Colonization History, Phylogeography and Conservation Genetics of the Gravely Endangered Tree Species *Hagenia abyssinica* (Bruce) J.F. Gmel from Ethiopia

Dissertation

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1. General introduction

1.1 Ethiopia in brief

Within an altitudinal range of 126 meters below sea level at Afar Depression to 4,620 meters above sea level (m asl) at the spectacular mountaintops of Ras Dejen, Ethiopia's varying physiographic features endowed the country with diverse fauna and flora. The climate of Ethiopia is varying from cool to hot and fundamentally governed by the Inter-tropical Convergence Zone (ITC). The rainfall pattern is influenced by two wind systems: monsoon from south Atlantic and the Indian Ocean, and winds from the Arabian Sea. The country is devided in 21 major Tree Seed Zones and 27 sub-Tree Seed Zones that were delineated based on ecological criteria to facilitate seed transfer within the country (Aalbæk 1993). The vegetation of the Ethiopian mountains belongs to the Afromontane phytogeographical region (White 1983). Ethiopia is a severely deforested country with only about 3.5% of its land currently covered by closed forests (WBISPP 2004). The low living standard of the people coupled with lack of options is the underlying factor causing severe decline in forest cover. There has been increasing pressure on the forest land for crop and animal husbandry, and wood for fuel and construction. New settlements in primary forests are becoming commonplace and hence resulted in the conversion of forest land into agricultural and other land use systems, subsequently causing forest fragmentation. Precious tree species such as *Hagenia abyssinica* are the prime victims of such malpractices.

1.2 Conservation genetics of tropical tree species

Deforestation, forest fragmentation and extraction of timber in the form of selective logging could have serious consequences on the long-term maintenance of genetic diversity and fitness in plants (Finkeldey and Hattemer 2007; Laikre and Ryman 1996; Young et al. 1996). The marvelous biodiversity that has captured our planet is being lost at a pace that is nearly unprecedented in the history of life (Ehrlich and Ehrlich 1991). Biodiversity is in a serious decline, with, for example, approximately 50% of the vertebrate animal species and 12% of all plant species now considered vulnerable to near-term extinction, mostly as a result of effects of habitat alteration associated with human population growth (Franklin et al. 2002).

The analyses of the amount and distribution of genetic variation within and among populations of a species can increase our understanding of the historical processes underlying the genetic diversity (Dumolin-Lapegue et al. 1997). The maintenance of natural tree populations with sufficient genetic variation to adapt to future changes in the environment is essential. Genetic variation is thought to be positively correlated with populations' ability to adapt to short-term environmental change, and populations with the highest levels of genetic variation are expected to suffer least from the negative effects of inbreeding depression or genetic drift (reviewed by Barrett & Kohn 1991, Ellstrand & Elam 1993). Examples of natural and dynamic evolutionary processes that shape genetic diversity are mutation, genetic drift, gene flow, natural selection, speciation and hybridization (Avise 2004). Sound knowledge of the biology and genetics of a given organism is therefore instrumental in providing a scientific basis to its conservation and management. The two major goals of conservation biology are (1) the preservation of genetic diversity at any and all possible levels in the phylogenetic hierarchy and (2) the promotion of the continuance of ecological and evolutionary processes that foster and sustain biodiversity (reviewed by Avise 2004). Conservation genetics is a discipline dealing with the characterization of a given taxon and the development of conservation measures to maintain its variation in order to adapt to changing environmental conditions. The present study investigates the pattern of genetic variation in *Hagenia abyssinica* at morphological and molecular genetic markers in order to identify populations for conservation and domestication.

1.3 Taxonomy and reproductive biology of Hagenia abyssinica

The monotypic *Hagenia abyssinica*, formerly/synonimously known as *Banksia abyssinica* Bruce, *Brayera abyssinica* Moq.-Tand, *Brayera anthelmintica* Kunth and *Hagenia anthelmintica* Kunth, is a wind-pollinated (anemogamous) and wind-dispersed (anemochorous) broad-leaved dioecious tree species belonging to the Rosaceae family (Hedeberg 1989; Legesse 1995). It is closely related to the monospecific genus Leucosidea from the same family in its taxonomic position (Eriksson et al. 2003). Locally, the tree is known as *Kosso, Heto* and *Habbi* in Amharic, Oromiffa and Tigrigna, respectively (major local languages in Ethiopia). It is also commonly known as African redwood, Brayera, Cusso, Hagenia, Kousso, and Rosewood in English; Mdobore and Mlozilozi in Swahili (http:/www.worldagroforestry.org), and Kosobaum in German (http://de.wikipedia.org/wiki/Hagenia_ab-yssinica). The specific name *abyssinica* refers to the former name of Ethiopia.


17/01/2006

Fig.1 Excellent quality timber tree growing in Checheba (Uraga) forest. Photo: Taye B. Ayele


29/09/2005

Fig. 2 compound leaf of *Hagenia*
Photo: Taye B. Ayele

Hagenia grows up to 35 meters in height (Fig.1). Hagenia trees exhibit varying architectures from croaked to slender, multi-stems or forked to single stem, and thick to thin crowns. The bark is brownish and readily peels in strips, sometimes very thick in old