

Tree density and germplasm source in agroforestry ecosystems in Meru, Mount Kenya

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Abstract

Farmers use and conserve a large variety of tree species. In Meru, a tree census on 35 farms covering 60 ha was conducted. This study included farmer interviews and biological measurements, with about 63,000 trees and 297 species being recorded. This paper discusses tree densities per species and germplasm sources for trees and species. The low densities and limited influx of germplasm from outside the farming community for some species, may result in an increased vulnerability to inbreeding and genetic erosion. This paper aims to provide some baseline data for understanding genetic resource management in agroforestry systems. It also provides suggestions for interventions to lower the vulnerability for species in Meru. Farmers need to have increased access to germplasm to diversify their farms in terms of species evenness, by substituting trees of more common species with trees of rarer species, or by increasing trees of rarer species.

Introduction

Farmers plant trees in pursuit of their livelihood goals of income generation, risk management, household food security and optimum use of available land, labour and capital (Arnold and Dewees 1995). Farmers use and conserve species to obtain many products such as food, wood, medicine and fodder, and for numerous services. Trees also play a crucial role in the cultural life of people. The many products, services and roles these trees provide cannot be delivered by a few species only. As a result, farmers have a wide variety of tree species on their farms. Farmers benefit from using all these species and thereby conserve the biological diversity on their farms. This conservation through use is increasingly important as the natural tropical forests are disappearing fast (Simons et al. 2000). Putting greater tree diversity into use is a method to

increase farmer benefits and to conserve biological diversity on farm (Kindt and Lengkeek 1999).

Farmers need biodiversity, including intra-specific diversity, for the productivity and sustainability of their agroforestry ecosystem. A broad genetic base provides the species with an adaptive capacity to respond to environmental fluctuations and changing farmer practices and markets. It ensures the vitality and long-term survival of the species in question and can be important for the vitality and sustainability of the entire agroforestry ecosystem (SGRP 2000).

Critically low densities may hamper adequate gene migration within species populations. Low densities may result in pollination problems, such as: (i) no pollination, (ii) increased selfing, resulting in inbreeding, or (iii) biparental inbreeding. There are, however, no baseline data available on what should be the 'minimum' tree densities to maintain

Table 1. Characteristics of the agro-ecological zones of the study area.

Farming community	Gaukune	Kigane	Ncoroiboro
Village name	Igoji	Nkubu	Ruiri
District	Central Meru	Central Meru	Central Meru
Zone	Sub humid	Humid	Semi arid
Land classification*	Upper Midlands 2	Upper Midlands 2	Upper Midlands 3
Annual rainfall (mm)	500–2200	500–2200	500–1800
Av. farm size (census)	2.2 ha	1.3 ha	2.4 ha
Soils	Well drained, very deep loam to clay	Well drained, extremely deep loam clay	Well drained, deep red cracking clay with humic topsoil
Distance of the community to the forest	25 km	12 km	0 km
Altitude farms (MAS)	1353–1586	1497–1674	1524–1761
GPS farms	037 66' E 00 11' S	037 65' E 00 04' S	037 63' E 00 09' N

*Land classification according to Pelley et al. (1985).

the genetic base. Some species specific information is available: Murawski et al. (1994) indicated that a reduction in population density of *Shorea megistophylla* P.S.Ashton following selective logging can significantly elevate the proportion of seeds produced through inbreeding. Whereas Cascante et al. (2002) found that in fragmented forest seeds from isolated trees of *Samanea saman* (Jack.) Merrill had less genetic diversity and were less likely to germinate, and the seedlings that did grow had smaller leaves. Regardless of this little information available, it should be clear that the lower the tree density of a species, the more chance for genetic erosion.

Gene flow materialises through seed transfer and pollen dispersal. Hamrick and Nason (2000) cite various studies to indicate that pollen dispersal is responsible for much higher levels of gene migration in natural populations. This may be different on the farm, since farmers actively collect their germplasm. Although there is some evidence for large-distance movement of seed along human migration patterns, most germplasm is obtained from local sources (Kindt 2002; Lengkeek and Carsan 1999; Brodie et al. 1997).

The hypothesis is that, due to critically low densities and limited influx of seed from outside the farming community, a percentage of the species will be vulnerable to inbreeding and genetic erosion in the landscape. This paper aims to provide some baseline data for farmers, conservationists and agroforesters to understand the genetic resource management of the tree component in agroforestry systems. These data may help to address this

vulnerability, with the objective of securing farmer benefits and conserving the biological diversity.

Materials and methods

In Meru district on the slopes of Mt Kenya, 35 farmers were questioned about all the trees currently on their farm. A tree census was conducted during the first half of 2001. The census team consisted of the farmer, an extension worker from the Meru office of the Ministry of Agriculture (MoA), a researcher from the International Centre for Research in Agroforestry (ICRAF), and an extra taxonomist (from ICRAF) often also accompanied the team.

Farms

Three farmer communities participated in the study, representing a large area of high agricultural potential based on Mount Kenya (Table 1; Figure 1). Participating farmers were representative of Meru farmers, but were likely to be biased because of a higher interest in tree planting trials (Lengkeek and Carsan 2003). The farmers had already been involved in ICRAF's tree domestication trials for two to three years. One reason for selecting them, rather than working from a random sample, was that farmers had to spend a significant amount of time explaining different aspects of all their individual trees, which ranged from 3 h to 2 days per farm. We therefore felt that the research benefits would not compensate the inputs a random set of farmers had to make. Second, we knew

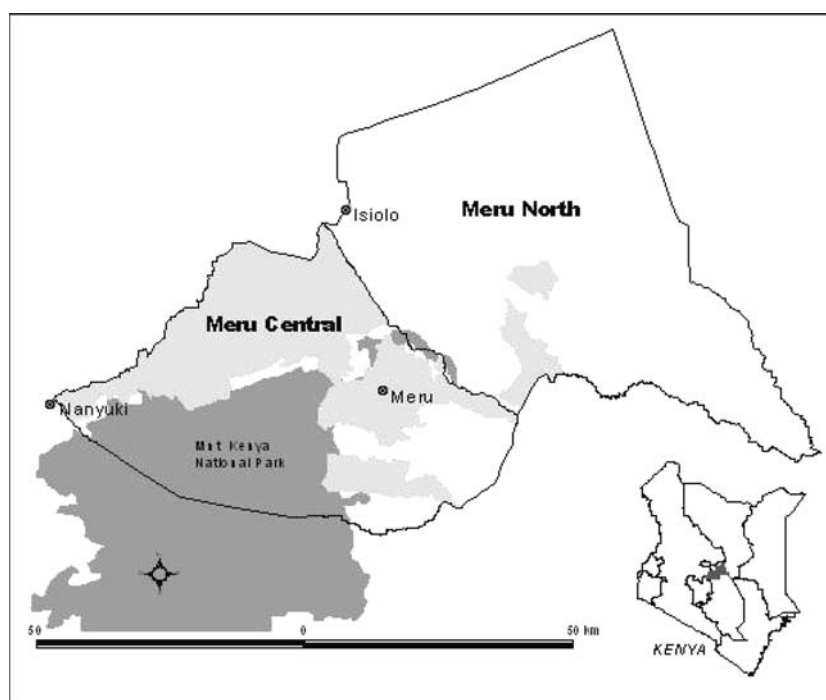


Figure 1. Map of Kenya showing Mt Kenya National Park and Meru Central District.

that a random sample would not be able to provide as detailed information on, for instance, cultural and medicinal uses of species, while a good and trusting relationship already existed with the trial farmers. Comparing our data with an earlier survey of randomly selected farmers to assess tree cover in Meru (Betser et al. 2000) showed great similarity, and therefore this data set can be seen as representative of the Meru farms.

Data

All trees were measured and farmer information was recorded through open-ended questionnaires. Data per tree included the species identification (by the farmer, extension worker and researcher), species origin – native range – (from the farmer, literature) source of germplasm and type of germplasm used (both from farmer interviews), reproductive capacity (from farmer interviews, visual recording by extension worker and researcher), age (from farmer interviews, visual measurements by extension worker), tree biomass (from diameter and visual measurements by researcher, using classes of tree shapes). Hedges with uniform vegetation were documented through multiplying

representative 5 m parts (from measurements by extension worker and researcher). Data per species included interviews about the species' uses (from farmer interviews). Data per farm included GPS coordinates (taken by researcher) and farm size (from farmer interviews, MoA data).

Definitions of 'trees' were similar to Beentje's (1994) criteria for species inclusion and comprised all woody perennials growing to over 1.5 m tall, but also included exotics. Because of the long-term cultivation of the sampled agroforests, (only Ncoroiboro was recently (50 years ago) brought under cultivation (MoA 2000)), it was not possible to ascertain whether indigenous species have occurred in the various farming communities. Species origin could therefore not be classified as endemic per farming community, but was classified as 'indigenous' if occurring in the UM2 and UM3 zones (see Table 1) in Meru district; hence, the rationale of the term indigenous instead of endemic in further analysis. Cultivars, for instance of *Coffea*, were not classified as indigenous (Maes 1993). The natural vegetation of the UM2 and UM3 zones was checked using farmer information and from literature such as Beentje (1994), Agnew and Agnew (1994) and Bussmann (1994).

Table 2. Number of families, species, trees and trees per hectare by origin on 35 Meru farms.

	Total	Indigenous (%)	Exotic (%)	Unknown (%)	Av. per farm (st. dev.)	Min. per farm	Max. per farm
Family	64	–	–	–	28 (6.8)	16	44
Species	297	61	29	10	54 (20)	28	97
Trees	62,946	32	67	1	1798 (1402)	294	5718
Trees, excl. coffee	42,135	47	51	2	1204 (1130)	240	4535
Density	1048*	32	67	1	1291* (775)	419	3645
Density, excl. coffee	702	47	51	2	868 (625)	229	2456

*Density for the total area versus the density based on farm averages.

For Ncoroiboro, a census of the nearby forest (Sjöberg and Swenson 1990) also assisted in identifying the original natural vegetation.

Analysis

Densities were calculated by dividing the total number of trees over the total number of hectares. Densities were compared between indigenous and exotic species and between the three communities. The origins of germplasm (categorised as from the own farm, from the same community or from outside the community) and types in which the germplasm was obtained (categorised as natural regeneration (wildings), transplanted wildings, forest remnants, cuttings or seedlings obtained from nurseries, the latter produced on or off of the farm) were compared between indigenous and exotic species.

The analysis was conducted for two categories: all tree species and indigenous species. The rationale behind this was that from a farmer's point of view, access to quality germplasm of all species is important (Lengkeek and Carsan 2003; DFSC 2003). However, the origin of the tree species is often seen as being less important; therefore, for short-term production purposes, genetic losses of exotic species can be just as harmful to the farmer. From a biological point of view, the conservation value of exotic tree species is less important than that of indigenous species.

The trees contributing offspring to the next generation determine the size of the genepool. As a result, non-seeding trees are not part of the effective population. However, this showed that the potential effective population size could be larger

Table 3. Number of families, species and trees per farming community in Meru.

Community	No. families	%	No. species	%	No. trees	ha	No. trees/ha
Gaukune	47	73	178	60	17,000	14	1200
Kigane	52	81	171	58	17,000	16	1100
Ncoroiboro	52	81	173	58	29,000	31	900
Total	64	100	297	100	63,000	60	1000

No differences among communities between the number of species and families ($P = 0.94$, $P = 0.89$). There were significant differences in the proportions of indigenous/exotic trees between communities, with a greater balance in Kigane, and even more indigenous trees if *Coffea* cultivars were excluded, in both cases (chi-square tests, $P < 0.001$).

than the current one. To address this, the potential effective population size was analysed as well.

The analysis was split up between the different farming communities. The tree cover could not be analysed as a meta population because of the geographical distance between the communities, and because the agro-ecological characteristics and farmer practices differed. Detecting possible differences between the farming communities was not an objective.

Results

Taking stock of species and trees

A total of 64 plant families was recorded. Major families were Rubiaceae (with 22 species), Euphorbiaceae (21) and the subfamily Papilionoideae (19). As many as 18 families were represented by a single species only. Family richness ranged from 16 to 44 families per farm with an

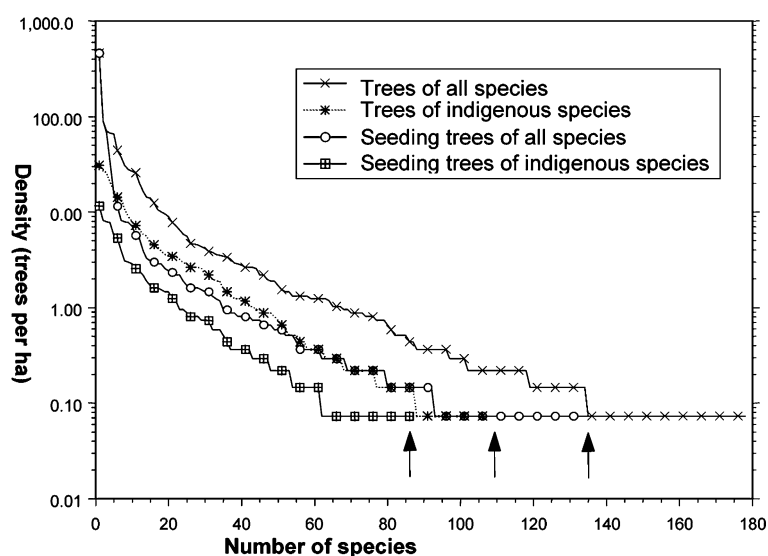


Figure 2. Tree densities per species in G aukune, Mt Kenya.

average of 28 families (see Table 2). A total of 297 species were recorded, ranging from 28 to 97 species per farm with an average of 54 species per farm. Not all species could be fully identified: 23 species were identified to the genus level, 13 species were identified by local name(s) only, six species remained unidentified ornamentals (most likely exotics) and another 12 species could not be identified (data not shown).

In total, almost 63,000 trees were recorded, 1/3 of these *Coffea* cultivars. The number of trees per hectare varied considerably, ranging from 419 to 3645, with a standard deviation of almost 800. The density based on the farm averages was 1291 trees/ha.

About 61% of the species were indigenous whereas 29% were of exotic origin, and 10% remained uncertain (Table 2). Nevertheless, there were more exotic trees on the Meru farms – 2/3 of the individual trees were exotic. The five most commonly occurring species were all exotic and formed 54% of the total number of trees on the farms (data not shown). Excluding *Coffea* cultivars, however, would result in almost an equal number of indigenous and exotic trees.

The results of the farming communities were consistent: the number of plant families ranged from 47 to 52, covering 73–81% of the total family diversity (see Table 3). The number of species per farming community ranged from 171 to 178, cover-

Table 4. Percentage of species that have fewer seeding trees per hectare averaged over three villages for various densities.

Density (trees/ha)	<10	<5	<2.5	<1	<0.5	<0.25	<0.1	No seed*
All species (%)	95	91	85	76	66	57	45	21
Indigenous species (%)	97	93	87	76	65	56	44	20

No differences between villages for all trees and indigenous trees (Chi-square test, $P = 0.38$, $P = 0.09$, resp.). *'No seed' represents the percentage of species that have no seeding trees.

ing 58–60% of the total tree species diversity. Due to larger farm size, the total number of trees in Ncoroiboro was larger; however, the number of trees per hectare was lower.

Densities

Figure 2 shows the densities of species by plotting the number of species against the numbers of trees for that species per hectare. Included are densities of all species as well as indigenous species alone for the total number of trees and for seeding trees. The graph only shows data from Gaukune, but other farming communities show similar profiles. Data presented in Figure 2, for instance, display the number of species with a density of more than one tree per hectare: these included 67 species,

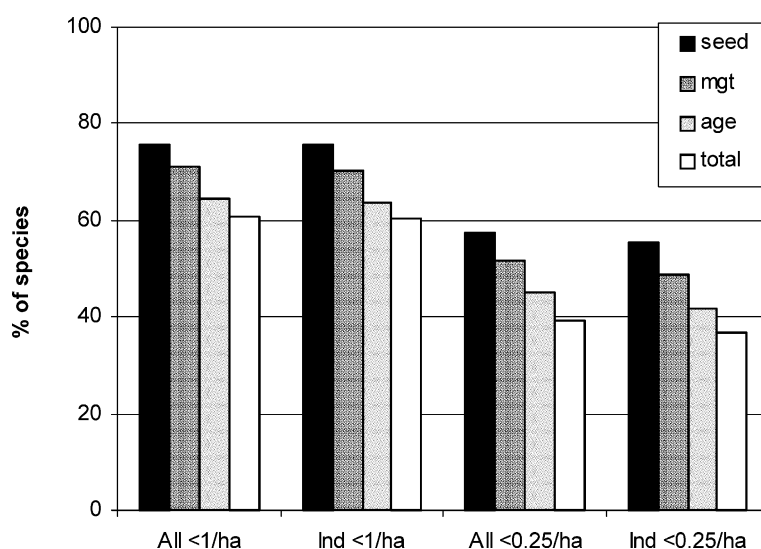


Figure 3. Percentages of species that have fewer trees or fewer seeding trees per given density, and the potential of management or ageing to increase the percentage of seeding trees per species. Densities include 1 tree per hectare and 1 tree per 4 hectares for all and indigenous (Ind) species. All data are averaged per species and per farming community. 'Total' represents the overall tree cover, whereas 'seed' represents seeding trees only. In between there are the potentials 'age' and 'mgt' representing the percentage of trees that may seed through ageing or a change in management practices.

which was 38% of the total amount of species recorded. For seeding trees, the numbers were, 34 (19%) for all species. For indigenous species only this density included 43 species (39%) and for seeding trees 22 species (20%). Averaged over all farmer communities, 76% of both all and indigenous species had less than a single seeding tree per hectare, representing 132 and 82 species for all and indigenous species, respectively.

Table 4 shows the percentage of species that had fewer seeding trees per hectare for various arbitrarily chosen tree densities. For example, averaged over the three communities, 97% of the indigenous species had less than 10 trees/ha whereas 44% had less than a single tree per 10 ha.

Although the three farming communities came from different agro-ecological zones and had different farming practices and species compositions, the results were consistent (Chi-square test, $P = 0.38$ for all species; $P = 0.09$ for indigenous species). For all and indigenous species only, approximately 20% of the species had no seeding trees.

Allowing trees to set seed would increase the density of seeding trees for many species. There is a potential for increasing the cover of seeding trees, for instance through a change in management (e.g., no pruning) or ageing. For example, 76% of the

indigenous species had less than one seeding tree per hectare; however the total for this density (including all non-seeding trees) is 60%. Figure 3 plots the overall tree density and the density of seeding trees against this potential. The results shown are for one species per hectare and one species per 4 hectares; other densities show similar patterns. Age was the most limiting factor; nevertheless, mortality, weeding and harvesting may remove many more seedlings and therefore the full potential of extra trees joining the gene pool is unlikely to be met.

Germplasm source

Farmers were questioned about the type and the source of germplasm of every single tree. Trees from indigenous species were more often wildings and rarely came from distant sources (see Table 5).

The 'unknown' source consisted of 95% wildings and 4% forest remnants for all species, and for indigenous species, the unknown source consisted of 94% wildings and 6% forest remnants. The data show that trees of unknown sources most likely originate from the farm itself or from the local area. Wildings were most likely

Table 5. Source of germplasm (GP) per species and source and main type of GP per seeding tree.

Source of Gp	Species (source in %)		Trees (source in %)		Main type of GP per source	Trees (type in %)	
	All	Indigenous	All	Indigenous		All	Indigenous
On-farm	25	20	15	14	Cutting	41	81
					Transplanted wilding	32	5
					Seedling on farm	24	15
Local	40	27	36	22	Cutting	59	64
					Seedling off farm	31	34
Distant	29	14	9	3	Seedling off farm	83	98
					Cutting	10	–
Unknown	77	91	40	60	Wilding	95	94
					Forest remnant	4	6
Total	100	100	100	100	Wildling	38	56
					Cutting	28	26
					Seedling off farm	19	11

Percentage of species with germplasm from a particular source averaged over the three farmer communities, focusing on 'all' and 'indigenous' species. Per individual tree, data represent all seeding trees ($n = 42,135$, this excludes *Coffea* cultivars,) and indigenous seeding trees ($n = 19,861$) at 35 Meru farms. All *Coffea* cultivars originate from distant sources and from seedlings produced off the farmers' farm. The trees sourced as 'local' originate from within the farmer community whereas distant sources come from outside the community. Significant difference between all and indigenous species in sources (Chi-square=8.39, $P = 0.038$).

Table 6. Percentage of species with less than a seeding tree per 1 and 4 ha, receiving germplasm (GP) from a distant source.

	All species					Indigenous species				
	No. of species	% of species		% of species with GP from a distant source		No. of species	% of species		% of species with GP from a distant source	
		1/ha	0.25/ha	1/ha	0.25/ha		1/ha	0.25/ha	1/ha	0.25/ha
Gaukune	178	81	62	15	16	109	80	57	7	8
Kigane	171	75	56	16	16	107	76	53	4	4
Ncoroiboro	173	71	54	32	29	111	71	56	14	13
Av.	174	76	57	21	20	109	76	55	8	8

No difference between the communities between indigenous and all species (Chi-square test, $P = 0.95$, $P = 0.755$, $P = 0.50$ and $P = 0.47$, resp.).

progeny of trees located on the farm or from other local trees; even if wildings were recorded under a seeding tree, they were classified as 'unknown'. Nevertheless, there is a chance that some of the trees of some species in Ncoroiboro derived from the adjacent forest (see also Table 1). Forest remnants are part of the founder population on the farm; these trees comprise the on-farm source itself. These results correspond with other findings that most trees are derived from the close vicinity (Kindt 2002; Lengkeek and Carsan 1999; Brodie et al. 1997).

Nurseries were an important mechanism for the influx of germplasm from distant sources. The vast majority of trees from distant sources were seedlings produced off the farm and these seedlings were derived from nurseries.

Table 5 also shows that only a limited number of species had one or more individual trees within their current population deriving from a distant source. On average, 29% of all species included trees from a distant source; for indigenous species, only 14% of the species included trees from a distant source.

Source of germplasm according to density

Table 6 combines densities (see Table 4) and the influx of external germplasm per species (see Table 5) for two arbitrarily chosen densities; i.e., a single species per hectare and per four hectares. For all species it shows that, for both densities, about 20% of the species included one or more trees from a distant source in the current population. For indigenous species, and both densities, 8% of the species included trees from a distant source.

Although the objective was not to detect differences between farmer communities, the variation increased here, which may subsequently increase the error margin. Nonetheless, no differences were found and other densities (data not shown) gave comparable results.

Discussion

The number of individual trees per species per hectare was low for many species – more than half of the species had only one tree or less per 4 ha. Although a change of management or ageing could increase the density of many species, this potential would make a minor difference (see Figures 2 and 3). Secondly influx of germplasm from a distant source for species with low densities only occurred for a few species, and rarely for indigenous species (see Table 6). No baseline data were available to provide information on the densities and gene flow needed for species populations to prevent inbreeding and genetic erosion. This baseline data were certainly not available for all 297 species involved, besides these would be dependant on too many other factors such as farmer decisions, incompatibility mechanisms, climatic conditions, pollinator populations, pollination processes, flowering patterns, possible subpopulation divergence, spatial structure of the tree populations and their various interactions, to name but a few. Nevertheless, species with very low tree densities are more vulnerable for inbreeding and genetic erosion than species with high tree densities, irrespective of the processes by which tree densities are determined.

Two additional factors further lowered the 'effective' density of seeding trees. In Meru, there are two clear and distinct rainy seasons, the long and the short rains (Pelley et al. 1985); therefore,

it is likely that most trees flower and set seeds at the same time. The extensive farmer interviews and interviews with seed collectors from the Kenyan Forest Seed Centre (KFSC) confirmed this. Nevertheless, asynchronous flowering cannot be excluded. Furthermore, not all recorded species were monoecious or hermaphrodite. It was however not possible to determine the sex of all individuals as the trees were not all flowering during the survey due to the time of year or due to management practices (e.g., hedges). Therefore, dioecious species were not treated as such.

'Tree domestication on the landscape level' is a concept recently developed at ICRAF (Simons et al. 2000; Kindt 2002; Lengkeek 2003). In contrast to the domestication of agroforestry species aimed at using the diversity present in individual species – (for instance, selection), domestication of the landscape proposes using the diversity of the tree component in agroecosystems. The data on densities and germplasm sources provide some baseline data that increase our understanding of the genetic resource management of tree and species diversity in the landscape. Furthermore, these baseline data may help farmers to address possible problems of inbreeding and genetic erosion.

Farmers' options

Farmers have four possible interventions available to them regarding domestication of the tree component of agroforestry ecosystems; these are 'replacement', 'addition', 'modifications in tree management' and 'substitution' (Simons et al. 2000).

1. Replacement of a tree by a tree of the same species would not increase the size of the gene-pool of the rarer species. If the germplasm is obtained from a distant source it may increase genetic diversity since small amounts of germplasm from the meta population can already prevent genetic drift in subpopulations (Wright 1931; Newman and Tallmon 2001). The number of species receiving germplasm from distant sources was, however, very limited, especially for indigenous species (see Tables 5 and 6). Additionally, the influx of germplasm from a distant source is not always effective, particularly not when species have low densities.

If no gene exchange occurs between the local trees and trees derived from distant sources, there will be no difference in vulnerability. For instance, genetic erosion will be independent of the source if a farming community only has a single tree of the species, as was observed in Gaukune for 44 species, 39 in Kigane and 28 in Ncoroiboro. The effect of the influx of germplasm from distant sources on lowering the vulnerability of genetic erosion is limited.

2. The addition of new trees is not effective either. Using the densities in Table 4 as an example, we can understand the effect of increasing tree densities in Meru. By defining – for example – a single tree per hectare as ‘critically low’, 76% of all species will have had a ‘critically low’ density. Doubling the tree cover on farm, which is similar to setting the density at 0.5 trees per hectare, 66% of the species would have a ‘critically low’ density. Doubling the tree cover once more – to 0.25 trees per hectare – the percentage of species with ‘critically low’ densities decreased to 57%. Similar results were found for indigenous species (see Table 4). Obviously, data on critically low densities are unknown and speculative, and doubling the current tree cover in Meru is next to impossible due to the high tree density already in place. This unrealistic ‘doubling’ would, however, decrease the number of species vulnerable to genetic erosion with 10% only, other, more realistic levels of tree addition would hardly make a difference. This example therefore shows that relatively independent of how the density is defined as ‘critically low’, the addition of new trees is not the most effective option.
3. A change in tree management, such as pruning, would not increase the effective population size substantially either. Only a limited number of trees would be able to seed in a different management regime (see Figure 3). Another management option farmers have is to change the location of the species in the landscape. For instance, farmers may choose to conserve their species by aggregating the species instead of segregating. However, the rule of thumb for species is 50 individuals for short-term productivity and long-term survival (FAO 1993). Averaged over the three farming communities,

only 25% of the species had more than 50 individual trees per community (data not shown). Therefore, aggregation of the current tree population per species does not seem to be enough. Aggregation will result in small-sized populations with an increased geneflow within the small population, leading to more genetic drift, and more incompatibility problems, and local species extinction, similar to the problems of fragmented forests (Young and Boyle 2000; Hall et al. 1996) or island populations (Hubbell 2001). Even if aggregation was possible, 50 trees of a species on one farm does not correspond with the farmer’s wish for risk management (Lengkeek and Carsan 2003). It should however be clear that the densities recorded did not imply that trees are distributed randomly over the sampled area, as farmer preferences and niche occurrence vary from farm to farm.

4. The best option seems to be a diversification in terms of species evenness of the agroforestry ecosystem through substitution; i.e., fewer trees of a few major species and more trees of the rarer species. Solely increasing the rarer species will give the same results, though this is more a ‘relative substitution’ than an increase as such.

Species substitution

Almost 300 species were recorded and it is unlikely that all farmers can or want to conserve all these species. In the case these species were evenly distributed over the almost 63,000 trees, then the density of each species would be: 3.53 trees/ha. In the current situation, almost 90% (Table 4) of species has a lower density. Substitution of trees of dominant species with trees of less dominant species will increase the densities of rarer species. However, to obtain the completely even distribution of 3.53 trees on average for each species, then over 46,000 (73%) of the 63,000 trees would need to be substituted. In no natural or agroforest ecosystem, perfect evenness of species is observed. A more realistic approach to model evenness is to use the broken-stick distribution (Hubbell 2001). In that case, over 32,000 trees would still need to be substituted. It may therefore not be realistic to expect farmers to make all these substitutions. A more

practical goal could be substitute some of the trees of the dominant species with some trees of rare species, but only targeting a subset of the rare species. One hypothetical suggestion could be that farmers substitute 1/3 of the trees of the 10 most dominant trees (over 13,000 individuals) with 50 rare species. The result would be that the density of these 50 rare species is increased by 4.43 trees/ha. Farmers' perceptions about individual species must be considered when planning such substitutions.

Interviews with the Meru farmers showed that they are eager to diversify to a large extent, in terms of species and evenness of distribution (Lengkeek and Carsan 2003). Especially where farmers have made deliberate management decisions to establish some species in high abundance and other species in low abundance – for instance based on their livelihood options – we may expect that farmers would not be interested in substituting most of their dominant species. It is, however, not sure if the current dominant species are also the most preferred species; Farmers have no choice but to plant or maintain what is available. Therefore there is a risk that well-preferred species may even become locally extinct, instead of the less preferred species that may have a better availability or regeneration capacity.

A large natural regeneration rate was observed; for indigenous species, 56% of the tree cover was derived from wildings and 91% of the indigenous species had one or more wildings and forest remnants in the population (see Table 5). For all species, 38% of the trees were wildings and 77% of the species had one or more wildings or remnants in the population. This regeneration capacity of species is however not sufficient to address the farmers' needs in search of preferred germplasm (Lengkeek and Carsan 2003). Therefore, to enable farmers to continue to use and conserve a reasonable subset of species, access to germplasm needs to be improved (see also Lengkeek and Carsan 2003; DFSC 2003). Additionally, farmers may need to increase their efforts to obtain germplasm.

Farmers should be guided in their use and conservation efforts to increase tree densities of the rarer species, however, because: (i) populations have been reduced to few individuals, so it is likely that there has been or will be a reduction in diversity among trees within populations, and (ii) the

germplasm of the current populations mainly comes from local sources and, therefore, probably has limited genetic diversity. As a result, species may have difficulties in re-establishing to larger population sizes from these small populations because of mating incompatibility. If by chance some of the genotypes have higher selfing compatibility rates, than the population could be re-established, but it would have a higher inbreeding coefficient. On the other hand, it is possible that selfing capacity tends to indicate selection against inbreeding depression. Since data on tree densities are unknown and dependant on many factors, it is however not clear to what level substitution must occur.

Some less preferred species will always have marginal numbers. Survival may occur in hedges and fallows, and indeed hedges often comprised the most diverse niches in Meru (e.g., Kindt 2002; van Oijen 2002). Hedges were also classified as niches for biodiversity conservation in comparable farming systems in western Kenya (Backes 2001). This may change, however, because invasive weeds such as *Tithonia diversifolia* (Hemsley) A.Gray and *Lantana camara* L. increasingly inhabit hedges, which does not help biodiversity conservation.

Vegetative propagation

About 28% of all trees were propagated vegetatively (see Table 5). Species that are solely reproduced vegetatively are also vulnerable for clone losses without the influx of new or the reintroduction of old clones. A certain number of individual clones are propagated more successfully and simple models show that after some generations only a few clones may dominate the area (Lengkeek, unpublished data). In short: with sexual reproduction one loses genes, and with vegetative propagation one loses clones. Note that the 20% of non-seeding trees (Table 4) were not able to seed due to age (56%), so these were not solely dependent on vegetative propagation. Only 11% of the vegetatively propagated trees were not able to seed.

Indigenous and exotic species

The analysis was split between all species and indigenous species only because farmers need access to

quality germplasm of all species. From a biological perspective, indigenous species are perhaps the most threatened group of species and merit more immediate attention for conservation. However, results on densities of all or indigenous species only were similar (see Table 4). Therefore, conservation from both the farmers' and biological perspective coincided and diversification in terms of species evenness sufficed to lower the vulnerability to genetic erosion.

The source of the germplasm differed between all species and indigenous species (see Table 5). Indigenous trees were markedly less often sourced from outside the community than exotic trees, both in terms of total amounts of germplasm and the proportion of species. Because minor gene migration per species from outside may already prevent narrowing of the genetic base (Wright 1931; Newman and Tallmon 2001), this indicates that indigenous species are relatively more vulnerable to inbreeding and genetic erosion. Therefore, if farmers would be aware of the advantages of the source of germplasm, it would benefit the genetic sustainability of indigenous species in particular.

Some factors may influence the vulnerability of indigenous species as compared to exotics. Indigenous species may receive geneflow from neighbouring forests, by pollen as well as by seed. In Uganda, Gerrits (1999) found increased densities of wildings of timber species closer to the forests. However, there is a rapid destruction of forests on Mt Kenya and surrounding areas, especially in the vicinity of settlements (Francis Ndiege, Meru forest officer, personal communication; KWS 1999). Seed sources for indigenous species used by the KFSC also suffer from illegal logging (Joseph Ahenda, personal communication). Similar to exotic species, the populations of indigenous species on farm will increasingly have to survive on their own. From a conservation point of view, on-farm populations are increasingly important. For exotics, there are generally more formal pathways for obtaining good quality exotic material for reintroduction.

Furthermore, exotics are more likely to be under cultivation in an area for a shorter period of time than indigenous species. Their long-term cultivation with possible bottlenecks may therefore be of less importance. On the other hand, exotics often get introduced in low numbers only,

resulting in a narrow genetic base of the founder population.

Conclusions and recommendations

It would be speculative to give a percentage of species that are vulnerable to inbreeding and genetic erosion since no data on species densities are known and the vulnerability is a product of many other factors as well. However, it is fair to conclude that with more than half of the species having less than an individual tree per 4 ha, the recorded tree densities of many species are low on Meru farms. Secondly, the influx of germplasm from a distant source is minimal, especially for indigenous species.

These two factors lead to a vulnerability to inbreeding and genetic erosion for some species in agroforestry ecosystems. This may cause short-term productivity and long-term stability loss. The best option to prevent this is to diversify the farm in terms of species evenness through an increased number of trees of rarer species, or through a substitution of the more common species. Farmers and researchers active in tree domestication could focus on improving access to quality germplasm of a wider range of species, instead of only concentrating the frequently mentioned domestication activities on a few successful or high potential priority species.

Due to the wide range of variables that may impact on tree genetic diversity levels on-farm, studies that mathematically simulate (Kindt 2002) or directly measure variation are useful. Direct measurements are however currently limited and have generally involved informal comparisons of native populations with exotic stands (e.g., Chamberlain 1998; Muluvi et al. 1999). Rarely have studies directly compared the diversity of natural and on-farm populations within the native range of a tree species (*Prunus africana* (Hook.f.) Kalkm.; Muchugi Mwangi 2001). Currently, farm and forest stands of the important and heavily exploited timber tree *Vitex fisheri* Grke (syn. *Vitex keniensis* Turrill) from central Kenya are being tested as a model for genetic erosion concerns on the farm by one of the authors (AGL), by employing molecular genetic markers. These molecular genetic data, although restricted to individual

species, can be used to increase the understanding of the genetic resource management of agroforestry systems.

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