END BINDING PROTEINS
IN ARABIDOPSIS THALIANA

All cells must regulate the orientation and timing of division throughout the life of an organism. An essential component of this regulation is the control of microtubules, filamentous structural proteins. Many proteins are known to interact with microtubules within the cell. One group of these proteins is the End Binding proteins (EB proteins). These proteins are members of a family of microtubule plus end tracking proteins. In yeasts and animal cells they have been shown to bind microtubules and increase the dynamicity of the microtubule. The dynamic polymerization and depolymerization of microtubules is an integral part of a cell's development. In yeast it is known that without this protein cell division does not occur correctly. In plants the role of this protein has yet to be characterized, in particular its role in asymmetric division.

Using Arabidopsis thaliana as a model for angiosperms work has begun on characterizing the function of these proteins. There are three genes in Arabidopsis that are members of the end binding protein family, named EB1, EB2, and EB3 respectively. One way to understand the function of these proteins is to isolate and study the development of plants with non-functional EB genes. Using a reverse genetics approach plants with T-DNA insertions within one of the EB genes were isolated via PCR screening techniques. Once obtained these plants were grown and re-screened to confirm that they indeed had T-DNA insertions within an EB gene. Three plant lines harboring T-DNA disrupted genes have been discovered to date (Figure 1). Plants that have only one of the three EB genes disrupted by T-DNA insertion have shown no gross observable phenotype. This leads us to believe that there is functional redundancy within this family of end binding proteins.

In order to further test this hypothesis we are currently developing plants with multiple EB gene mutations via a rigorous plant crossing strategy. We predict that plants with multiple disrupted EB genes will exhibit a phenotype that will lead us to further understand the role of the End Binding Protein family.