



Assessment and integration of genetic, morphological and demographic variation in *Hagenia abyssinica* (Bruce) J.F. Gmel to guide its conservation

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ABSTRACT

Assessing and integrating genetic, morphological and demographic variation is instrumental for planning conservation, tree improvement and domestication programs. We discuss the variation of the gravely endangered tropical tree species *Hagenia abyssinica* in Ethiopia with regard to its morphological and genetic traits as well as its population demography in a conservation context. An analysis of variance (ANOVA) revealed a highly significant differentiation among 22 natural populations of *H. abyssinica* in all quantitative morphological traits assessed. Multivariate and univariate taxonomic distances of leaf traits among populations are not correlated with the corresponding genetic distances at AFLP markers (multivariate $r = -0.03484$ at $p = 0.3926$), showing that the genetic differentiation at AFLPs is not associated with the morphological differences among populations. Chloroplast microsatellite data allowed us to identify lineages and to reconstruct population history, while the AFLP data enabled us to identify populations of high genetic diversity. A weighted-score population prioritisation matrix (WPPM) that integrates genetic, morphological and demographic criteria was developed and used for the first time to prioritise populations for conservation and domestication. Action is needed to launch conservation and domestication programs of *H. abyssinica* to ensure the long-term survival of the species and to boost its economic and ecological value.

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Introduction

Conservation of tropical forest ecosystems in general, and that of critically endangered tree species and their genetic resources in particular, is a challenging task in the face of high pressure from local communities on forest land. It is imperative to know the extent and distribution of genetic variation within a species in order to develop appropriate conservation strategies that *inter alia* preserve maximum genetic diversity (Bawa & Krugman 1990; Loveless & Hamrick 1984). Investigation of intraspecific genetic variation may help to assess extinction risks and evolutionary potential (Bawa & Krugman 1990; Hedrick 2001) and can be instrumental in identifying appropriate units for conservation of rare and threatened species (Allendorf & Luikart 2007; Frankham, Ballou, & Briscoe 2002; Newton, Allnutt, Gillies, Lowe, & Ennos 1999; Watanabe, Kanagawa, Kakioka, Takahiko Itai, & Mori 2009). The preservation of germplasm in genebanks and the establishment of *in situ* and *ex situ* conservation stands requires sound knowledge of the genetic structure of a given species. Whereas genetic variation estimates have been used to formulate some general rules of thumb about

viable population size (Franklin 1980; Lande 1995; Lynch, Convey, & Bürger 1995), demographic analyses of individual species are more often used to assess short-term population health and to suggest management alternatives (McCarthy, Burgman, & Ferson 1995; Menges 1990). The need to integrate demographic and genetic criteria in plant conservation has been recognised during the last two decades (e.g., Delgado, Eguiarte, Molina-Freaner, Alvarez-Buylla, & Piñero 2008; DeSalle & Amato 2004; Hoebee, Thrall, & Young 2008; Lande 1988; Oostermeijer, Luijten, & den Nijs 2003).

High genetic diversity enhances a population's survival probability (Avisé 2004). Small population sizes reduce genetic variation and might therefore lead to a decreased ability of populations to adapt to ecological challenges (Amos & Balmford 2001; DeSalle & Amato 2004). When populations are few in number and small in size, the possibility of species extinction through stochastic demographic fluctuations can be of immediate concern (Gilpin & Soulé 1986; Hanski & Gilpin 1997). Reduced fitness may be a direct consequence of low individual heterozygosity (Amos & Balmford 2001). On the other hand, in some endangered species such as the northern elephant seal, low genetic variation has not seriously inhibited population recovery from dangerously low levels (Avisé 2004).

The assessment of both phenotypic traits and genetic markers is of high interest for the selection of genetic resources. Phenotypic traits including those describing the demography of

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populations are used to characterise the state of adaptedness of populations to particular environments. The potential of populations to undergo evolutionary adaptation depends on genetic variation (e.g., Finkeldey & Hattemer 1993).

This paper describes the association and integration of morphological and molecular genetic variation in *H. abyssinica* and proposes various conservation and domestication measures. *H. abyssinica* is a monotypic tree species of the Rosaceae family native to Africa (Hedberg 1989; Negash 1995). It is an anemogamous and anemochorous broad-leaved dioecious tree species with distinct male and female flowers. Fossil pollen records suggested that *H. abyssinica* recolonised Ethiopia from the south during the late Pleistocene (since 16,700 years Before Present (BP)) and became abundant in the southern regions of Ethiopia about 2500 years BP (Beuning, Talbot, & Kelts 1997; Bonnefille et al. 1995; Olago, Street-Perrott, Perrott, Ivanovich, & Harkness 1999; Umer et al. 2007). *H. abyssinica* is one of the best timber species in Ethiopia preferred for its strength, fine texture and attractive appearance (Bekele-Tessema, Birnie, & Tegnäs 1993; Desalegn 2006). A concoction made from the powder of dried female inflorescences is used as a purgative and taenicide against tapeworm in Ethiopia (Abebe & Ayehu 1993; Abegaz, Ngadjui, Merhatibeb, & Mdee 1999; Hedberg 1989; Jansen 1981; Pankhurst 1969). Honey obtained from beehives placed on or located near *Hagenia abyssinica* trees is also effective in expelling tapeworms. The leaves, seeds and barks are used as fodder, condiment or spice, and for dyeing textiles to yellowish red, respectively (<http://database.prota.org/PROTAhtml/Hagenia%20abyssinica.En.htm>). In some areas farmers retain some *Hagenia* trees on their farms to control soil erosion and enhance soil fertility by generously shedding old leaves (personal observation, first author). *Hagenia* is a graceful ornamental tree particularly when in blossom.

H. abyssinica has been logged heavily mainly due to its superior timber; it is currently one of the endangered tree species in

Ethiopia (Negash 1995). According to the present inventory, only about 7000 individuals were left in Ethiopia and natural regeneration was observed in only 2 out of 22 natural populations. Furthermore, planting efforts were very limited and unsuccessful in most cases. This is an alarming situation for the genetic resources of the species, and may eventually lead to extinction in Ethiopia. The genetic diversity of *H. abyssinica* was investigated by using cpSSR (Ayele, Gailing, & Finkeldey 2009), AFLP (Ayele, Gailing, & Finkeldey submitted for publication), ISSR (Feyissa, Nybom, & Bartish, et al. 2007) and RAPD (Kumilign 2005) markers. The latter two studies covered a small spatial scale relative to the widespread distribution of the species in Ethiopia and were also limited to a comparatively small number of individuals per population.

Here we present information on the amount and distribution of diversity at morphological, molecular genetic markers and simple traits characterising population demography with the objectives to (1) identify conservation units for *in situ* conservation and populations for collection of germplasm for *ex situ* conservation, and (2) provide a basis for the domestication and improvement of *H. abyssinica*.

Materials and methods

Twenty-two natural populations were sampled from diverse forest types including closed forests (12 populations), open forests/woodlands (six populations), wooded grasslands (two populations), and farmlands/homesteads (two populations), representing most of the extant distribution of the species in Ethiopia (Fig. 1 and Table 1). The distance between populations ranges from 21 to 806 km within an altitudinal range of 2200 m asl at Bonga to 3200 m asl at Wofwasha. Temperatures range from an absolute minimum of -1°C at Dinsho to a maximum of 33.5°C at Kosso Ber. Differences of annual minimum and maximum mean temperatures between population pairs ranged from approximately 0.2 to

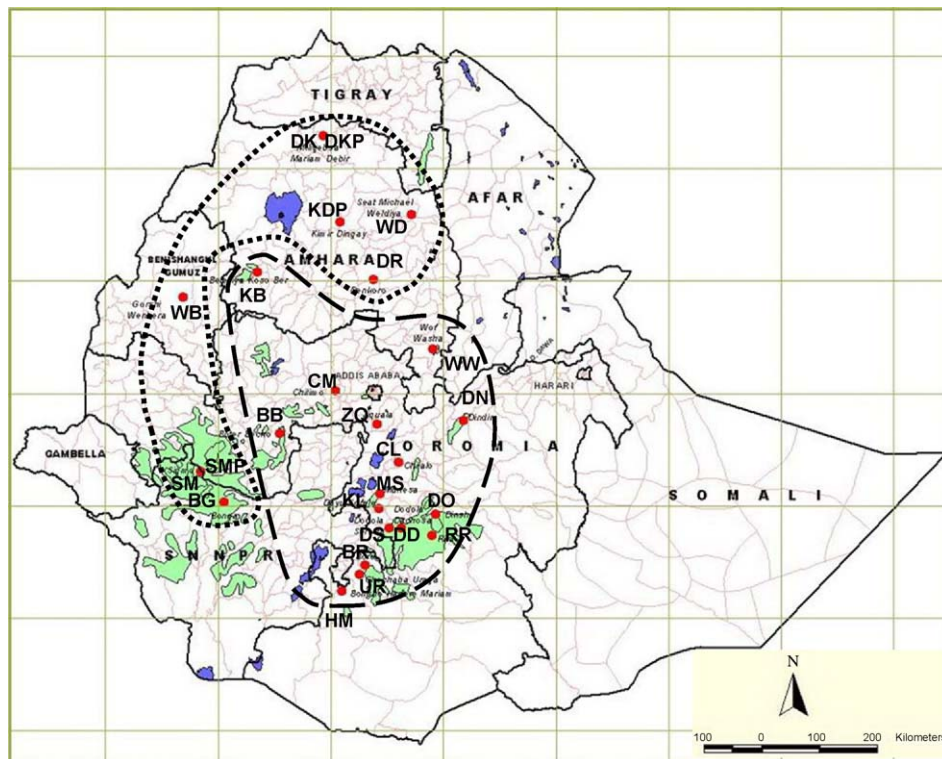


Fig. 1. The distribution of populations of *H. abyssinica* showing the two chloroplast lineages observed in Ethiopia (Ayele et al. 2009). Square-dotted enclosure shows the northern lineage; long-dashed enclosure shows the southern lineage. Small filled-circles indicate the locations of the populations; population codes are provided in Table 1. Bright shaded areas show extant closed forests; dark shaded areas show lakes.

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