Study Of Gene Regulatory Network in Maize Endosperm Development

Abstract

In flowering plants, second fertilization gives rise to the endosperm which is an absorptive structure that supports embryo development and seedling germination. Endosperm in cereal grain contains large amounts of carbohydrates and protein storage product that serves as an important source of food, feed, and industrial raw materials. Despite it’s obvious importance for grain yield, little is known of the GRNs that direct the pattern of early endosperm development. Prior studies showed that opaque2 (o2) mutants and nkd1, nkd2 double mutants dramatically altered the endosperm cell fate, tissue differentiation, nutrient biosynthesis and storage, and germination rate. As transcription factors, they directly control and indirectly influence a large number of downstream genes that form a gene regulatory network. Weighted gene co-expression network analysis (WGCNA) was performed that identified several gene modules (a group of co-expressed genes) correlated well with a specific sample, indicating that tissue types, mutants and development stages may influence a specific group of co-expressed genes. Further, within a specific module, the analysis identified several hub genes, which may play central role in the module. Therefore, an understanding of how gene network functions will provide deeper insights into maize endosperm development that will contribute both direct and indirect beneficial effects on human nutrition and economic development.

Biography

Bibechana received a MS in Biotechnology from Bangalore University. Bibechana is a third year IPB graduate student in the Becraft lab.