

# Unique Contributions

The availability of next-generation sequence data has dramatically accelerated the pace of discovery in all fields of genomics. With the exception of human medicine, nowhere is the potential for new discovery greater than in agriculture. Maize, in addition to being the single most valuable crop in the US, is also one of the oldest genetic model organisms. An impressive number of scientific discoveries have been made in maize, including heterosis [1], crossing over [2], meiotic drive [3], transposable elements [4], and the first cloned QTL in any plant [5].

## 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.