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1975	B.A., Smith College, Hispanic Studies (Cum Laude)
1982	M.S., University of Massachusetts, Plant Pathology
1990	Ph.D., Cornell University; Plant Breeding and Genetics

Honors
1996

Cornell Young Faculty Teaching Excellence Award

## Wild Alleles for Crop Improvement

A strategy for discovering and recombining agronomically favorable QTL alleles from agronomically inferior phenotypes was based on the use of advanced backcross QTL analysis. An accession of O. rufipogon, a relative of cultivated rice, was chosen as a donor and crossed with three high performing, elite cultivars adapted to different rice growing environments in China, Korea, and Colombia. Interspecific BC2 testcross populations consisting of approximately 300 lines each were developed. These populations were evaluated for 12 key agronomic traits under field conditions in each country to which they were adapted. Transgressive segregants were observed that outperformed the original (recurrent) elite variety in all cases. RFLPs and microsatellites, or simple sequence length polymorphisms (SSLPs) covering the whole genome were used to identify QTL for the 12 traits. O. rufipogon alleles were consistently associated with significant increases in grain yield per plant, grain quality, early maturity, and plant height in different genetic backgrounds and different environments. Efforts to identify the genes underlying these QTLs are in progress. This discovery suggests that the innovative use of genomic information can alter the way in which wild and exotic germplasm is used in plant breeding and that these reservoirs of genetic diversity may hold a key to future productivity increases in rice and possibly other crop species.