

# Genomic tool development for the Fagaceae.

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## Plants to be studied:

Principal: *Castanea mollissima* (Chinese chestnut)

Secondary: *Castanea dentata* (American chestnut)

Tertiary: *Quercus rubra* (Northern red oak), *Quercus alba* (White oak), *Fagus grandifolia* (American beech).

## Project Objectives:

The family of forest trees (the Fagaceae) 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 study the chestnut genome as a model for the Fagaceae and we will compare chestnut to oaks, beeches and other forest trees. A major goal is to advance the production of an American chestnut (*Castanea dentata*) resistant to chestnut blight. Chestnut blight, caused by *Cryphonectria parasitica*, was the greatest ecological disaster in our nation's history. Our work will focus on genetic and physical mapping of the chestnut genome. We hope to identify the physical locations of genetic loci that contribute to blight resistance, by the integration of genetic and physical maps. An integrated map would become a platform for targeted genome sequencing. This project would be the first genome project directed to ecosystem restoration and could provide a model using genomics for a large number of ecological crises caused by pathogens and pests that threaten the world's forest resources.

## Experimental Approaches:

1. GS20/454 sequencing of nine cDNA libraries from four species of the Fagaceae.
2. Development of an expanded set of genetic markers for *Castanea*.
3. Establishment of new mapping populations in Chinese and American chestnut.
4. Genetic mapping in Chinese and American chestnut and derived hybrids.
5. QTL mapping for resistance to chestnut blight.
6. Creation and analysis of a BAC library of Chinese chestnut.
7. Construction of a physical map for Chinese chestnut.
8. Integration of the genetic and physical maps.

## Information/Materials to be generated:

1. Database of expressed sequences for the Fagaceae.
2. New genetic maps in Chinese and American chestnut.
3. Improved identification of loci affecting blight resistance.
4. Physical map of Chinese chestnut.
5. An integrated genetic and physical map of Chinese chestnut.

## Contact Information for Outcomes:

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**Internet Addresses (Web or Email) for Project Information:**

1. A Fagaceae database and web interface has been set up at CUGI (<http://www.genome.clemson.edu/projects/fagaceae/>).

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**Informatics Contact Person(s):**

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**Practical Applications of Research:**

The work we propose would accelerate chestnut breeding for urban and rural forestry, food crops, timber, high quality wood products and ecological restoration. Scientific progress would be accelerated for all species of the Fagaceae, and breeding would be advanced for oak species, as well. A disease resistant chestnut would have value for rural communities in the Appalachian Mountains, a region of the USA that is in need of economic development. A fully resistant chestnut could restore a vast damaged ecosystem, provide nutrients for wildlife, and create major new economic resources.

**Project Participants:**

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