COLLOQUIUM

Department of Statistics and Probability
Michigan State University

Yuehua Cui
Michigan State University

A Statistical Variance Components Framework for Mapping Imprinted Quantitative Trait Loci Underlying Endosperm Traits in Flowering Plants

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Refreshments: 10:00 a.m.

Abstract

Genomic imprinting has been thought to play an important role in seed development in flowering plants. Empirical studies have shown that some economically important endosperm traits are genetically controlled by imprinting genes. However, the number and location of the imprinting genes are largely unknown due to the lack of efficient statistical mapping methods. The unique triploid inheritance structure of the endosperm genome presents challenges in modeling. Methods developed for the diploid genome can not be directly applied to the endosperm genome. In this talk, I will present a statistical variance components framework, by utilizing the nature of sex-specific alleles shared identical-by-decent among sibpairs in experimental crosses, to map imprinted quantitative trait loci (iQTL) underlying endosperm traits. We propose a new variance components partition method based on the nature of the triploid inheritance pattern, and apply a restricted maximum likelihood estimation method in a genome-wide interval scan for estimating and testing iQTL effects. Cytoplasmic maternal effect with primary influences on yield and grain quality, is also considered when testing for genomic imprinting. Extension to multiple iQTL analysis is also proposed. Extensive simulation studies are performed to evaluate the model performance. The utility of the method is demonstrated with a real data analysis.

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