

The Classical Genetic Map of *Arabidopsis thaliana*

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In recognition of the 20th International Conference on *Arabidopsis* Research, I describe here the current status of the classical genetic map of *Arabidopsis*, which was first published 26 years ago by Koornneef et al. (J. Heredity, 74: 265-272). The updated map includes 340 loci associated with a defined mutant phenotype, a significant increase beyond the 76 markers included on the original map. Consistent with the working definition of a classical genetic map, the current dataset is limited to mutant genes mapped using recombination data obtained with other visible markers. Genes localized only in relation to molecular or physical markers are for the most part excluded. Forty percent of the genes included on the classical map exhibit a seed phenotype. Seventy percent of these mapped *EMB* genes remain to be cloned. Recent progress towards identifying these genes is described in a separate poster from my laboratory. Almost 90% of mapped visible markers with other mutant phenotypes have been cloned. An updated list of mapped and cloned genes is presented here. Ultimately, the classical map needs to be replaced by a comprehensive, sequence-based map of cloned *Arabidopsis* genes associated with a mutant phenotype. The first version of such a map was published 6 years ago (Meinke et al., Plant Physiol., 131: 409-418). My laboratory is currently updating this dataset based on information obtained from TAIR and the published literature. Eventually, we hope to incorporate the list of cloned genes with a loss-of-function mutant phenotype into TAIR so that it can be widely used, thoroughly checked, and regularly updated by members of the community