

Understanding the genetic basis and adaptive significance of natural variation in organismal form is a fundamental challenge in biology. Leaves of seed plants present attractive opportunities to address this challenge because they show tremendous diversity in their size, shape and complexity both between and within species. However, little is known about the genetic factors and evolutionary forces driving this variation within species. In contrast to the well-studied model plant *Arabidopsis thaliana*, its close relative *Cardamine hirsuta* exhibits compound leaves that consist of leaflets. Natural strains of *C. hirsuta* show substantial genetic variation in leaflet number and therefore, display an attractive system to study the genetic basis of leaf complexity in an evolutionary and ecological context. In this thesis, I perform quantitative trait locus (QTL)-mapping in a recombinant inbred line-population derived from a cross between the reference strain from Oxford and the conspicuously low leaflet number strain from the Azores. I show that leaflet number variation has a polygenic basis and I report the identification of QTLs that have not been detected in previous mapping attempts. All QTLs affect age-dependent variation in leaflet number which can be characterized as heterochronic and act at distinct stages of the development of the plant. Two cloned leaflet number QTL were previously shown to affect shoot maturation. Together these results indicate that heterochronic variation is the major source of intraspecific variation in leaf complexity. By fine mapping and transgenic validation, I found a novel candidate gene putatively underlying leaflet number variation. This QTL together with an already cloned heterochronic QTL is part of a QTL cluster containing in total four neighboring QTLs that together reduces leaflet number. Analyses of genetic polymorphisms in 759 natural strains indicate that this cluster might be involved in local adaptation along an environmental cline on the Azores. Another conspicuous leaflet number QTL is likely based on a *FRIGIDA* loss-of-function-allele that similar to *Arabidopsis thaliana* shows a latitudinal cline and is associated with a large selective sweep. These results together with correlation analyses of leaflet number with fitness-relevant traits help formulate new hypotheses on the evolutionary processes driving this leaf shape variation.