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# Marker Assisted Selection For Drought Tolerance And Striga Resistance Introgressing Quantitative Trait Loci Qtl In Farmer Preferred Varieties Of Sorghum

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## MARQUIS JAMARI

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*Advances in Molecular Breeding Toward Drought and Salt Tolerant Crops* Editions Quae

Drought is a major environmental stress factor that affects the growth and development of plants. Most of the physiological

traits associated with drought tolerance are quantitative in nature. An important research strategy that has been widely used to deal with such complexity is to use molecular markers to identify quantitative trait loci (QTLs) in appropriate mapping populations. In response to drought brought about by soil water deficit, plants can exhibit either drought escape or drought resistance mechanisms, with resistance further classified into drought avoidance and drought tolerance. Drought escape is the ability of plants to complete the life cycle before severe stress arrives. Drought avoidance is the maintenance of high tissue water potential in spite of soil water deficit. Drought avoidance is consequence of improved water uptake under stress and the capacity of plant cells to hold acquired water that reduces water loss. Drought tolerance is the ability to withstand water deficit with low tissue water potential. Plant water status that includes leaf water potential, osmotic potential and relative water content (RWC) represents an easy measure of water deficit and provides best sensor for stress. Genomics-assisted breeding (GAB) approaches, such as marker-assisted selection (MAS), can greatly improve precision and efficiency of selection in crop breeding. Molecular markers can facilitate indirect selection for traits that are difficult or inconvenient to score directly, pyramiding genes from different sources and combining resistance to multiple stresses. Conventional breeding for developing drought-tolerant crop varieties is time-consuming and labor intensive due to the quantitative nature of drought tolerance and difficulties in selection for drought tolerance. The identification of genomic regions associated with drought tolerance would enable breeders to develop improved cultivars with increased drought tolerance

using marker-assisted selection (MAS). This requires integration of knowledge from plant physiology and biotechnology into plant breeding. The availability of a large number of molecular markers, dense genetic maps and markers associated with traits and transcriptomics resources have made it possible to integrate genomics technologies into chickpea improvement.

[DNA Marker Assisted Selection to Improve Drought Tolerance in Alfalfa \(Medicago Sativa L.\)](#) John Wiley & Sons

Alfalfa (*Medicago sativa* L.) is the most important cultivated forage crop in the world. However, large proportions of alfalfa acreage in the western USA experience water deficit on a regular basis. Consequently, the current studies investigated the application of both molecular and conventional plant breeding approaches to improve alfalfa productivity under limited water conditions. The objectives of these studies were to: i) conduct marker assisted selection for favorable biomass QTL and to select against unfavorable biomass QTL that were segregating in three different elite alfalfa genetic backgrounds, ii) assess the impact of one cycle of phenotypic selection for drought resilience on frequencies of marker alleles linked to biomass QTLs, iii) determine the productivity of 24 elite alfalfa germplasms under fully irrigated, chronic (deficit irrigation throughout the season) and acute (mid-summer irrigation termination) water stress conditions, and iv) determine if elite alfalfa populations vary in their response to variable irrigation management regimes.

*Molecular Breeding for Rice Abiotic Stress Tolerance and Nutritional Quality* MDPI

Alfalfa is a perennial forage legume grown extensively under both rainfed and irrigated conditions. It is the most important forage

crop and the third most valuable crop in the United States of America. Alfalfa production is affected by abiotic stress factors such as drought that causes plant yield reduction. Because of this, plant breeding efforts are geared towards breeding for crop drought tolerance. Most traits governing drought tolerance are influenced by multiple genes, referred to as quantitative trait loci (QTL), and environmental factors. The NMSU alfalfa genetics and breeding program previously conducted forage and root biomass QTL mapping experiments in two segregating alfalfa populations grown under drought-stressed field conditions. Ten shoot and root biomass QTLs were identified in that research and represented by 10 simple sequence repeat (SSR) DNA markers. These markers were selected for use in a marker assisted selection (MAS) experiment in alfalfa in the current study. MAS was imposed on the unselected control (C0) (base population) by selecting plants that possessed (+), or did not possess (-), specific combinations of DNA marker alleles associated with high shoot (HS), low shoot (LS), high root (HR), and low root (LR) biomass, all designated as Cycle 1. The Cycle 1 populations that possessed (+) the marker alleles and the C0 population were then crossed to the three cultivars Malone, Melton and Multileaf to develop 18 cultivar-MAS hybrids (referred to as Malone-MAS, Melton-MAS, and Multileaf-MAS). A total of 32 populations were evaluated for shoot biomass production under normal irrigation (NI) and limited irrigation (LI) field conditions during 2011 and 2012. The goal of this research study was to validate if these drought tolerance QTLs can be used to improve the performance of three elite cultivars for yield under NI and LI management. The impact of MAS on forage quality factors and leaf relative water

content was also monitored. Results show that selection for high shoot biomass markers and high root biomass markers in the MAS-derived Cycle 1 populations improved forage yield by 23% and 20%, respectively in the LI study. In addition, selection for the low shoot and low root biomass marker alleles in the same populations decreased forage yield by 3% and 15%, respectively, in the LI study. In the NI study, selection for HS3+ improved forage yield by 9% (not significant) while all other population yield differences were small. For the cultivar-MAS hybrids two superior Malone-MAS and Multileaf-MAS hybrids outperformed their respective parent cultivar by 6% and 19% in the LI study, and 6% and 7% in the NI study. While no Melton-MAS hybrids outperformed their drought tolerant Melton parent in the LI study, one of the hybrids yielded 7% more than Melton in the NI study. Forage quality results indicated that most of the MAS-derived Cycle 1 populations had significantly higher leaf to stem ratio (LSR) than the three cultivars and their cultivar-MAS hybrids under the LI and NI management. For the cultivar-MAS hybrids, results show that under the LI and NI studies, one and two Multileaf-MAS hybrids, respectively, had a significantly higher LSR than the Multileaf cultivar; five and six Malone-MAS hybrids, respectively, had a significantly higher LSR than the Malone cultivar; and four and six Melton-MAS hybrids, respectively, had a significantly higher LSR than the Melton cultivar. For leaf relative water content (RWC), no significant year by entry, or main entry effect on leaf RWC were detected among the 32 populations under LI and NI management. The rankings among the populations were inconsistent in both studies. The overall results presented in this study validated the past QTL experimental

outcome that the marker effects were in the same direction as previously determined under well-watered and water-limited environments. This study also demonstrated that DNA MAS was effective at improving forage yield of three existing cultivars in both limited irrigation and normal irrigation management.

*Application of Marker Assisted Selection to Improving a Quantitative Trait in Common Bean (phaseolus Vulgaris L.)*

Springer Science & Business Media

The latest update on improving crop resistance to abiotic stress using the advanced key methods of proteomics, genomics and metabolomics. The wellbalanced international mix of contributors from industry and academia cover work carried out on individual crop plants, while also including studies of model organisms that can then be applied to specific crop plants

IITA

This book focuses on early germination, one of maize germplasm most important strategies for adapting to drought-induced stress. Some genotypes have the ability to adapt by either reducing water losses or by increasing water uptake. Drought tolerance is also an adaptive strategy that enables crop plants to maintain their normal physiological processes and deliver higher economical yield despite drought stress. Several processes are involved in conferring drought tolerance in maize: the accumulation of osmolytes or antioxidants, plant growth regulators, stress proteins and water channel proteins, transcription factors and signal transduction pathways. Drought is one of the most detrimental forms of abiotic stress around the world and seriously limits the productivity of agricultural crops. Maize, one of the leading cereal crops in the world, is sensitive to

drought stress. Maize harvests are affected by drought stress at different growth stages in different regions. Numerous events in the life of maize crops can be affected by drought stress: germination potential, seedling growth, seedling stand establishment, overall growth and development, pollen and silk development, anthesis silking interval, pollination, and embryo, endosperm and kernel development. Though every maize genotype has the ability to avoid or withstand drought stress, there is a concrete need to improve the level of adaptability to drought stress to address the global issue of food security. The most common biological strategies for improving drought stress resistance include screening available maize germplasm for drought tolerance, conventional breeding strategies, and marker-assisted and genomic-assisted breeding and development of transgenic maize. As a comprehensive understanding of the effects of drought stress, adaptive strategies and potential breeding tools is the prerequisite for any sound breeding plan, this brief addresses these aspects.

Genetic Diversity Assessment and Marker-Assisted Selection in Crops Springer

Marker Assisted Selection for Drought Tolerance and Grain Yield in Rice (*Oryza Sativa* L.) DNA Marker Assisted Selection to Improve Drought Tolerance in Alfalfa (*Medicago Sativa* L.)

Molecular Marker Analysis of Perennial Ryegrass (*Lolium Perenne* L.) Genetic Diversity Analysis, Linkage Map Construction, and Quantitative Trait Loci Mapping Springer Science & Business Media

This superb volume provides a critical assessment of genomics tools and approaches for crop breeding. Volume 1 presents the

status and availability of genomic resources and platforms, and also devises strategies and approaches for effectively exploiting genomics research. Volume 2 goes into detail on a number of case studies of several important crop and plant species that summarize both the achievements and limitations of genomics research for crop improvement.

**Identification of Drought-related Quantitative Trait Loci (QTLs) in Sugarcane (Saccharum Spp.) Using Genic Markers** John Wiley & Sons

Presents the latest knowledge of improving the stress tolerance, yield, and quality of rice crops One of the most important cereal crops, rice provides food to more than half of the world population. Various abiotic stresses—currently impacting an estimated 60% of crop yields—are projected to increase in severity and frequency due to climate change. In light of the threat of global food grain insecurity, interest in molecular rice breeding has intensified in recent years. Progress has been made, but there remains an urgent need to develop stress-tolerant, bio-fortified rice varieties that provide consistent and high-quality yields under both stress and non-stress conditions. *Molecular Breeding for Rice Abiotic Stress Tolerance and Nutritional Quality* is the first book to provide comprehensive and up-to-date coverage of this critical topic, containing the physiological, biochemical, and molecular information required to develop effective engineering strategies for enhancing rice yield. Authoritative and in-depth chapters examine the molecular and genetic bases of abiotic stress tolerance, discuss yield and quality improvement of rice, and explore new approaches to better utilize natural resources through modern breeding. Topics include

rice adaptation to climate change, enriching rice yields under low phosphorus and light intensity, increasing iron, zinc, vitamin and antioxidant content, and improving tolerance to salinity, drought, heat, cold, submergence, heavy metals and Ultraviolet-B radiation. This important resource: Contains the latest scientific information on a wide range of topics central to molecular breeding for rice Provides timely coverage molecular breeding for improving abiotic stress tolerance, bioavailability of essential micronutrients, and crop productivity through biotechnological methods Features detailed chapters written by internationally-recognized experts in the field Discusses recent progress and future directions in molecular breeding strategies and research *Molecular Breeding for Rice Abiotic Stress Tolerance and Nutritional Quality* is required reading for rice researchers, agriculturists, and agribusiness professionals, and the ideal text for instructors and students in molecular plant breeding, abiotic stress tolerance, environmental science, and plant physiology, biochemistry, molecular biology, and biotechnology.

**Improving Crop Resistance to Abiotic Stress** LAP Lambert Academic Publishing

Genetic mapping and marker assisted selection (MAS) is considered as one of the major tools in genetic improvement of crop plants in this genomics era. This book describes basics in linkage mapping, step-by-step procedure to perform MAS, achievements made so far in different crops, and limitations and prospects of MAS in plant breeding. It summarizes all this in a simple but comprehensive mode using suitable examples so as to explain the concept and its historical developments. To summarize, this book describes technologies for identification of

genes of interest through genetic mapping, recaps the major applications of MAS to plant breeding; lists examples in which MAS is being applied to various breeding programs, and emphasizes the various difficulties that limit the application of MAS in plant breeding, providing possible solutions to overcome these difficulties, and finally tries to illustrate the future prospects. This book would be a valuable guide to the undergraduates and post-graduates of agricultural universities and institutes that are interested and/or involved in genetic improvement of crop plants using modern tools. Bibliography listed in this book constitutes two parts: literature cited and further reading. Literature cited contains references cited in the text and further information on the given concept/technique can be obtained from these references. Further reading provides a list of suggested readings for in-depth coverage of the topics.

*Drought Stress in Maize (Zea mays L.)* John Wiley & Sons

The abiotic stresses like drought, temperature, cold, salinity, heavy metals etc. affect a great deal on the yield performance of the agricultural crops. To cope up with these challenges, plant breeding programs world-wide are focussing on the development of stress tolerant varieties in all crop species. Significant genomic advances have been made for abiotic stress tolerance in various crop species in terms of availability of molecular markers, QTL mapping, genome-wide association studies (GWAS), genomic selection (GS) strategies, and transcriptome profiling. The broad-range of articles involving genomics and breeding approaches deepens our existing knowledge about complex traits. The chapters are written by authorities in their respective fields. This book provides comprehensive and consolidated account on the

applications of the most recent findings and the progress made in genomics assisted breeding for tolerance to abiotic stresses in many important major crop species with a focus on applications of modern strategies for sustainable agriculture. The book is especially intended for students, molecular breeders and scientists working on the genomics-assisted genetic improvement of crop species for abiotic stress tolerance.

Selection of Drought-tolerant Soybean Lines Using a Field Screening Method and Identification of QTLs for Slow Wilting and Nitrogen Fixation Associated with Drought-tolerance Food & Agriculture Org.

A comprehensive description and assessment of the use of marker-assisted selection for increasing the rate of genetic gain in crops, livestock, forestry and fish, including the related policy, FAO's tradition of dealing with issues of importance to agricultural and economic development in a multidisciplinary and cross-sectoral manner.

Marker Assisted Selection in Advanced Segregating Lines for Drought Tolerance in Chickpea (Cicer Arietinum L.) [With CD Copy] John Wiley & Sons

Chapter Seven then describes the identification of QTL for morphological traits, water soluble carbohydrate content and photosynthetic traits as a first step towards the utilisation marker assisted selection (MAS) for the improvement of drought tolerance in perennial ryegrass.

*Molecular Marker Technology for Crop Improvement* Springer

There is an increasing need to improve crop water-use efficiency (WUE) (ratio of whole-plant biomass to cumulative transpiration) due to decreased water availability and increased food and

energy demands throughout the world. The objective of the study was to estimate the genetic variation and genetic basis for transpiration efficiency A:E (CO<sub>2</sub> assimilation rate (A) divided by transpiration rate (E)) trait and its relationship to WUE related to pre-flower drought tolerance in recombinant inbred lines (RILs) of sorghum and associated QTLs. A greenhouse study was conducted at Bushland, TX, 2008, using 71 RILs derived from cross of Tx430 x Tx7078. A randomized complete block experimental design was used, with both genotype and water regime (40 and 80 percent water regime) as experimental factors, and four replications. Genotype had a significant effect on A, E and A:E under both the environments. Among the RILs, entry means for A:E ranged from 1.58 to 3.07 mmol CO<sub>2</sub> mol<sup>-1</sup> H<sub>2</sub>O and 1.18 to 4.36 mmol CO<sub>2</sub> mol<sup>-1</sup> H<sub>2</sub>O under 80 percent and 40 percent water regime, respectively. Heritability estimates based on individual environments for A:E, A and E were 0.77, 0.45 and 0.37 under 80 percent water regime and 0.90, 0.33 and 0.71 under 40 percent water regime, respectively. A genetic map was constructed by digital genotyping method using Illumina GAI sequencer with 261 informative indel/ single-nucleotide polymorphism (SNP's) markers distributed over 10 linkage groups. Three significant QTLs associated with transpiration efficiency were identified; two on SBI-09 and one on SBI-10 with one logarithmic of odds (LOD) interval length ranging from 5.3 to 5.7 cM and accounting for 17 percent - 21 percent of the phenotypic variation. In field and greenhouse evaluation of agronomic of traits at College Station and Halfway, TX, 91 QTL that control variation in six major agronomic traits such as plant height, flowering, biomass, leaf area, leaf greenness and

stomatal density were identified. Co-localization of transpiration efficiency QTLs with agronomic traits such as leaf area, biomass, leaf width and stomatal density indicated that these agronomically important QTLs can be used for further improving the sorghum performance through marker assisted selection (MAS) under pre-flowering drought stress conditions. Genomics-Assisted Crop Improvement John Wiley & Sons The first edition of this book, Genetic Mapping and Marker Assisted Selection: Basics, Practice and Benefits, was widely appreciated as the first of its kind on this topic and has been listed as a reference work in several agricultural universities' curricula. A great deal has happened over the last five years, making it high time to incorporate recent developments in genetic mapping and report on novel strategies in marker assisted selection in crop plants as a second edition. This book addresses a range of topics, including: new marker types and their genotyping methods based on high-throughput technologies, advances in genomics and their role in new marker development, improvements in genetic mapping strategies and software updates, developments in phenomics and their applications in QTL mapping, and how to incorporate these developments and advances in marker assisted selection in crop plants. Similar to the first edition, each technique and method is explained using a step-by-step method, allowing the book to serve as a self-study guide for scholars whose work involves the genetic improvement of crop plants for any trait of interest, particularly for biotic and abiotic stress resistance. In addition, the book offers a valuable guide for undergraduate and graduate students at agricultural universities and institutes that are



interested and/or involved in the genetic improvement of crop plants using modern tools. In addition, the bibliography includes a list of suggested works for pursuing further research on the topics covered.

Marker Assisted Selection for Drought Tolerance and Blast Disease Resistance and Detection of QTL Controlling Silicon and Zinc Content in Rice (*Oryza Sativa* L.) Springer Science & Business Media

Marker-assisted plant breeding involves the application of molecular marker techniques and statistical and bioinformatics tools to achieve plant breeding objectives in a cost-effective and time-efficient manner. This book is intended for beginners in the field who have little or no prior exposure to molecular markers and their applications, but who do have a basic knowledge of genetics and plant breeding, and some exposure to molecular biology. An attempt has been made to provide sufficient basic information in an easy-to-follow format, and also to discuss current issues and developments so as to offer comprehensive coverage of the subject matter. The book will also be useful for breeders and research workers, as it offers a broad range of up-to-the-year information, including aspects like the development of different molecular markers and their various applications. In the first chapter, the field of marker-assisted plant breeding is introduced and placed in the proper perspective in relation to plant breeding. The next three chapters describe the various molecular marker systems, while mapping populations and mapping procedures including high-throughput genotyping are discussed in the subsequent five chapters. Four chapters are devoted to various applications of markers, e.g. marker-assisted

selection, genomic selection, diversity analysis, finger printing and positional cloning. In closing, the last two chapters provide information on relevant bioinformatics tools and the rapidly evolving field of phenomics.

Marker Assisted Selection for Drought Tolerance and Grain Yield in Rice (*Oryza Sativa* L.) Springer Science & Business Media

Drought causes significant yield reductions in soybean. The development of drought-tolerant cultivars is an effective alternative to overcome this abiotic stress. Slow wilting, prolonged nitrogen fixation, and minimal yield reduction under water stress play an important role in evaluating breeding materials. Despite advances in knowledge about plant responses to drought conditions, there is little information on effective methodologies for phenotype screening in the field, and some QTLs have been identified for drought tolerance. Field screenings under drought and irrigated conditions are necessary to detect drought tolerant lines. In addition, QTLs and molecular markers associated with drought tolerance traits will greatly facilitate the development of tolerant lines through marker-assisted selection (MAS). The objectives of this study were: 1) to evaluate whether selection of high-yielding lines under irrigation in the preliminary stage is a positive predictor of the performance of these lines under drought conditions, and 2) to identify/confirm QTLs associated with slow wilting and nitrogen fixation for drought tolerance. For the first objective, yield performances of 87 genotypes derived from three different populations were evaluated under rain-fed conditions versus standard irrigation. The second objective was to identify QTLs associated with slow wilting, shoot ureides and nitrogen concentrations in soybeans.



For this objective, 148 lines from an F4-derived population (R07-7044 x R01-581) were screened with SNP markers and molecular analysis was conducted. Results for the first project showed four different types of yield performance on the lines. The high-yielding lines under full irrigation also had high yields under drought indicating that the selection of high-yielding lines in initial stages under irrigation is a good indicator of the profitable yielding lines under moderate drought conditions. In the second project, results showed two new QTLs for shoot nitrogen on chromosomes 6 and 11, and confirmed two shoot ureide QTLs on chromosomes 10 and 13. Four new QTLs for wilting were identified on chromosomes 11, 13, 14, and 18. These newly confirmed QTLs and molecular markers will be useful for marker-assisted selection for drought tolerance improvement in a soybean breeding program.

#### **Plant Breeding Reviews** MDPI

Plant Breeding Reviews presents state-of-the-art reviews on plant genetics and the breeding of all types of crops by both traditional means and molecular methods. Many of the crops widely grown today stem from a very narrow genetic base; understanding and preserving crop genetic resources is vital to the security of food systems worldwide. The emphasis of the series is on methodology, a fundamental understanding of crop genetics, and applications to major crops. It is a serial title that appears in the form of one or two volumes per year.

#### **Techniques and Uses of Molecular Markers** Springer Science & Business Media

This book deals with the major scientific challenges facing rice researchers are to raise the maximum yield potential, close the

yield gaps between potential yields and those achieved in farming practice and sustain current high yields. To check for drought resistance for rice plants, is very beneficial to plant breeders and application of modern tools like DNA markers such as SSR to these genotypes will help for further insight into rice genome and to develop rice with more resistance to the biotic and abiotic constraints of modern ecosystem.

#### *Marker-Assisted Plant Breeding: Principles and Practices* Springer Nature

This book provides comprehensive information on the latest tools and techniques of molecular genetics and their applications in crop improvement. It thoroughly discusses advanced techniques used in molecular markers, QTL mapping, marker-assisted breeding, and molecular cytogenetics.

#### **Genetic Analyses of Wheat and Molecular Marker-Assisted Breeding, Volume 1** Springer

Population based association studies in crops that were established by domestication and early breeding can be a valuable basis for the identification of QTLs. A case control design in a population is an ideal way to identify maximum candidate sites contributing to a complex polygenic trait such as drought. In the current study, marker loci associated with drought related QTLs were identified in sugarcane (*Saccharum* spp), one of the most complex crop genomes, with its polyploid nature (>8), chromosome number (>100) and interspecific origin. The objectives of this investigation were: 1) development of genic markers, which can be used for marker-assisted selection of drought tolerant genotypes of sugarcane. 2) genotypic characterization of sugarcane population at drought related loci

using EST-SSR markers. Using 55 microsatellite markers, 56 polymorphisms were scored among 80 modern sugarcane genotypes. Homogeneity of the population was confirmed by determining the distribution of allele frequencies obtained by random genomic microsatellite markers. This analysis was conducted in the STRUCTURE program and the population was divided in 3 subgroups based on the allelic distribution. Phenotypic data to evaluate drought tolerance among the genotypes was collected by measuring chlorophyll content, chlorophyll fluorescence, leaf temperature and leaf relative water content. A generalized linear model in SPSS was used to find

association between marker loci and phenotypic data. Markers with significant association (less than or equal to P 0.001 level) with the trait were subjected to linear regression to screen the spurious associations. Based on the results, 21 EST-SSR markers and 11 TRAP markers related to drought-defining physiological parameters were considered as genuine associations in this study. Fifty-six polymorphisms produced by 13 EST-SSR primers were used to produce genetic similarity matrix for 80 genotypes. Dendrogram prepared from this genetic similarity matrix will be useful in selecting parents carrying diversity at drought specific loci.