A comparison of the genetic diversity of yellowwood (Cladrastis kentukea[(Dum.Cours.)_Rudd] trees sampled from captive and wild populations.

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Abstract

Yellowwood (Cladrastis kentukea), a commonly used ornamental in cities and towns in the Midwest, is found in the wild only in small highly scattered populations. Despite its popularity as an ornamental and its status as endangered or threatened in two states at the center of its range, little is understood about the ecology of this species. Using microsatellite markers we designed, we are determining the genetic diversity, relatedness and local spatial genetic structure of yellowwood populations sampled from Indiana, Kentucky, and Arkansas. We will compare the genetic diversity of wild populations to that of trees in "captivity" or in urban areas. We will study the genetic composition of wild populations in the edge of the yellowwood range to determine if these populations show the effects of recent bottlenecks or founder effects to determine if they were recently introduced or if they are what is left of a wider population. We will attempt to estimate the level of gene flow, if any, between populations in Indiana and Kentucky.

Introduction

Yellowwood, Cladrastis kentukea (Dum. Cours.) Rudd (Andrews, 1999) is a small to medium-sized tree in the Leguminosae (bean) family native to the eastern United States. The species is considered rare in most of the 21 states in which it grows because natural populations are often small and highly scattered, especially those found outside the Appalachian ridge. Because of its limited abundance, the species is listed as endangered in Illinois, threatened in Indiana and is a species of concern in various other parts of its range. There are no active conservation efforts trying to maintain or restore yellowwood populations, and the ecology of this species is not well understood. In order to increase our understanding of the species and enable better management of it, I am using genetic markers (microsatellites) to describe the genetic composition and diversity found among and within various yellowwood populations.

Study Area

Yellowwood has been determined to be native from Indiana and southern Illinois, southwestern Missouri, north and central Arkansas, extreme eastern Oklahoma, and east to eastern Tennessee, North Carolina, and northern Georgia (Hill 2007)

The populations we will study are located in(Fig 1):

- · Hoosier National Forest, IN
- Central Kentucky (Tom Dorman State Nature Preserve)
- Hot Springs, Arkansas (Private property near Remmel Dam)
- Urban population from: KY,VA,IL, IN, MO,OH etc.



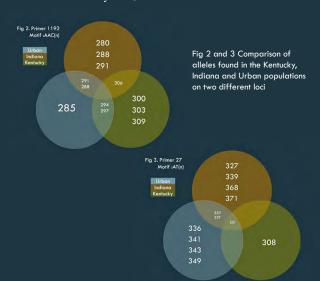
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Methods

Using 10 primers developed to amplify yellowwood DNA we will:

- Complete the identification of microsatellite loci for Yellowwood.
- 2. Complete the genotyping of all yellowwood samples collected in urban areas, Indiana, Kentucky and Arkansas
- Determine if they differ in terms of genetic diversity, and if any populations show evidence of inbreeding, genetic isolation, or genetic bottlenecks.

DNA samples where extracted from fresh leaves. Leaves were ground in CTAB extraction buffer using a DNA Fastprep (BIOSAVANT) and DNA extracted using a phenol-chloroform extraction method; DNA amplification and all other methods were as described in Victory et al., 2006.



Results and Next Steps

We developed thirty-two primer pairs that can be used to amplify specific microsatellite regions in yellowwood DNA. Eight of these were highly polymorphic and are useful for studying diversity in yellowwood populations. We have obtained preliminary allelic data for three yellowwood populations (KY, IN and the urban forest population) (Fig 2 and Fig 3). The next steps in the project are to complete the genotyping of the Indiana, Kentucky and urban populations and to collect samples from a population in Arkansas. We also expect to test the ability of our primers to amplify polymorphic microsatellites in other species of the Fabaceae, including *Cercis*, the redbud. We will use population genetic software to determine the genetic distance between the sampled populations.

Discussion

Preliminary results show that the loci we have chosen amplify and are polymorphic in all populations tested, so we expect them to be informative for determining the population genetic structure of yellowwood. We observed high levels of heterozygosity in the Indiana (HNF) population, probably indicating that yellowwood is an outcrossing species (unlike many of the Fabaceae). Surprisingly, the number of alleles at some loci from the population in KY was small compared to the HNF population; additional tests will be used to show if this result is statistically significant. Yellowwood trees from the urban forest do not represent a true "population" in that they do not share common ancestors, but we should be able to compare its allelic diversity with other wild populations as a measure of its diversity. The results of our research will guide conservation efforts for yellowwood and help determine if yellowwood in Indiana requires consideration as a genetically distinct population from trees at the center of the species' range. Our results may also help determine if the captive population in urban forests represents a genetically diverse and viable source of germplasm for future restoration, if necessary.

Acknowledgement

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Literature Cited

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