Quantitative Genetics, Genetical Genomics, and Plant Improvement

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Overview of This Material

Plant improvement is one of man's oldest, and most important, technologies. Indeed, the amazing economic growth in China owes much of its success to the green revolution, which allowed a smaller fraction of the population to feed the country, providing the rich labor pool behind much of China's recent growth to an economic superpower.

Quantitative Genetics is the study and analysis of traits whose variation is influenced by both genetic and environmental variation. This includes essentially all agriculturally-important traits, such as yield, lodging, flowering times, etc. The machinery of quantitative genetics, which classically has relied upon **variance components** estimated by using *sets of relatives* underpins most of plant and animal improvement, and well as much of human genetics and evolutionary genetics. The machinery of quantitative genetics, while largely statistical in nature (indeed, much of modern statistics comes from the roots of quantitative genetics) easily incorporates information from molecular markers. Indeed, a major growth area in quantitative genetics has been the search for **QTLs** – **quantitative trait loci** – whose variation influences the variation in a trait of interest. Equally important, although less flashy, has been the development of powerful statistical tools (typically based on **mixed models**) such as BLUP estimation of breeding and combining values, and mixed-model-based approaches for the analysis of complex genotype $\times$ environment interaction.

Genetical genomics is a term coined by Risert Jansen, and is simply the application of quantitative-genetic ideas and techniques to genomic traits, such genome-wide transcription data, the genomic patterns of methylation, and metabolomic/ proteomic data. For all of these traits, we are interested in *variation* – how do these features change over tissues/individuals/populations/species. Such variation is influenced by both genetic and environmental factors. The machinery of quantitative genetics can be used to find QTL influencing these traits, as well as exploring how much of the observed variation is heritable, and how we can exploit this variation for plant improvement.

The propose of this series of lectures in the broader context of this workshop is to provide some background in these tools and ideas. Future lectures will explore the exciting fields of functional genomics in much greater detail. Keep in mind these genomic features (no matter how apparently complex) are simply traits, really no different from classically-measured traits such as yield. The goal is to understand how best to use this information for (i) a deeper understanding of plant biology and (ii) enhancement of plant improvement.

Table of Contents for Lecture Notes

Additional Textbooks on Quantitative Genetics

General

Falconer, D. S. and T. F. C. Mackay. 1996. *Introduction to Quantitative Genetics*, 4th Edition

Lynch, M. and B. Walsh. 1998. *Genetics and Analysis of Quantitative Trait*s. Sinauer.

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Bernardo, R. 2002. *Breeding for Quantitative Traits in Plants*. Stemma Press.

Hallauer, A. R., and J. B. Miranda. 1986.*Quantitative Genetics in Maize Breeding*. Iowa State Press.

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Saxton, A. M. (Ed). 2004. *Genetic Analysis of Complex Traits Using SAS*. SAS Press.

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