

Integrating the Genetic and Physical Maps of *Arabidopsis*: Identification of Mapped Alleles of Cloned Essential (*EMB*) Genes

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More than 130 genes with an embryo-defective (*emb*) knockout phenotype are included on the classical genetic map of *Arabidopsis*. Many of these genes remain to be cloned. Hundreds of additional *EMB* genes have been cloned and catalogued (www.SeedGenes.org) but not mapped. To facilitate *EMB* gene identification and assess the level of saturation for essential genes in *Arabidopsis*, we updated the classical map, compared the physical and genetic locations of all mapped loci, and performed allelism tests between mapped (but not cloned) and cloned (but not mapped) *emb* mutants with similar map locations. Initial efforts focused on chromosomes 1 and 5. Two hundred pairwise combinations were tested and more than 1100 total crosses were screened. Sixteen of 51 mapped *emb* mutants examined were found to be disrupted in a known *EMB* gene. Informative alleles of a wide range of published *EMB* genes (*YDA*, *GLA1*, *TIL1*, *AtASP38*, *AtDEK1*, *EMB506*, *DG1*, *OEP80*) were discovered. Two EMS mutants isolated 30 years ago, T-DNA mutants with complex insertion sites, and a mutant with an atypical, embryo-specific phenotype were resolved. The frequency of allelism encountered was consistent with past estimates of 750 to 1000 *EMB* loci. New *EMB* genes identified among mapped insertion mutants included *CHC1*, which is required for chromatin remodeling, and the *Arabidopsis* ortholog (*SHS1*) of the maize *BRITTLE1* locus required for normal endosperm development. The alignment of genetic and physical maps presented here should facilitate the continued analysis of essential genes in *Arabidopsis* and further characterization of a broad spectrum of mutant phenotypes in a model plant.