



Polyploidy and Hybridization for Crop Improvement

Annaliese S. Mason (*Ed.*)



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Polyploidy and
Hybridization for
Crop Improvement

Preface

Polyploidy and interspecific hybridization are critical processes in plant evolution and speciation. Polyploidy refers to the presence of more than two sets of chromosomes or the presence of more than one genome within a single organism, and interspecific hybridization refers to the process by which two different species come together to form a new organism with genetic information from both parents. When two different species each contribute a complete set of chromosomes to make a new, stable species with all the genetic information from both parents, this is referred to as "allopolyploid" formation, while "autopolyploids" have three or more sets of chromosomes from the same species. However, categorization of individuals or species as "auto" vs "allo" polyploid or as "intra" or "inter" specific hybrids is on some level arbitrary, depending on species definitions and genetic divergence between the parent genomes. In the middle are hybrids between subspecies or genetically distinct populations of individuals, or between geographically isolated taxonomic species with conserved genome structure.

Many of our current agricultural crops are either natural or agricultural hybrids or polyploids, including potato, oats, cotton, oilseed rape, wheat (and triticale), strawberries, kiwifruit, banana and many others. There is also a great deal of potential to utilise these natural evolutionary processes for targeted crop improvement, for example through introgression of desired traits from wild species into crops, production of seedless fruits, or even creation of entirely new crop types.

Polyploidy and interspecific hybridization are increasingly being revealed as both complex and common phenomena in plants. Characterization of crop genomes with modern genetics and genomics technologies has revealed that polyploidy and interspecific hybridization processes shaped many of our extant crop species. In parallel, breeding approaches utilizing polyploidy and interspecific hybridization as tools for crop improvement are becoming more and more common. Some crop genera have hundreds of years of manipulation of interspecific hybridization and polyploidy processes behind

them, while in others use of these processes for crop improvement is still at the theoretical stage. As our knowledge grows and technology advances, it is increasingly important to bring together expert researchers and plant breeders to form a cohesive picture of how best to utilize these evolutionary processes for crop improvement across diverse genera. Which processes and problems are crop-specific, and which are widely applicable? Answering these questions has potential to not only aid in our understanding of plant evolutionary processes, but to add additional fundamental tools to the plant breeding tool kit, helping the agricultural processes on which we all rely for life. This book will provide a comprehensive summary of how the processes of polyploidy and hybridisation have shaped the foods we eat, and how these processes have been and can be used for crop improvement. This book is targeted to both researchers and breeders, facilitating sharing of knowledge and stories across the wide range of crops where polyploidy and hybridization processes are relevant and potentially useful for crop improvement.

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Interspecific Hybridization for Upland Cotton Improvement

Peng W. Chee^{1,*}, Andrew H. Paterson², Joshua A. Udall³ and Jonathan F. Wendel⁴

ABSTRACT

Interspecific hybridization has been central to the evolution, domestication, and improvement of Upland cotton, the cultivated form of *Gossypium hirsutum*. As the world's most important fiber crop species, *Gossypium hirsutum* belongs to the allotetraploid *Gossypium* clade that consists of six additional species. The lint fiber evolved only once in the history of *Gossypium*, in the ancestor diploid A-genome species, and this trait was passed on to the allopolyploid species when the A-genome united in a common nucleus with a D-genome from the other ancestor that produced no lint fibers. The domestication history of *G. hirsutum* involved the collection and use of lint fibers by indigenous people for the purpose of making strings and other textile products; hence, spinnable lint fibers were likely to have evolved under domestication. The geographical distribution of *G. hirsutum* overlaps with *G. barbadense* and *G. mustelinum*, and gene flow among these species has been documented. Therefore, the introgression of novel alleles into *G. hirsutum* possibly contributed to greater ecological adaptation in colonizing new habitats and providing important sources of genetic variation for artificial selection in the early domestication efforts. In modern Upland cotton, numerous germplasm lines have been developed from crossing with *G. barbadense*. However, reproductive barriers such as reduced fertility, segregation distortion, and hybrid breakdown are often observed in later

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generation hybrids between *G. hirsutum* and the other polyploid species, complicating the task of introgressing new, stably inherited allelic variation from inter specific hybridization. Recent efforts in molecular genetic research have provided insights into the location and effects of QTLs from wild species that are associated with traits important to cotton production. These and future research efforts will undoubtedly provide the tools that can be utilized by plant breeders to access novel genes from wild and domesticated allotetraploid *Gossypium* for Upland cotton improvement.

The Cotton Crop

The cotton plant is a source of both food and fiber, contributing to two basic needs of humanity. Cotton fiber in the form of textile products has contributed greatly to the comfort, style, and culture of human society. Although not commonly viewed as a food source, cotton is an important source of vegetable oil used extensively in foodstuffs such as baking and frying fats, mayonnaise, margarine, and snack food. Furthermore, after oil extraction, the seed by-product is used as raw material in livestock feed, fertilizer, and paper. This versatility has made cotton one of the most important field crops in the world.

According to the International Cotton Advisory Committee (ICAC), which collects statistics on world cotton production, consumption and trade, about 36 million hectares of cotton are planted in over 100 countries from latitudes 45°N in Ukraine to 32°S in Australia (ICAC, 2015). The top five cotton producing countries in the 2014-15 season include, in order of importance, China, India, the United States, Pakistan and Brazil, which collectively account for nearly two-thirds of the world's cotton production. Total cotton fiber production has now reached 106 million bales, and contributes about 40% of the world fiber market (ICAC, 2015), thus making cotton the single most important natural fiber in the textile industries and a vital agricultural commodity in the global economy. The aggregate value of the world's cotton crop is estimated to be about US\$30 billion/yr, with 90% of its value residing in lint fiber. More than 350 million people are engaged in jobs related to the production and processing of cotton. The economic importance of cotton as a natural fiber for the global textile industry has fueled considerable interest in improving the inherent genetic potential of the crop through breeding for cultivars with higher levels of biotic and abiotic tolerance as well as higher lint yield and the further enhancement of fiber quality.

Interspecific hybridization has been central to the evolution of cotton, and to its improvement. As a crop, cotton is unique in that four different species in the genus *Gossypium* (Malvaceae) were domesticated independently on two separate continents for lint fiber production (Wendel and Cronn 2003; Wendel and Grover 2015). Therefore, the word "cotton" in the textile industry can apply equally to the two allotetraploid species *G. hirsutum* L. and *G. barbadense* L., endemic to the Americas, and the two diploid species