

# Unique Contributions

High-throughput sequencing has accelerated the pace of discovery in all fields of genomics. Agricultural plants provide a particularly excellent system for basic discovery, with their rich history of basic genetic research, ample modern genetic resources, and the opportunity to sample or replicate genotypes across a wide array of environments. The country's most economically valuable crop, maize, is also one of the oldest model organisms, famous for its phenotypic and genetic diversity. This diversity has led to a number of scientific discoveries, including heterosis [1], recombination and crossing over [2], meiotic drive [3], transposable elements [4], and the first cloned QTL in a plant [5]. Though other groups are using high-throughput sequencing to accelerate applied breeding, my group is uniquely poised to exploit maize diversity using population genetic approaches to understand fundamental processes of evolutionary change in plant genomes. Familiar basic questions — such as the origin and nature of adaptive mutations or whether most adaptive evolution is geographically local — can now be re-addressed genome-wide across a number of populations. But genomic data also enable us to investigate processes that were previously intractable, such as the mechanisms that govern transposable element transposition and spread, how demographic change shapes the fitness consequences of new mutations, how selection drives genome size variation across environments, or how individual deleterious variants may combine to explain heterosis. Going beyond crop improvement, pursuing these questions in the wild ancestral populations of maize will also advance our understanding of evolution and conservation in natural systems.

## References

- [1] George H Shull. The composition of a field of maize. *Journal of Heredity*, (1):296–301, 1908.
- [2] Harriet B Creighton and Barbara McClintock. A correlation of cytological and genetical crossing-over in *zea mays*. *Proceedings of the National Academy of Sciences of the United States of America*, 17(8):492, 1931.
- [3] MM Rhoades. Preferential segregation in maize. *Genetics*, 27(4):395, 1942.
- [4] Barbara McClintock. The origin and behavior of mutable loci in maize. *Proceedings of the National Academy of Sciences*, 36(6):344–355, 1950.
- [5] J Doebley, A Stec, and L Hubbard. The evolution of apical dominance in maize. *Nature*, 386(6624):485–488, 1997.