

Preface

Plant breeding is a science of evolution. The scientific basis of plant breeding started in the 1900s. The rediscovery of Mendelian genetics and the development of the statistical concepts of randomization and replication had considerable impact on plant breeding methods. They provided a genetic basis for the variation observed among individuals, separating genetic and environmental effects, and valid experimental techniques for measuring those differences. Breeders work with traits and environments and their major task is to increase the frequency of favorable alleles of quantitative traits, controlled by a large, unknown number of genes interacting with target environments.

Maize is an economically important crop for feed, fiber, fuel, and food. It is used as an ingredient in an endless list of manufactured products that affect the nutrition of the world's population. Maize is a cross-pollinated species with unique and separate male (tassel) and female (ear) organs. Maize breeding has unique features that are different from the other extensively cultivated grain species which are primarily self-pollinated. Techniques from both self- and cross-pollinated crops are utilized in maize that allow production of large sample sizes easily and a diversity of breeding methods. These methods are geared toward the development of improved populations, inbred lines, and their hybrids for different types of markets.

Maize breeding is one of the successful examples of breeder-directed evolution. Breeders have been effective in developing improved cultivars to meet the changing cultural and environmental conditions of the past 150 years. Modern maize breeding methods are primarily a 20th century phenomenon. Applied maize breeding has been effective in developing improved hybrids during the past 100 years. The inbred-hybrid concept was developed in the public sector and is still considered one of the greatest achievements in crop breeding. It is considered one of the most successful plant breeding breakthroughs as a consequence of private-public research cooperation and business vision. Development of the commercial seed industry is testimony of breeding methods that have evolved for the economical production of high-quality hybrid seed that is accepted and demanded by the modern farmer. In order to meet the increasing and divergent uses of maize, breeding methods have evolved to increase the effectiveness and efficiency of selection for several quantitative traits in multiple stages and environments often at a rate of more than one season per year due to winter nurseries.

Maize breeders decide which combination of traits and environments is needed to breed for both inbreds and hybrids. A trait controlled by genes that are not significantly affected by the environment can be improved very effectively. For instance, breeders have the option to improve flowering date for earliness at a rate of 2–3 days per year at a minimum cost by stratified mass selection (e.g., less than a penny per plant screened) or utilized cloned genes (e.g., *vgt1*) for a more expensive procedure (e.g., if a grant is awarded). Scientists have also decided to invest federal funds in understanding the genetic basis of flowering time in a specific maize population (e.g., NAM) which should alert us of the need to increase maize sampling while linking classical and modern quantitative genetic approaches. However, most traits that concern the breeder (e.g., yield, drought tolerance) are economically very important, difficult to measure, and quantitative in nature often with significant environmental influence on the trait's expression. For instance, breeding approaches for drought tolerance exploiting polygenic effects with possible transgenes would seem desirable. Though single-gene transgenic approaches are currently being proposed by industry, choosing the right methodology (e.g., may be an interaction of both) will demonstrate there is no limit to genetic improvement for drought tolerance when most tolerance genes are targeted in the breeding process and not just a single-gene approach. Drought-tolerance efforts on polygenic effects do not have a limit on genetic improvement and quantitative traits, at the moment, are better explained by polygenes rather than quantitative trait loci (QTL).

Quantitative traits are controlled by a large, but unknown, number of genes, each having a small effect on the total expression of the trait. The environment in which they are measured determines their effects and it is dependent on genetic background as each hybrid has its own genetic effects. These traits are characterized by degree differences among phenotypes that do not fall into distinct categories. They have a complex inheritance including dominance, epistasis, linkage, and the interaction of genetic and environmental effects. Quantitative traits are controlled by the joint action of many genes, and genetic improvement of plants has been successful even though the knowledge of genes controlling these traits was minimal.

Unlike other crops maize is a model crop for achieving significant genetic gain with large genetic variability. Genetically broad-based public germplasm has significantly been utilized and recycled by industry before intellectual property rights were available. B14, B37, B73, and B84 are examples of publicly developed inbred lines that have generated billions of dollars to the agricultural sector via their use in hybrids. They were derived from a breeding scheme that integrated germplasm improvement (e.g., five cycles of half-sib intra-population recurrent selection before developing B73) with inbred line development. The development of these lines needed continuous federal and state funding through decades for creating the genetically broad-based synthetic variety Iowa Stiff Stalk Synthetic (BSSS), improving it by five cycles of half-sib recurrent selection with a tester, conducting several years of inbreeding and extensive hybrid testing, and producing seed increases for release and industry distribution. Few of these programs are left due to public funding restrictions and lack of commitment from breeders to conduct long-term

programs for germplasm improvement. Moreover, such programs are often indirectly discouraged due to land-grant University tenure and royalty concerns as well as encouragement for short-term grants with indirect costs often leading scientists to avoid unbiased decisions and research. But, scientists are also encouraged to keep long-term breeding goals active as they provide an extensive and annual production of peer-refereed high-quality manuscripts with applied science impact.

Although the basic breeding methods for development of maize inbred lines and hybrids were described by 1910, significant contributions have been visualized and tested for modernizing the basic breeding methods including transgenic maize for single genes. However, as for the drought example, there is no limit to genetic improvement when most genes are targeted in the breeding process. Even though choice of base germplasm continues to be the priority we still have the challenge to integrate effective molecular tools for selecting quantitative traits that are either difficult or expensive to measure with low heritability (e.g., root traits, fast dry down). Definitively, modern technology should target the right traits, those currently challenging to phenotype. The genome of B73 has been sequenced. The application of this discovery, however, still is not fully realized in breeding programs. Therefore, there might be alternative and/or complementary options to speed up the development of maize hybrids. We definitively need the integration of basic and applied science for common long-term goals directed at better cultivars. Heterotic effects are unique for each hybrid and sequencing efforts on only B73 and others alike might limit the identification of useful and unique alleles (e.g., tropical and/or early maturing genetic backgrounds) for complex traits, ultimately the desirable ones to broaden our germplasm base.

Similar to other scientific disciplines, many changes have occurred in the methods, techniques, information available, and germplasm used in maize breeding since the first edition of this volume. Interest in the inheritance of quantitative traits of maize was one of the basic areas of maize research during the 30-year span of 1945–1975. During this time frame, there were areas of maize breeding of concern because of the seemingly yield plateau of double-cross hybrids; the germplasm available for breeding purposes and how they could be improved; selection and breeding methods to enhance effectiveness of developing inbred lines and hybrids; and the one area of common interest in all facets of maize breeding – the genetic basis of heterosis. Extensive data have been reported for the types of genetic effects important in quantitative trait expression across different types of maize populations and hybrids. However, against predictions and multi-million dollar grants a uniform theory on heterosis remains inconclusive. It is generally agreed, however, that the presence of non-additive genetic effects (dominance and epistasis) are necessary even though measuring epistasis continues to be challenging to also predict at the molecular level. Because non-additive effects seem so important for heterosis expression, it seems that relative importance of the different non-additive genetic effects will vary among hybrids because of the combination of genes and alleles that is unique for each highly productive hybrid.

Our main concern in this volume is to describe how the principles of quantitative genetics and cyclical selection schemes have been used in maize breeding

research. In addition to the principles discussed, data are summarized and updated from reported studies. It is not intended that the breeding methods discussed in this volume will, or should, replace those currently used in the public and private sectors; they are intended to supplement those currently used and help devise new ones. The integration of the breeding methods discussed herein with those currently used should enhance future breeding efforts to maintain the level of genetic gain of the past 70 years and help achieve industry targets (e.g., double genetic gains in 30 years). Future genetic gains in maize hybrid yields are dependent on the incorporation of useful and unique genetic diversity. The integration of breeding methods discussed in this volume should enhance future breeding efforts to maintain and create active public breeding programs, not only adapting for improving genetically broad-based germplasm, but also developing products and training the next generation of maize breeders. There are fewer applied public maize breeding programs than generally thought. It will require the combine support of industry, grower associations, grant agencies, and land-grant systems to help keep applied public maize breeding programs strong.

One aspect of genetics that has dramatically changed how maize breeders design and conduct breeding programs is the vast and rapid developments in molecular genetics and the generation of genotypic data at a lower cost. Similar to the study of quantitative genetics for the types of genetic variation and inheritance of maize traits, certain techniques of molecular genetics also have been extensively studied and applied to maize breeding programs (e.g., marker-assisted backcrossing for single-gene trait integration). Quantitative genetics and molecular genetics represent the opposites. Data for the quantitative genetic studies were collected on the phenotypes of families and progenies replicated within and across environments. In contrast, the molecular geneticists study gene and allele effects at the DNA level. The disparity between the two facets of genetics may seem irreconcilable, but they are becoming more interwoven with continued advancements in molecular genetics and the need for 'phenotyping.' Interest and emphasis on the study on the inheritance of quantitative traits decreased rapidly with the advent and rapid expansion of molecular genetics. However, they seem to be different approaches for a similar information generation. Initially, molecular genetics had the desire to study complex traits but emphasized the study of traits with major effects, such as resistance and/or tolerance to major pests (insects, diseases, and weeds) that affect maize production. If molecular genetics was to have greater impact it became obvious that it had to examine how molecular genetic techniques could be used to improve the important economic traits, such as grain yield. The identification and use of molecular markers to assist in selection of quantitative trait loci (QTLs), genome-wide selection, and association mapping have become common areas of research. Breeders are trying to sort out what can be applied. The integration of quantitative and molecular genetic information will only increase in the future as sample sizes approach those of the past quantitative genetic studies. Cooperation between the public and private sectors for latest technology seems to be a solution to avoid spending precious resources with state and federal funds in labs that become obsolete quickly. It also allows the public scientist to generate basic research as a matter of weeks

vs. years. The maize genome has over 60,000 genes (number increases annually). Therefore, all aspects of genetics will be needed for continued genetic advances. The integration of molecular biologists, geneticists, physiologists, and breeders is key. Maize breeders will need all the resources available to them to manipulate the large number of genetic factors that affect the traits important in developing elite inbred lines to produce genetically superior hybrids with consistent performance in changing environments. Exploiting unique environments (e.g., North Dakota) can accelerate desirable evolution toward adaptation to climate change.

The objective of this volume, as part of the *Handbook of Plant Breeding*, is to increase awareness of the relative value and impact of applied maize breeding for all crop uses and its security and sustainability. The topics included should be of interest of graduate students in plant breeding and to breeders conducting research on not only breeding and selection methods but also developing pure lines and hybrid cultivars in maize and other crop species. Because of rapid development of the inbred line–hybrid concept in maize, chapters pertain mostly to maize but are applicable to other crop species. The volume's main contribution will be to breeders, geneticists, students, and policy makers willing to work together for the long-term sustainable crop improvement and production for various environments. We hope long-term genetic maize improvement programs with genetically broad-based genetic materials (e.g., GEM/ EarlyGEM programs) are encouraged.

The authors wish to acknowledge the contributions and suggestions others have provided in the preparation of this volume. This project was initiated to commemorate 20 years of the last edition of this book, a very useful resource for research, teaching, and breeding. Our target was to update content and make a unique style presentation. Corrections of errors detected by the authors and others have been made, some changes were made in notation for consistency, rewriting was done for clarity, and content and references on the subject matter were added.

The authors owe a deep gratitude to Mary Lents for all of her efforts for the past 30 years, which made this book possible. Her diligence, talents, interests, persistence, attention to details, typing skills, and editing link 'between Iowa and North Dakota' are sincerely appreciated. She accomplished these tasks in addition to her regular duties as secretary. We sincerely appreciate all her past contributions and wish her only the best in the future, especially at this moment of uncertainty.

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