The main objectives of my Ph.D. dissertation were to investigate the several aspect of genetic diversity in maize (Zea mays ssp. mays) and its wild relative, Teosinte (Zea mays ssp. parviglumis). In my dissertation research, I wanted to investigate (a) if novel alleles from teosinte have a potential for improving the nutritional traits of the modern maize germplasm, and (2) statistical evidence for bi-locus epistatic interactions for several agronomically and nutritionally important traits, and decipher the complex genetic network underlying these traits.

Maize is one of the most important grain crops in the world. Teosinte is the wild progenitor of maize and has greater genetic diversity than maize inbreds and landraces. Maize was domesticated from teosinte about 9,000 years ago in central Mexico, and has been subjected to modern plant breeding over the past 100 years. In the recent years, extensive scientific breeding practices have led to remarkable yield increases in maize. However, domesticated and artificial genes have greatly reduced genetic diversity and cannot contribute to variation for agronomically important traits. Teosinte readily forms hybrids with maize and thus, offers a unique pool of allelic diversity for maize improvement, yet limited genetic resources were available to efficiently evaluate and tap this diversity. To broaden resources for genetic diversity studies in maize, two novel populations: the teosinte near isogenic lines (Teo-NILs) and the Teosinte Synthetic (Teo-Syn) were developed derived from maize (B73) and 11 accessions of teosinte founders. In order to understand the relationship between genetic diversity from teosinte and grain composition, I evaluated kernel starch, protein, and oil content in bulk intact kernels in the teosinte NILs using a non-destructive, robust and high-throughput phenotyping calibration models that I developed to phenotype the kernel composition traits. In the genetic analysis, I identified a wide range of strong allelic effects relative to the maize allele; supporting our hypothesis, that teosinte harbors stronger alleles for kernel composition traits than maize. We found that some of the regions of the genome that control grain composition in our population were previously identified in maize, but we also found several new regions of the genome from teosinte that control grain composition. For the improvement of kernel composition traits in modern maize germplasm. Ultimately, these novel regions of the teosinte genome can be mined for useful variation to improve corn for producers and consumers, as well as many industrial applications such animal feed, biofuel, sweetener and, food and seed. I further investigated for statistical evidence for epistatic (gene × gene) interactions for various agronomic and domestication traits in the Teo-Syn population. My results show an accumulated evidence for epistasis to be a major determinant of phenotypic variance for kernel composition traits and significantly important for adaptation and fitness related traits in the Teosinte Synthetic population.

Maize plays a central role in the US agriculture and food production, as well as has the greatest molecular and phenotypic diversity than any crop species. My research study strongly suggests that teosinte bears novel alleles, which can be utilized for the improvement of kernel composition traits in modern maize germplasm. These teosinte alleles will also provide unique source of variation to breeders and geneticist for further QTL and molecular studies accelerating in the development of future elite maize germplasm as well as provide insight to predict maize hybrid performance. Furthermore, my findings in this dissertation will encourage other researchers to mine for novel variations in the wild relatives of other crop species for increased production, better fertilizer uptake efficiency, increased tolerance and resistance to various biotic and abiotic stresses, and improved nutrition.