Heterosis and combining ability in corn (*Zea mays* L.). *Bangladesh Journal of Botany* 35(2): 109 - 116.

- United States Agency for International Development. (2009). *Silage making for small scale farmers*. Retrieved from USAID: https://pdf.usaid.gov/pdf_docs/PNADQ897.pdf
- USDA. (2015). *Malaysia grain and feed annual Corn, Wheat, and Rice update*. Retrieved from <https://www.fas.usda.gov/data/malaysia-grain-and-feed-annual-1>
- USDA. (2016). Germplasm Resources Information Network - (GRIN) Retrieved 8 March 2016, from United States Department of Agriculture, Agricultural Service <https://npgsweb.ars-grin.gov/gringlobal/search.aspx>
- van Bueningen, L.T., and Busch, B.H. (1997). Genetic diversity among North American spring wheat cultivars: I. Analysis of the coefficient of parentage matrix. *Crop Science* 37: 570 - 579.
- Van Soest, P.J. (1994). *Nutritional ecology of the ruminants* (2nd ed.). Ithaca, London: Cornell University Press.
- Vasal, S.K., Srinivasan, D.L., Beck, D.L., Crossa, J., Pandey, S., and De Leon, C. (1992a). Heterosis and combining ability of CIMMYT's tropical late white germplasm. *Maydica* 37: 217 - 223.
- Vasal, S.K., Srinivasan, D.L., Pandey, S., Cordova, H.S., Han, G.C., and Gonzales, C.F. (1992b). Heterotic patterns of ninety-two white tropical CIMMYT maize lines. *Maydica* 37: 259 - 270.
- Virk, P.S., Newbury, H.J., Jackson, M.T., and Ford-Lloyd, B.V. (2000). Are mapped markers more useful for assessing genetic diversity? . *Theoretical Applied Genetics* 100: 607 - 613.
- Virmani, S.S., Pandey, M.P., Singh, I.S., and Xu, W.J. (2004). *Classical and molecular concepts of heterosis, plant breeding mendelian to molecular approaches*. New Delhi: Narosa Publishing House.
- Vos, P., Hogers, R., Bleeker, M., Reijans, M., Van De Lee, T., Hornes, M., et al. (1995). AFLP: a new technique for DNA fingerprinting. *Nucleic Acids Research* 23: 4407 - 4414.
- Wan Zahari, M., and Wong, H.K. (2009). Research and development on animal feed in Malaysia. *Wartazoa* 19(4): 172 - 179.

- Wang, H., Nussbaum-Wagler, T., Li, B., Zhao, Q., Vigourous, Y., Faller, M., *et al.* (2005). The origin of the naked grains of maize. *Nature* 436: 714 - 719.
- Watson, L., and Dallwitz, M.J. (1992). *Grass genera of the world: Descriptions, illustrations, identifications, and information retrieval; including synonyms, morphology, anatomy, physiology, photochemistry, cytology, classification, pathogens, world and local distribution, and references* Retrieved from <http://delta-intkey.com/>
- Weising, K., Nybom, H., Wolff, K., and Kahl, G. (2005). *DNA fingerprinting in plants: Principles, methods, and applications* (2nd ed.). Boca Raton: CRC Press, Taylor & Francis Group.
- Wen, Z., Ding, Y., Zhao, T., and Gai, J. (2009). Genetic diversity and peculiarity of annual wild soybean (*G. soja* Sieb. Et Zucc.) from various eco-regions in China. *Theoretical Applied Genetics* 119: 371 - 381.
- Wende, A., Shimelis, H., Derera, J., Mosisa, W., Danson, J., and Laing, M.D. (2013). Genetic interrelationships among medium to late maturing tropical maize inbred lines using selected SSR markers. *Euphytica* 191: 269 - 277.
- Westman, A.L., and Kresovich, S. (1997). Use of molecular marker techniques for description of plant genetic variation. In J. L. Callow, B. V. Ford-Lloyd, and H. J. Newbury (Eds.), *Biotechnology and plant genetic resources* (pp. 9 - 45). Birmingham: CAB International.
- Wilkinson, J.M. (1980). Ensiling forage maize. In E. S. Bunting (Ed.), *Production and utilization of the maize crop* (pp. 229 - 244). The Grassland Research Institute, Hurley, Maidenhead, Berkshire SL6 5LR, England: Hereward and Stourdale Press.
- Wright, S. (1968). *Evolution and the genetics of populations. Vol. I. Genetic and biometric foundations*. Chicago: University of Chicago Press.
- Wu, K.-S., and Tanksley, S.D. (1993). Abundance, polymorphism and genetic mapping of microsatellites in rice. *Molecular and General Genetics* 241: 225 - 235.
- Xia, X.C., Reif, J.C., Hoisington, D.A., Melchinger, A.E., Frisch, M., and Warburton, M.L. (2004). Genetic diversity among CIMMYT maize inbred lines investigated with SSR markers: I. Lowland tropical maize. *Crop Science* 44: 2230 - 2237.

- Xia, X.C., Reif, J.C., Melchinger, A.E., Frisch, M., Hoisington, D.A., Beck, D., *et al.* (2005). Genetic diversity among CIMMYT maize inbred lines investigated with SSR markers: II. Subtropical, Tropical Midaltitude, and Highland maize inbred lines and their relationships with elite U.S. and European maize. *Crop Science* 45: 2573 - 2582. doi:10.2135/cropsci2005.0246
- Xie, H.L., Ji, H.Q., Liu, Z.H., Tian, G.W., Wang, C.L., Hu, Y.M., *et al.* (2009). Genetic basis of nutritional content of stover in maize under low nitrogen conditions. *Euphytica* 165: 185 - 193.
- Xu, Y., Skinner, D.J., Wu, H., Palacios-Rojas, N., Araus, J.L., Yan, J., *et al.* (2009). Advances In Maize Genomics and Their Value for Enhancing Genetic Gains from Breeding. *International Journal of Plant Genomics* 2009. doi:10.1155/2009/957602
- Yeh, F.C., Yang, R.C., and Boyle, T. (1999). Popgene: Microsoft windows-based freeware for population genetic analysis (Version Release 1.31). Alberta: University of Alberta
- Young, E. (2016). Comparing corn silage hybrids. <https://www.progressiveforage.com/forage-types/silage/comparing-corn-silage-hybrids>
- Young, J., and Virmani, S.S. (1990). Heterosis in rice over environments. *Euphytica* 51: 87 - 93.
- Yu, S., Zhang, F., Wang, X., Zhao, X., Zhang, D., Yu, Y., *et al.* (2010). Genetic diversity and marker-trait associations in a collection of Pak-Choi (*Brassica rapa* L. ssp. *chinensis* Makino) accessions. *Genes and Genomics* 32(5): 419 - 428. doi:10.1007/s13258-010-0033-6
- Zhang, L., Chia, J.M., Kumari, S., Stein, J.C., Liu, Z., Narechania, A., *et al.* (2009). A genome-wide characterization of microRNA genes in maize. *PLoS Genetics* 5(11): e1000716. doi:10.1371/journal.pgen.1000716
- Zhang, Y., and Kang, M.S. (1997). DIALLEL-SAS: A SAS program for Griffing's diallel analyses. *Agronomy Journal* 89: 179 - 182.
- Zhang, Y., and Kang, M.S. (2003). DIALLEL-SAS: A program for Griffing's diallel methods *Handbook of formulas and software for plant geneticist and breeders* (pp. 1 - 19). New York: The Haworth Press. Inc.

Zhang, Z.M., Zhao, M.J., Ding, H.P., Rong, T.Z., and Pan, G.T. (2005). Quantitative trait loci analysis of plant height and ear height in maize (*Zea mays* L.). *Russian Journal of Genetics* 42(3): 391 - 396.

Zsubori, Z., Gyenes-Hegyí, Z., Illés, O., Pók, I., Rácz, F., and Szőke, C. (2002). Inheritance of plant and ear height in maize (*Zea mays* L.). *Agricultural Research Institute of the Hungarian Academy of Science, Martonvásár*: 1 - 5.

