Characterization of the *BTB* E3 Ubiquitin-Ligase Gene Families in Viridiplantae

Ubiquitylation, the attachment of ubiquitin to proteins to mark for degradation by proteasomes, is crucial for proper organism function. One family of complexes that play a role in this process are the BTB/Cullin 3/RBX E3 ubiquitin-protein ligases, which catalyze attachment of ubiquitin to target proteins. The BTB (Bric-a-Brac, Tramtrack, Broad Complex) domain-containing proteins are the target-adapters, binding to the proteins to be ubiquitylated via motifs appended to the BTB domain. Genes encoding BTB proteins have been identified in wide range of eukaryotic organisms (including fungi, protists, animals, and plants) but the *BTB* gene families in different organisms show great variability in size, complexity, and composition. In land plant genomes thus far studied *BTB* gene families are large (~75-150 members) and complicated (with multiple BTB subtypes encoded based on the presence of a diverse set of putative target-binding motifs). We are interested in when the particular *BTB* family composition seen in the higher plants may have arisen in evolution. To help answer this question we are currently working to identify the complete *BTB* families in representative members of the Viridiplantae clade (including land plants and algae). Our analyses thus far have shown that while the size of the *BTB* families in land plant genomes vary significantly (~40 to more than 200 members in species thus far analyzed), they all share a relatively similar set of BTB types (as defined by domain organization). However, the algal genomes we have analyzed encode a distinctly different set of BTB types. Collectively these data show that there have been dramatic changes in both the size and composition of this E3 ubiquitin-ligase gene family during Viridiplantae evolution and that significant changes in the suite of BTB types may have occurred as plants colonized land.