

Public Abstract

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Title:Quantitative trait loci mapping and analysis of adaptive traits in northern red oak (*Quercus rubra* L.)

Genomic resources are becoming increasingly important in combating the adverse effects of climate change and invasive pathogens on forest species. Efforts to breed a blight-resistant American chestnut are spearheaded by these new resources. Like the American chestnut once was, red oaks (*Quercus* section *Lobatae*) are economically and ecologically important to eastern North America. Identifying genomic regions associated with adaptive traits is an important step in breeding better oaks. To this end, the current study utilized resources previously developed in European white oak species pedunculate oak and sessile oak to better identify the genetic basis of adaptive traits. A northern red oak mapping population was created by grafting replicates of full-sibling (same parents) seedlings. A subset of the population was surveyed for various adaptive traits including bud burst date, leaf morphology, stomatal density and winter leaf retention (marcescence). Three genomic regions, or quantitative trait loci, associated with bud burst date were identified in the population. Two of these regions were similar to those identified in pedunculate oak. Additionally, winter leaf retention was discovered to likely be associated with growing season length. These results suggest that oaks growing later into the season are more likely to retain dead foliage. This study illuminates a level of similarity in significant associations between genome and trait between two oak sections, and provides new information on a scarcely-studied trait.