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P505 : Forest Trees

Genomic Tool Development For The Fagaceae

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The Fagaceae family of forest trees that includes the chestnuts, oaks and beeches, dominates the hardwood forests of the northern hemisphere. These tree species have significant economic value and represent a major natural resource. We will carry out comparative sequencing and DNA marker development for Chinese chestnut: (*Castanea mollissima*), American chestnut (*Castanea dentata*), Northern red oak (*Quercus rubra*), White oak (*Quercus alba*), and American beech (*Fagus grandifolia*). We will use the chestnut genome as a model for the Fagaceae. A BAC library and physical map of Chinese chestnut will be constructed. Our work will focus on genetic and physical mapping of the Chinese chestnut genome to identify the physical location of genetic loci that contribute to resistance to Chestnut Blight Disease. An integrated genetic and physical map would become a platform for targeted genome sequencing of resistance genes. A Fagaceae database and web interface have been set up at Clemson (<http://www.genome.clemson.edu/projects/fagaceae/>). This project is supported by a grant from the NSF (DBI-PGRP-TRPGR 0605135).