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The goal of this project is to contribute towards the understanding of how genetic architecture (the structure of the mapping from genotype to phenotype) affects the evolution of quantitative traits (e.g. morphology). According to quantitative genetics theory, the evolution of phenotypic traits depends on the strength of selection and the amount of genetic variation. However, part of this variation may be constrained by correlations with other traits that are under conflicting selection regimes. In consequence, the ability to respond to selection may be limited, even if a trait has high variation. However, the extent to which genetic architecture limits phenotypic evolution remains an open question. Likewise, it is unknown whether it affects only evolution on the short time scale and is easily overcome by selection, or if the genetic architecture is an important long-term determinant of the direction of evolution. In this project we aim to answer these questions using two plant species from the carrot family (Apiaceae), wild carrot (*Daucus carota*) and giant fennel (*Ferula communis*), as a model system. Both species are characterized by different distributions and contrasting levels of phenotypic variation. This disparity will be used to test whether our hypothesis can be generalized to organisms with very different patterns of trait divergence. We also intend to verify if the genetic architecture is reflected in the history of the group. We assume that traits should adapt faster to changing conditions at longer time scale if they exhibit high evolutionary potential at interpopulation level. These analyses will be done on a dated phylogeny of *Daucus* (<10 million years) and *Ferula* (<6 Ma), and on the entire tribe Scandiceae (<35 Ma) to which both genera belong. This will determine the time frame in which the impact of genetic architecture is the most influential. To reach our goals, we will use state-of-the-art computational and DNA sequencing methods.