

Molecular and Functional Diversity of Maize

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SUMMARY

The maize genome is a source of tremendous phenotypic and molecular diversity. Indeed, when considering nucleotide polymorphism in genes, two maize lines are on average as diverged from one another as humans are from chimpanzees. Such abundant variation was first used by Native Americans for domestication and continues to be harnessed today by modern breeders for crop improvement. Here, we discuss recent advances in studies on the molecular and functional diversity of maize, including an increased understanding of genome rearrangements and the first large-scale identification of the genes that are involved in domestication and maize improvement.

INTRODUCTION

In the past few years, maize researchers have made tremendous strides in the identification of genes and nucleotides that control quantitative variation. Most of the phenotypic variation in a species is controlled by polymorphisms at numerous genes; these polymorphisms are the functional basis of quantitative trait loci (QTL). Most crop improvement relies on selecting these numerous QTLs. QTL mapping in particular, has been pioneered in maize over the past two decades, with roughly 100 research studies published in this area during the past two years alone. Given that the average maize gene houses a couple of hundred common polymorphisms and even 20–30 amino acid polymorphisms that segregate among a diverse collection of lines, geneticists must decipher how all of these genes affect quantitative traits. Three major approaches are being used to evaluate this tremendous diversity: F2-derived QTL mapping, positional cloning, and association mapping. *Zea mays* (maize or corn) is the third most important food crop of global importance after wheat and rice in terms of production and the second most widespread genetically modified (GM) crop after soybean. Maize has been known to have evolved from teosinte, a wild grass occurring naturally in isolated patches of central Mexico (Sherry A. Flint-Garcia, 2013). The International Maize and Wheat Improvement Center (CIMMYT) holds the world's largest repository of tropical and semitropical maize germplasm maintaining more than 23,000 maize landrace accessions (Anami *et al.*, 2009). Integration of advances in biotechnology, genomic research and molecular marker applications with conventional plant breeding practices have opened tremendous avenues for genetic modifications and fundamental research in tropical maize. Among all the types of markers, SNP markers are increasingly the marker of choice for all genomic applications in maize breeding. Utilizing the rapidly advancing genome sequencing and genotyping technologies along with phenotypic characterization through a global phenotyping network are required for identifying trait-specific donors as well as favourable genes/alleles that can be channelized in breeding strategies to develop concerned hybrids (Yunbi *et al.*, 2009).

On the DNA sequence level, exotic and elite maize genotypes contain more diversity than humans, *Drosophila* and many wild plants. The maize genome is a source of tremendous phenotypic and molecular diversity. Major approaches are being used to measure the molecular diversity of maize: allozymes, microsatellites (simple sequence repeats [SSRs]) or DNA sequences. Functional diversity is evaluated by three major approaches: F2-derived QTL mapping, position cloning, and association mapping (Buckler *et al.*, 2006). Fu and Dooner (2002), uncovered the substantial differences in bacterial artificial chromosome (BAC) sequences from the bronze (bz) region of two maize inbred lines, B73 and McC. Of the 10 genes identified originally in the McC *bz* genomic region, only the proximal 6 have had allelic counterparts in B73. Therefore, a B73_McC hybrid is supposed to be hemizygous for 4 of the 10 genes in the region. Clearly, this type of variability is only possible for those genes with relatively minor quantitative effects. In agreement with this, all 4 genes are members of small gene families and they have concluded that the Helitron-induced diversity may contribute to differences in gene expression between lines, dosage effects and heterosis.

Wright *et al.* (2005), compared SNP diversity between maize inbreds and teosinte in 774 genes. They identified 5 major QTLs which have undergone modification during domestication. The teosinte branched1 locus on chromosome 1 and the barren stalk1 locus on chromosome 3 interact to control lateral meristem formation, thus converting the lateral branches of teosinte into the maize ear. The selection at the teosinte glume architecture1 (*tga1*) locus was responsible for transforming the hard copulate fruitcake of teosinte into the uncovered grain of the maize ear, a key step in making teosinte an edible crop. The role of a fourth gene, *ramosa1*, in shaping maize ear morphology has also been recently discovered (Xuehui Huang and Bin Han, 2012).

Xu *et al.* (2016) characterized and complemented *Arabidopsis* ago1-27 mutant with ZmAGO1a indicating that constitutive over-expression of ZmAGO1a could restore the smaller rosette, serrated leaves, later flowering and maturation, lower seed set and darker green leaves at late stages of the mutant to the wild-type phenotype. Based on the existing functional annotations, four OsAGO1 genes from rice, one AtAGO1 gene from *Arabidopsis*, and one TaAGO1 gene from wheat were chosen for analysis of their phylogenetic relationships with the four predicted putative ZmAGO1 genes. Phylogenetic analyses revealed a close evolutionary relationship among the predicted *Zea mays* AGO1 genes with those from rice, wheat, and *Arabidopsis*. Their analysis indicated that only four of the maize AGO1 genes likely have biological activity and were highly conserved and were closely related to other rice and wheat AGO1 homologs.

CONCLUSIONS

The future of maize research is a promising approach. Advances in experimental design and the increased availability of germplasm resources can help one move ever closer to dissecting the molecular and functional diversity of maize. Mapping QTLs to the level of individual genes will provide newer insights into the molecular and biochemical basis for quantitative trait variation and will identify novel targets for crop improvement in the 21st century. Now the day's availability of resources in areas of biotechnology has led to exploring more functional genomics in the case of maize.

REFERENCES

- Anami Sylvester, Marc De Block, Jesse Machuka and Mieke Van Lijsebettens, 2009, Molecular improvement of tropical maize for drought stress tolerance in sub-Saharan Africa. *Critical Reviews in Pl. Sci.*, 28(1-2): 16-35.
- Buckler, E.S., Gaut, B.S. and McMullen, M.D., 2006, Molecular and functional diversity of maize. *Current Opinion in Pl. Biol.*, 9(2):172–176.
- Fu, H and Dooner, H. K., 2002, Intraspecific violation of genetic colinearity and its implications in maize. *Proc. Natl. Acad. Sci. USA.*, 99:9573-9578.
- Sherry A. Flint-Garcia, 2013, Genetics and Consequences of Crop Domestication. *J. Agric. Food Chem.*, 61 (35): 8267–8276.
- Wright, S.I., Bi I. V., Schroeder S.G., Yamasaki M., Doebley J.F., McMullen M.D., and Gaut B.S., 2005, The effects of artificial selection on the maize genome. *Sci.*, 308:1310-1314.
- Xu, D., Yang H., Zou C., Wen-Xue Li., Xu, Y., and Xie, C., 2016, Identification and functional characterization of the AGO1 ortholog in maize. *J. Integr. Pl. Bio.*, 58: 749–758.
- Xu, Yunbi Jianbing Yan, Debra J. Skinner, Shibin Gao, Huixia Wu, Natalia Palacios-Rojas, Marilyn L. Warburton and Jose Luis Araus and Jonathan Crouch, H., 2009, Advances in Maize Genomics and Their Value for Enhancing Genetic Gains from Breeding. *Int. J. of Pl. Genomics*, 1155: 957602.