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Full Length Research Paper

Genetic diversity of *Sclerocarya birrea* subspecies *birrea* populations in Burkina Faso detected by RAPDs

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***Sclerocarya birrea*, multipurpose plant is characteristic of the Sahel-Sudanian savanna and is widespread in West Africa. Although this species has a high socio-economic importance, its genetic organization was not well characterized in Burkina Faso. In this study, the intra and interpopulation genetic diversity of *S. birrea* was determined by random amplified polymorphic deoxyribonucleic acid (RAPD) markers. We found a high average of intra population genetic diversity (He = 0.20) among *S. birrea* populations. The species populations were also characterized by their low genetic differentiation (Gst = 0.24), indicating a significant exchange of genes flow between populations. The whole population was clustered into four groups without reference of site and climatic zone. The Mantel test suggested that genetic distances between populations were not correlated to geographic distances. Our results strongly suggest that the structure and the level of this species' genetics diversity may be due to its mode of dissemination involving ruminants.**

Key words: Genetic, variation, *Sclerocarya birrea* subspecies *birrea,* populations, RAPDs markers, Burkina Faso.

INTRODUCTION

Africa prunus *Sclerocarya birrea* (A. Rich.) Hochst, from the family of Anacardiaceae is widespread in sahelo-sudanian Africa. The species spans from Senegal in West Africa to Uganda in East Africa (Arbonnier, 2000; Hall, 2002). *S. birrea* is divided into three subspecies (Kokwaro, 1986). The subspecies *birrea* is endemic to Western Africa with, subspecies *multifolialata* being found mainly in Tanzania, and subspecies *caffra* in Southern Africa. In Burkina Faso, the subspecies *birrea* is generally found in all the climatic regions and is used for multiple purposes. These include human and animal consumption, fuel, artisanal and medicinal uses (Kokwaro, 1976; Boffa, 1999; Atangana et al., 2001; Eloff, 2001; Hall and O'Brien Sinclair, 2002; Ojewole, 2003; Okole et al., 2004; Soloviev et al., 2004; Ganaba, 2005 et Neya, 2006).

Despite the many advantages of *S. birrea* for local communities, the sustainability of the species is threatened by human pressure and climate conditions. This is noticeable through the aging of its populations, characterized by degradation and absence of regeneration (Bationo-Kando et al., 2008). Measures to preserve the species are in need, because *S. birrea* is among the wild fruit species in extinction in Burkina Faso (Leipzig, 1996). During the last years, the promotion of wild fruit trees and *in situ* management of natural plant populations has been developed in various countries,

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including Burkina Faso. These strategies require a good knowledge of the genetic potential of the species throughout its range and should take into account the needs of the populations that use these plants. For a better conservation and use of a species, knowledge of genetic variation within and between populations is essential (Dawson et al., 1995). Many studies have already been done on the diversity of woody species in semi-arid areas using molecular markers (Diallo et al., 2007; Sanou et al., 2005; Bouvet et al., 2004). Techniques using molecular markers to study variation within and between populations of trees are available. Among the various available techniques, random amplified polymorphic deoxyribonucleic acid (RAPD) is the most widely used technique (Bekessy et al., 2002; Martin and Hernandez, 2000); it also has the advantage of being simple and fast. The diversity assessed by RAPD is comparable to that obtained with allozyme or restriction fragment length polymorphism (RFLP) (Wu et al., 1999). However, RAPD has some limitations such as the inability to differentiate homozygous and heterozygous individuals.

Previous studies on the diversity of *S. birrea* were not only concentrated in the South of the African continent, but also in East Africa (Namibia, Tanzania, Kenya), especially on the subspecies *caffra* (Agufa, 2002; Emanuel et al., 2005; Gutman et al., 1999; Hillman et al., 2008; Kadu et al., 2006; Leakey et al., 2002, 2005a, 2005b; Leakey, 2005; Moganedi, 2007; Muok et al., 2007). The current study is based on the diversity of *S. birrea* species and its organization in Burkina Faso. The aim of the study was to quantify the genetic variation using RAPD markers and its implication for the conservation and the domestication of the species.

MATERIALS AND METHODS

The sites of interest were chosen to stand apart 30 km along a north-south transect. The north-south transect chosen includes the ecological gradient defined by Fontes and Guinko (1995). The location and determination of the number of sites for a genetic evaluation generally follows an ecological gradient (Palmberg, 1985). In each phytogeographical territory, the number of sampling sites was based on its size (Figure 1). In total, 11 sites were identified along the transect. The characteristics of climate and ecological eleven sites are given in the Table 1. 85 of 138 plants of *S. birrea* previously studied morphologically and biochemically (Bationo-Kando et al., 2008, 2009) were genetically characterized.

Plant material and deoxyribonucleic acid (DNA) extraction

The total genomic DNA samples were extracted from silica-dried leaf, according to strains using the DNeasy Miniprep kit (QIAGEN), following the manufacturer's instructions. DNA concentration and quality were, respectively given by direct reading of the spectrophotometer at 260 nm and by migration on a 1% agarose gel. DNA samples were then stored at -20°C for further investigations.

RAPD

10 primers (Kit A and B from operon technologies) were tested for polymerase chain reaction (PCR) profiles on DNA samples from eight different individuals. Muok et al. (2007) used the same primers to characterize collections of *S. birrea* subspecies *caffra* from Kenya and Tanzania. Nine primers that gave strong, reproducible and clearly detectable bands were selected for an assessment of all the DNA samples: OPA02, OPA03, OPA08, OPA18, OPB04, OPB05, OPB06, OPB07 and OPB08.

The amplification protocol was the same used by Dawson et al. (1995), with minor modifications. PCR was carried out at 25°C in a final volume of 20 µl containing 50 ng of genomic DNA, 200 µM each dATP, dCTP, dGTP and dTTP, 200 µM primers, 1x Taq polymerase buffer (10 mM Tris-hydrochloric acid (HCl) pH 8.8, 50 mM potassium chloride, 1.5 mM magnesium chloride, 0.1% non-ionic detergent) and 5 U/µl Taq polymerase (Hot Start, Qiagen). Each reaction was overlaid with 40 µl mineral oil. The thermal cycler was programmed for an initial denaturation step at 94°C for 5 min and 45 cycles, 92°C for 1 min, 36°C for 2 min, 72°C for 2 min, followed by a final extension step of 72°C for 5 min. The amplification products were separated by electrophoresis on a 2% agarose gel with Tris-borate buffer at 180 Volts. The gels were stained with ethidium bromide using standard methods (Sambrook et al., 1989) and imaged under ultra violet (UV) light. The DNA ladder (Bioline GmbH, Germany) was used in each gel as molecular size standard.

Data analysis

Amplified DNA bands were scored for presence (1) and absence (0), only strong bands were scored. Each PCR product was assumed to represent a single locus as the homology is generally high at the intraspecific level (Païvi, 2000). Data were subjected to analysis using population genetic analysis (POPGENE) 3.2 (Yeh et al., 1999), assuming diploid inheritance and Hardy-Weinberg equilibrium. This assumption is also made by other researchers assessing RAPD data from *S. birrea* (Kadu et al., 2006, Muok et al., 2007). The frequency of each band and the percentage of polymorphic loci were calculated in each population. To assess molecular variation, the Shannon's diversity index (Lewontin, 1972) was used. This parameter, also used without the need to make an assumption regarding Weinberg equilibrium (Aide and Rivera, 1998; Martin and Hernandez, 2000), is defined as $I = \Sigma\ pi\ \log_2 pi$ where pi is the frequency of the RAPD phenotype (presence (1), or absence (0) of the band). It was calculated for each locus, and averaged over loci to quantify the degree of variation within each population. Shannon's index was also estimated for the whole sample considered as a single population.

To analyse genetic structure, genetic distances were constructed using the Nei's original measures of genetic identity and genetic distance (Nei, 1972). The degree of differentiation among populations was also estimated using the parameter genetic differentiation (Gst). The dendrograms were constructed based on Nei's genetic distance method (unweighted pair-group method with arithmetical averages (UPGMA), modified from NEIGHBOR procedure of PHYLIP version 3.5). Mantel test (Mantel, 1967) was used to study correlation between genetics and geographical distance among *S. birrea* populations.

RESULTS AND DISCUSSION

The nine primers generated a total of 42 RAPD polymorphic ranged in sizes from 300 bp to 2000 bp. Such

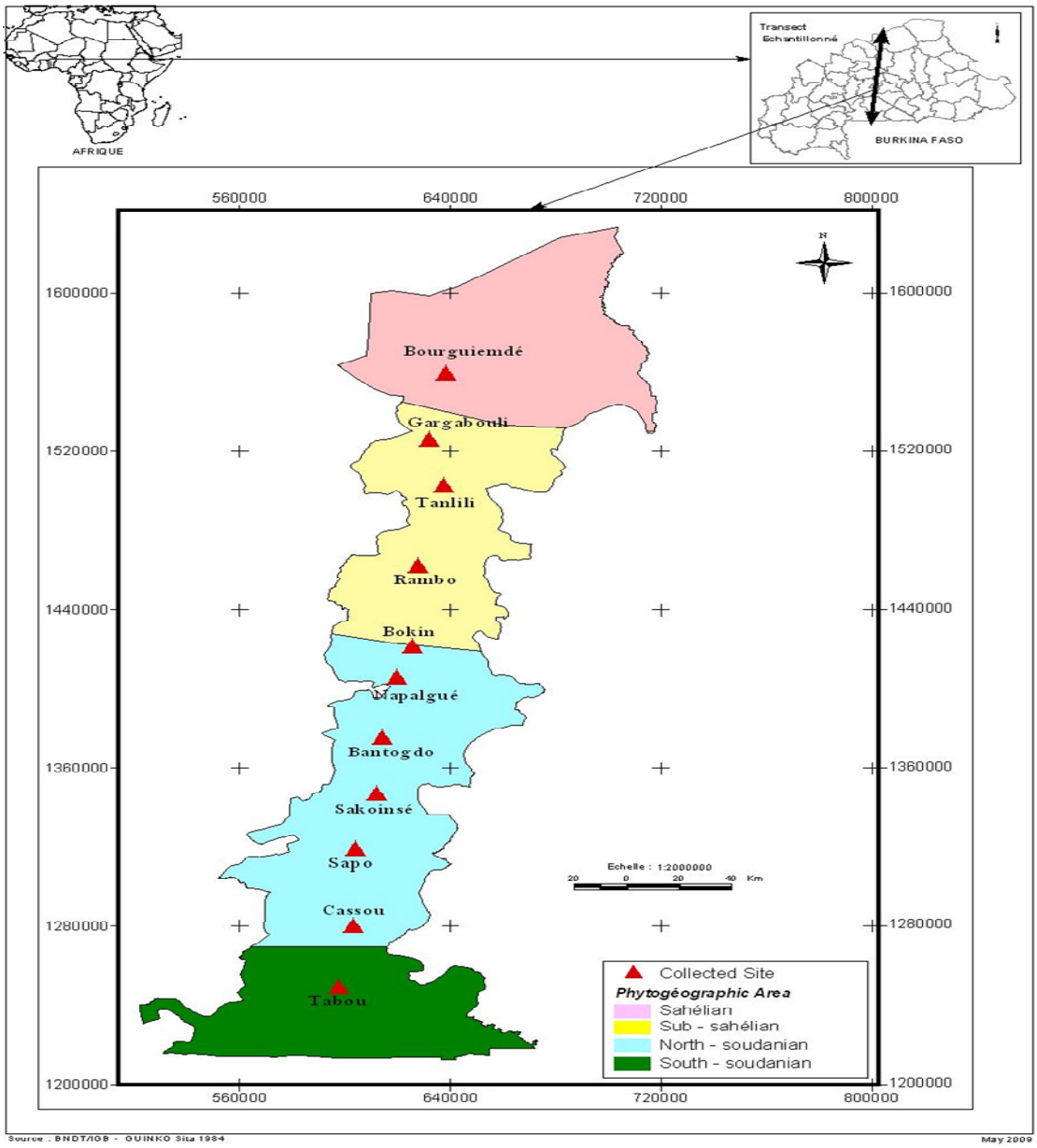

Figure 1. Geographic localisation of study area.

Table 1. Geographical location and climatic condition of *S. birrea* populations samples in natural range.

Population location	Climate	Geographical co-ordinate	Rainfall (mm)	Number of sample
Tabou (TB)	South-sudanian	11° 21' N, 2°10' W	900 - 1000	7
Cassou (KA)	North-sudanian	11° 34' N, 2° 02' W	700 - 900	7
Sapo (SP)	North-sudanian	11° 56' N, 2° 02' W	700 - 900	8
Sakouinsé (SK)	North-sudanian	12° 11' N, 1° 59' W	700 - 900	11
Bantogdo (BA)	North-sudanian	12° 29' N, 1° 57' W	700 - 900	9
Napalgué (NP)	North-sudanian	12° 41' N, 1° 54' W	700 - 900	8
Bokin (BK)	North-sudanian	12° 20' N, 1° 47' W	700 - 900	7
Rambo (RA)	South-sahelian	13° 14' N, 1° 48' W	600 - 700	10
Tanlili (TA)	South-sahelian	13° 35' N, 1° 44' W	600 - 700	9
Gargabouli (GA)	South-sahelian	13° 47' N, 1° 48' W	600 - 700	7
Bourguièdé (BR)	Sahelian	14° 06' N, 1° 44' W	500 – 600	2

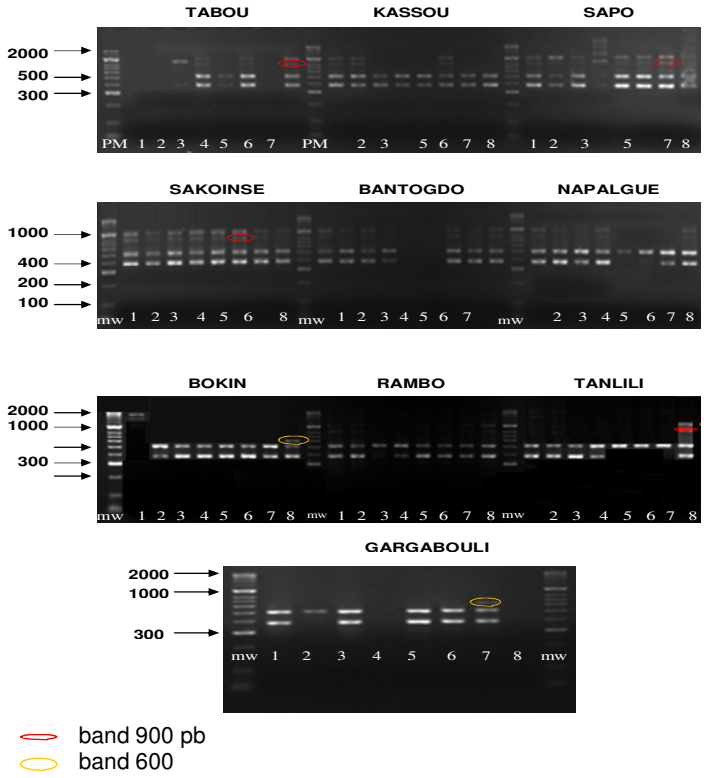

Figure 2. RAPD profiles obtained after amplification of ten populations of *S. birrea* with OPA06. Where mw, molecular weight Hyper Ladder II Bioline.

set of loci is expected to give a good sampling of the total genome and a suitable assessment of the genetic diversity. An example of the polymorphism detected with OPA06 is given in Figure 2. The number of bands per primer ranged from one (OPB08) to seven (OPA018 and OPB04). Six loci were polymorphic and were found in each of 10 populations examined, and 36 loci were found only in certain populations (Table 2). 25 loci were present at a frequency of less than 0.1 across bands. The locus APA06-4 had the highest overall frequency of occurrence (0.7625), while the locus OPB04-6 had the lowest of the overall frequency (0.0181). The percentage of polymorphic loci varied from 38.1% in Kassou up to 73.81% in Sakouinse (Table 3). Shannon's diversity parameter (I) for total population was equal to 0.33 (standard deviation (SD) = 0.20) and varied from 0.16 (SD = 0.19) for the population of Tanlili to 0.37 (SD = 0.28) of Sakouinsé. The diversity parameter which is genetic diversity (He) varied among the population from 0.11 (SD = 0.17) for the population of Kassou to 0.25 (SD = 0.20) for the population of Sakouinsé. It was 0.20 (SD = 0.15) for the total population. The differentiation assessed among populations was not marked (Gst = 0.24) indicating that 76% of individuals in the population was identical.

The genetic identity coefficient between pairs of population ranged from 0.8642 between Tabou and Sakouinsé to 0.9871 between Kassou and Napalgué (Table 4). The unrooted neighbour-joining tree obtained with whole population exhibited four clusters (data not shown). Genetic relationships among the 11 populations were summarized using UPGMA cluster analysis on similarity coefficients (Figure 3). UPGMA clustered the 11 populations into two groups. A Mantel test suggested that genetic distances between populations were not correlated to geographic distances (R = 0.252, p = 0.0638).

This study of *S. birrea* populations' genetic variation in Burkina Faso showed a high genetic diversity of the species. Furthermore, the interpopulation genetic differentiation was low and consistent with the reproductive biology and geographical distribution of the species. Our study shows a high genetic diversity of *S. birrea* in Burkina Faso through a percentage of a polymorphism and a Shannon diversity index (He = 0.20, P = 100% I = 0.33) higher than the average estimated by Agufa (2002) for populations of *S. birrea* subspecies *caffra* in Tanzania and Namibia (He = 0.06 and He = 0.18), the subsp. *birrea* in Mali (He = 0.148) and those reported by Hamrick et al. (1992) for tropical woody species (He = 0.125). However, our results are identical to those obtained in other populations of *S. birrea* by Kadu et al. (2006) and Muok et al. (2007). The values of *S. birrea* genetical diversity obtained in Burkina Faso are also comparable to woody species from wet tropical zone (Lengkeek et al., 2006;

Table 2. RAPD product frequencies for ten populations of *S. birrea* from Burkina Faso.

Polymorphism	RAPD product frequency in each population										RAPD product frequency in total population
	Tabou	Kassou	Sapo	Sakouinsé	Bantogdo	Napalgué	Bokin	Rambo	Tanlili	Gargabouli	
OPA02-1	0	0.1548	0.1343	0.2023	0.0572	0.2094	0	0.0573	0	0.1548	0.0961
OPA02-2	0.1548	0.0742	0.0646	0	0	0	1 000	0.4523	0.2546	0.4655	0.2258
OPA02-3	0	0.4655	0.3876	0.6985	0.4226	0.5	0.2441	0	0	0	0.2570
OPA02-4	0	0.1548	0.3876	0.0465	0.0572	0.1340	0.3453	0.0513	0.1181	0.1548	0.1253
OPA02-5	0	0	0.1343	0.0465	0	0.1340	0.0742	0	0	0.0742	0.0658
OPA06-1	0.3453	0.2441	0.5	0.5736	0.5286	0.2929	0	0.0513	0.1181	0	0.2780
OPA06-2	0.0742	0	0.0646	0	0.0572	0	0	0	0	0	0.0182
OPA06-3	0.2441	0.2441	0.2929	0.6985	0.4226	0.0646	0	0	0.1181	0	0.2215
OPA06-4	0.3453	1 000	0.6464	1 000	0.5286	1 000	1 000	0.5528	1 000	0.6220	0.7625
OPA06-5	0.4655	1 000	0.6464	0.6985	0.6667	0.5	1 000	0.5528	0.4226	0.4655	0.6269
OPA08-1	0.2441	0.3453	0.2929	0.5736	0.4226	0.2929	0.3453	0.1633	0.1181	0.0742	0.2889
OPA08-2	0	0	0	0.3258	0.1181	0	0.1548	0.0513	0.0572	0.0742	0.0856
OPA08-3	0	0	0.0646	0.0955	0.0572	0.0664	0.0742	0.0513	0.0572	0	0.0488
OPA08-4	0.0742	0	0.0646	0	0.1835	0	0.2548	0.0513	0	0	0.0573
OPA08-5	0	0	0.2094	0.6985	0.1835	0.0664	0.3453	0.1633	0.1181	0.1548	0.2085
OPA18-1	0.1548	0.2441	0.3876	0.6985	0.4226	0.2929	0.3453	0.2254	0.1181	0.2441	0.3196
OPA18-2	0	0	0	0	0	0	0	O	0	0.1548	0.0196
OPA18-3	0	0.1548	0.3876	0.4778	0.1835	0.2094	0.3453	0.2254	0.1181	0.1548	0.2373
OPA18-4	0	0	0.0646	0	0	0	0	0	0.0572	0.0742	0.0182
OPA18-5	0.0742	0	0	0	0.1181	0	0	0	0	0	0.0255
OPA18-6	0	0.2441	0.2929	0.6985	0.3333	0.2929	0.4655	0.1633	0.0572	0.4655	0.3029
OPA18-7	0	0.0742	0.2929	0.4778	0.2546	0.2929	0.4655	0.0513	0.0572	0.1548	0.2132
OPB04-1	0	0.0742	0.1340	0.3970	0.2546	0	0	0	0	0	0.0971
OPB04-2	0.0742	0.0742	0.2929	0.6985	0.1835	0.0666	0.2441	0.0513	0	0	0.1818
OPB04-3	0	0	0	0.0955	0	0	0.0742	0	0	0	0.0185
OPB04-4	0.2441	0	0	0.0465	0.0572	0	0.0742	0.1056	0	0	0.0742
OPB04-5	0.1548	0	0	0.2615	0.1181	0	0	0.0513	0	0.0742	0.0712
OPB04-6	0	0	0	0.0465	0	0.0646	0	0.0513	0	0	0.0181
OPB04-7	0	0	0	0.5736	0.0572	0	0.0742	0.1056	0.0572	0	0.1049
OPB05-1	0.0742	0	0	0.0465	0	0.0646	0	0.0513	0	0	0.0242
OPB05-2	0.0742	0	0	0.0465	0.1181	0	0	0.0513	0	0	0.0376
OPB05-3	0	0	0	0	0.1181	0.0646	0	0	0	0	0.0186
OPB05-4	0.0742	0	0	0.1472	0.0572	0.1340	0	0	0	0	0.0507
OPB05-5	0	0	0	0.2615	0	0.0646	0	0	0	0	0.0468
OPB06-1	0	0	0	0.4778	0.0572	0.1340	0	0	0	0	0.0805
OPB06-2	0.0742	0	0	0.0465	0	0	0	0.0513	0	0	0.0417
OPB06-3	0.0742	0	0	0	0	0	0	0.0513	0	0	0.0352

Table 2. Contd.

Polymorphism	RAPD product frequency in each population										RAPD product frequency in total population
		Tabou	Kassou	Sapo	Sakouinsé	Bantogdo	Napalgué	Bokin	Rambo	Tanlili	Gargabouli	
OPB07-1	0	0	0	0	0	0	0.0742	0	0.0572	0.0742	0.0183
OPB07-2	0	0	0.2094	0	0	0	0.2441	0	0.0572	0	0.0459
OPB07-3	0.1548	0.3453	0.3876	0.3258	0.3333	0.2094	0.3453	0.2929	0.1835	0.2441	0.2842
OPB07-4	0	0.3453	0.2094	0.3258	0.3333	0.2094	0.3453	0.2254	0.1181	0.2441	0.2398
OPB08-1	0.0742	0.3453	0.3876	0.3977	0.2546	0.1340	0.3453	0.2254	0.1835	0.0742	0.2201

Table 3. Size of populations (N), Shannon's Index (I), genetic diversity (He), percentage of polymorphic RAPD loci (%P).

Population	N	ne	I	He	%P
Tabou	7	1.17 (0.26)	0.19 (0.22)	17 (0.15)	47.62
Kassou	7	1.18 (29)	0.18 (0.24)	0.11 (0.17)	38.1
Sapo	8	1.35 (0.37)	0.31 (0.29)	0.21 (0.21)	59.52
Sakouinsé	11	1.44 (0.39)	0.37 (0.28)	0.25 (0.20)	73.81
Bantogdo	9	1.35 (0.36)	0.33 (0.26)	0.21 (0.19)	71.43
Napalgué	8	1.24 (0.30)	0.25 (0.25)	0.16 (0.17)	57.14
Bokin	7	1.29 (0.36)	0.25 (0.28)	0.17 (0.20)	50
Rambo	10	1.21 (0.28)	0.23 (0.23)	0.14 (0.16)	64.29
Tanlili	9	1.13 (0.20)	0.16 (0.19)	0.16 (0.19)	47.62
Gargabouli	7	1.21 (0.30)	0.21 (0.25)	0.13 (0.17)	47.62
Bourguièmdé	2	1.18 (0.31)	0.16 (0.27)	0.11 (0.18)	26.19
Total population	85	1.30 (0.26)	0.33 (0. 20)	0.20 (0.15)	100

Lowe et al., 2000, Newton et al., 2002) and dry tropical zone with the same biological and ecological charac-teristics as *Vitellaria paradoxa* (Fontaine et al., 2004) and *T. indica* (Diallo et al., 2007). *S. birrea* appears thus as a species with a high diversity compared to most of tropical species which were studied using RAPD markers. The average values of intra-population genetic diversity were high (ranging from He = 0.11 to 0.25). The level and structure of species diversity is determined by its genetics and ecological characteristics (Hamrick et al., 1992; Loveless, 1992; Yeh, 2000). The reproduction system of *S. birrea* and its population density may impact on the intra population's diversity. The species' pollination mode is mainly allogamous and could explain the relatively high level of intra-population diversity founded in S. *birrea* populations in Burkina Faso. According to Hamrick et al. (1992), allogamous species pollinated by animals have higher level of genetic diversity than other species. The relatively high density of individuals in our study (10 to 25 trees / ha) combined with synchronized flowering trees, promote the mixing

Table 4. Néi's genetic identity (above diagonal) and genetic distance (below diagonal) for pair-wise differences between eleven populations of *S. birrea* from Burkina Faso.

Population	Tabou	Kassou	Sapo	Sakouinsé	Bantogdo	Napalgué	Bokin	Rambo	Tanlili	Gargabouli	Bourguièmdé
Tabou	_	0.9625	0.9631	0.8642	0.9715	0.9654	0.9193	0.9845	0.9845	0.9741	0.9140
Kassou	0.0382	_	0.9788	0.9114	0.9793	0.9871	0.9471	0.9717	0.9767	0.9687	0.8610
Sapo	0.0376	0.0214	_	0.9295	0.9867	0.9811	0.9471	0.9693	0.9690	0.9555	0.8547
Sakouinsé	0.1460	0.0928	0.0731	_	0.9379	0.9172	0.8810	0.8778	0.8792	0.8750	0.7479
Bantogdo	0.0289	0.0209	0.0134	0.0641	_	0.9776	0.9298	0.9674	0.9632	0.9611	0.8647
Napalgué	0.0353	0.0130	0.0190	0.0865	0.0227	_	0.9401	0.9728	0.9820	0.9742	0.8684
Bokin	0.0842	0.0543	0.0544	0.1267	0.0728	0.0618	_	0.9608	0.9507	0.9615	0.8189
Rambo	0.0156	0.0287	0.0312	0.1304	0.0332	0.0276	0.0399	_	0.9898	0.9928	0.9015
Tanlili	0.0202	0.0236	0.0315	0.1287	0.0375	0.0182	0.0505	0.0102	_	0.9864	0.8857
Gargabouli	0.0263	0.0318	0.0351	0.1335	0.0397	0.0262	0.0392	0.0073	0.0137	_	0.8853
Bourguièmdé	0.0899	0.1497	0.1570	0.2905	0.1414	0.1411	0.1999	0.1036	0.1214	0.1218	_

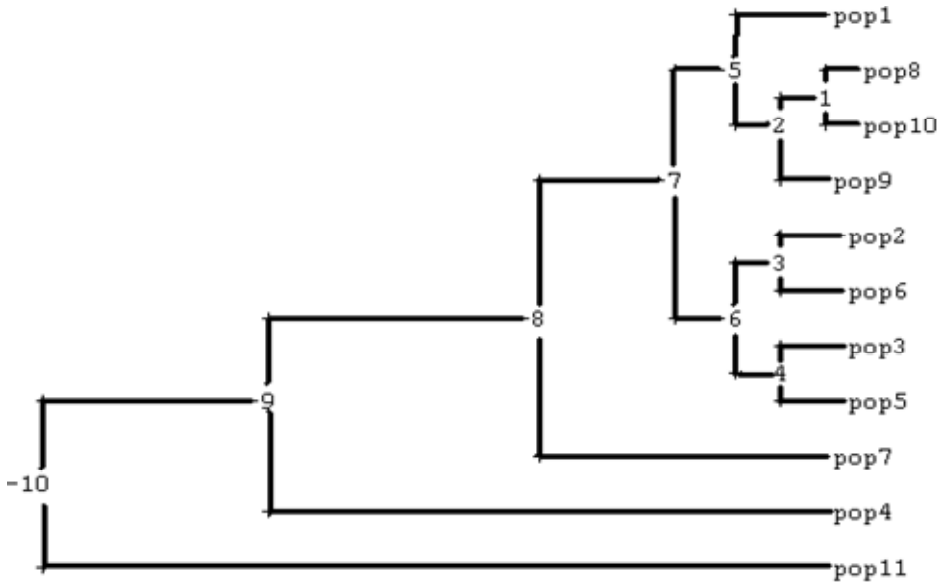

Figure 3. Dendrogram generated by a UPGMA of RAPD genetic similarity matrix, based on bands amplified using nine primers on 85 leaf samples from eleven populations of *S. birrea* subspecies *birrea* from Burkina Faso.

of genes in populations and thus helps in maintaining a high level of genetic diversity.

The present study found a relatively low genetic differentiation between populations of 0.24 for *S. birrea*. This value is comparable to that reported for *V. paradoxa*, a sudano-sahelian woody species, with a Gst = 0.23 (Fontaine et al., 2004). Given *S. birrea* pollination system, one would have expected a greater genetic differentiation between populations. The main pollinator of *S. birrea* is *Apis mellifera* (Hall and O'brien, 2002), which can only ensure the movement of pollen over short distances (few hundred meters), but the pollination could be also ensured by dipterans. Dipterans are known to move less frequently from one tree to another. This mode of foraging focuses on gene mixing within populations rather than between populations and the consequence could be the low gene flow between populations and the increase of gene flow within populations. The low level of inter-population diversity obtained in this study could not be due to pollinating agents, but probably to the spread of grains by hoofed animals along transhumance areas. The period during which *S. birrea* fruits are ripe corresponds to intense pasture period. The seeds are thrown in the nature close or far from harvest areas. The seeds dissemination may have greater impact on gene flow compared to pollen spread.

Contrary to the study of Kadu et al. (2006), we showed that the genetic structure of *S. birrea* can be influenced by direct or indirect actions of animals as shown in the studies of Leakey (2005), Leakey et al. (2005a, 2005b), Lewis (1987) Missana and Mukamuri (1996) Nghitoolwa et al. (2003); Shone (1979) and Walker (1989). Hamrick et al. (1992) showed that by order of importance, geographical distribution was the first factor responsible for inter population genetic differentiation. We found low values of inter-populations genetic distances, showing that *S. birrea* populations were very close; this is in accordance with the results obtained by Hamrick et al. (1992). The dendrogram established for all individuals genotyped, divided *S. birrea* populations in four groups without reference to site or climatic zone. RAPD polymorphisms of *S. birrea* obtained in the present report suggested that the intra and inter populations variation previously described for morphological and biochemical characteristics (Bationo-Kando et al., 2008, 2009) were probably associated with environmental than genetics factors. Only environmental conditions are likely to cause a gradual degradation of *S. birrea* populations and its genetic erosion. A long term management of *S. birrea's* genetic resources at the local level will necessarily involve the *in situ* management of the existing settlements in various agro-ecosystems.

The low differentiation among populations of *S. birrea* could be explained by the geographical extent of their range. The species that have an extended range have a low differentiation between populations (Hamrick et al., 1992). It is also established that most people are far from each other and they tend to be genetically differentiated, reflecting a decrease of gene flow (Loveless, 1992). This implies that the more people are close, the more they will tend to be genetically identical. This is also sustained by the results of Hall et al., (1994), who found for *Carapa guianensis* a very low Gst of 0.05 for very close populations (distant of few kilometers) and high differentiation between high distant populations. Likewise, the lack of correlation between genetic and geographical distances found in this study is thus explained by the fact that populations were close as they were separated each other by only 30 km, corresponding to a short distance for trees. According to Bekessy et al. (2002), a strong correlation between genetic and geographical distances is observed in populations separated by distances above 50 km and no significant correlation is observed for populations separated by short distances (1 to 50 km) (Scheirenbeck et al., 1997).

Conclusion

The present report enabled us to highlight a high level of intra-population genetic diversity of *S. birrea* in Burkina Faso. Two essential factors among many others, including anthropic activities and the species reproduction (seeds dissemination mode) may explain *S. birrea* genetic structure. As *S. birrea* populations are generally degraded, the capture of this variation within the species could constitute the first stage for a conservation program. The conservation strategies should integrate valorization, domestication and pro-tection of the species by rural populations (the local communities).

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