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Study of the Molecular Biodiversity of the Saharan Bread Wheat in Algeria

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Climate change has significantly affected wheat yield. Many studies have suggested that rising temperatures could be harmful to cereals around the world. Thus, the valorization of the desert wheat resources is essential to improve the resistance of this species to climate change. In this context, twenty-eight different local Saharan bread wheat (*Triticumaestivum* L.) genotypes were described using ten preselected SSR markers. The tested SSRs produced a total number of 20 alleles with an allelic size ranged from 100 pb (WMC261) to 400 pb (WMC257). The allele frequency varied from 0.1 for the allele 230 pb (WMC156) to 1 for the alleles 187 pb, 310 pb (WMC97, WMC168). Likewise, the PIC values ranged from 0 (WMC97, WMC168) to 0.5 (WMC327, WMC233), with an average of 0.34 and the observed heterozygosity (Ho) from 0 to 0.88, with an average of 0.55. The molecular variance (AMOVA) revealed the highest level of intra-population differentiation of local Saharan bread wheat (97%) and the statistical geometric distributions based on PCoA, NJ method and structure analysis confirmed the existence of four major classes of bread wheat. These results substantiate the previous researches based on the morphological markers and contribute for the first time in Algeria to create the genetic fingerprint of the Saharan bread wheat resources and to valorize their drought resistance potential through breeding programs.

Keywords: Algerian desert, biodiversity, climate change, SSR, *Triticum aestivum* L.

Introduction

Nature hides the secrets of the resistance of many living beings to the harsh climate. Plants and animals have to adapt to the scarcity of water and high temperatures to subsist. The genetic pools of these species constitute a precious treasure to cope with the negative effects of climate change on living beings. Algeria presents the largest hot desert in the world, with more than 3.5 million square miles. Human has lived within or on the edge of the desert and still today many nomadic tribes in Algeria call the Sahara home. The arrival of this nomad population to Algeria may extend as far back as 30,000 B.C. and marked the beginning of wheat cultivation. The introduction of semolina wheat by the

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Carthaginians led the Berbers to create couscous, Algeria's national dish. The Romans, who eventually took over Algeria, also grew various grains (such as wheat and barley). All these factors led to the creation of typical wheat genetic resources adapted to the Algerian Sahara climate and drought conditions. Therefore, the Saharan wheat genetic pool may constitute a real genetic matrix to improve the resistance of this species to drought stress. Exceptionally, that the negative impacts of climate change will be so severe in hot and dry areas were the rise in temperature and the decrease in rainfall have been more severe (Parry et al. 2004; Gregory et al. 2005; Sivakumar et al. 2005).

Nevertheless, durum wheat was the only crop grown by local Algerian people before the settlement of French colonization in 1830 (Boeuf 1932). The botanists as Ducellier 1930; Laumont and Erroux 1962, have pointed out the ancient presence of bread wheat under the name 'Farina' as opposed to durum wheat, 'Guemh', and described various forms such as 'Bou-Zeloum', 'Hachadi', 'Sahraoui', 'Dahra' wheat as well as on the Saharan borders and in the oasis where the local people have long used early bread wheat (Ducellier 1930; Laumont and Erroux 1962). The first investigation of local wheat resources in Algeria was based on morphological and physiological traits. Ducellier (1930) described the overall wheat crop species in Algeria: durum wheat with and without beards and the oasis bread wheat with and without beards. Boudour et al. (2011) characterized a collection of 1019 accessions of durum wheat from different Algerian regions and recently, Bellatreche et al. (2017), have conducted genetic divergence studies in thirty different local bread wheat accessions cultivated in western Algeria with a check based on morphological traits.

The creation of the genetic fingerprint database of the local bread wheat resources is paramount to predict the performance of the succeeding generation, to study their genetic diversity, relationships, and the heritage mechanisms (Hamdi 1992). SSR markers have been widely accepted as useful tools to estimate genetic diversity and divergence within and among populations (FAO 2011). The high-level polymorphism, the apparition of a large number of alleles per locus and the co-dominant inheritance of SSR markers have facilitated their use in genome mapping, phylogenetic inference, and population genetics (Kandemir et al. 2010; Brbaklih et al. 2014; Ozlem and Begum 2018).

However, so far, limited studies of genetic diversity on Algerian bread wheat have been conducted using molecular markers. Consequently, an inventory of the existing genetic diversity has been launched to establish a breeding plant and removed the ambiguity of the designation of accessions. Therefore, the current study aims at estimating for the first time in Algeria the coefficient level of the genetic variation of twenty-eight different local Saharan bread wheat genotypes and exploiting their genome short tandem repeats sequence to investigate the level of their genetic variability and employ their drought resistance potential through breeding programs.

Materials and Methods

Plant materials collection

In total, twenty-eight local wheat accessions were collected from twenty-one locality of South Algeria, representing almost half of Algeria's surface area (Table 1). The field survey was conducted at the level of Saharan ecotype zones to describe the types of agrosystems in which local bread wheat accessions are evolving, and subsequently to evaluate the effect of agricultural practices on the management of the diversity of wheat. These regions were made based on their situations in different climatic stages.

DNA isolation and SSR analysis

Total DNA was extracted from fresh leaves using the CTAB method according to Saghai-Maroof et al. (1984). The extracted DNA was checked for quality and quantity using 0.8% agarose gel electrophoresis and Nanodrop spectrophotometer (BioSpec-nano; Shimadzu Biotech). Ten SSRs primers (Table 2) were used to analyze the genetic profile of the tested bread wheat accessions and to test their resistance to drought, salinity and heat stress (Ashraf et al. 2015; Alhosein et al. 2012 and Shahzad et al. 2012).

The PCR reaction was performed in a 25 µl volume consisting of (50 ng genomic DNA, 1.5 mM $MgCl_2$, 0.2 mM each dNTP, 0.25 µM forward primer, 0.25 µM reverse primer, 0.04 U PromegaTaq DNA polymerase in 1X PCR buffer). Afterwards, the amplification were performed using the thermo-cycler (BIO-RAD C1000 Tm) with the program (94 °C for 2 min, followed by 35 rounds of 94 °C for 1 min; the amplification temperature varied between 50 °C and 60 °C for 1 min depending on the primer and 72 °C for 1 min, with a final step of 72 °C for 3 min). Finally, the amplified PCR products were screened by electrophoresis using a 3% agarose (1x Tris-Acetate-EDTA buffer pH 8.3) gel, stained with 0.5 mg/ml ethidium bromide, and visualized under UV light by Gel Documentation System (GDS). A 50 pb DNA ladder (Promega) was used as a molecular marker of standard sizes.

Molecular data analysis

The allelic profiles of the twenty-eight analyzed wheat cultivars generated by ten SSR markers were used to create a matrix based on the allelic size of the different microsatellite markers. These data were used by GenAlEx 6.5 software (Peakall and Smouse 2006) to determine the number of alleles per locus, the principal allele frequency (PAF), the observed heterozygosity (Ho), the Shannon index (I), the number of private alleles per variety, the probability of identity (PI) per locus and the cumulative PI for all loci (Waits et al. 2001). For the sake of creating the graphic dispersion of the studied varieties via the Principal Coordinates Analysis (PCoA) and determining the analysis of molecular variance (AMOVA). The statistical calculations of the polymorphic information content (PIC) and the allelic diversity (AD) were determined by the use of Power marker Version 3.25 (Liu and Muse 2005).

Table 1. Accessions name and country of origin for the bread wheat used in this study

Varieties	Code	Region	Localities	Longitudes	Latitudes	Altitude
Zraa Labled	A1	Adrar	Zaouiat Abd El Kader	0°14′18.29E″	29°15′41.81N″	288 m
Bahamoud	A2		Zaouia	0°14′18.29E″	29°15′41.81N″	288 m
Belmabrouk	A3		Zaouiat Kounta (El Mnasir)	0°12′00.52E″	27°13′00.28N″	189 m
Omrokba	A4		Tamantit	0°16′00.19″E	27°46′00.31N″	241 m
Belmabrouk d5	A5		Tamantit (Sidi Youcef)	0°16′00.19E″	27°46′00.31N″	241 m
Bahmoud AM	A6		Badrian	0°13′19.13E″	29°15′46.36N″	263 m
Djaghloul	A7		Zaouiat Debagh	0°42′38.05E″	29°42′43.47N″	356 m
Ali Ben Makhlouf	A8		Zaouiat Abd El Kader	0°14′18.29E″	29°15′41.81N″	288 m
Omrokba	A17		Ouled El Hadj Zaouiat Kounta	0°12′00.52E″	27°13′00.28N″	189 m
Sabagha	A18		Touat	0°14′12.69E″	27°51′25.92N″	269 m
Bahamoud	A19		Aougrout	0°15′00.00E″	28°45′00.00N″	298 m
El Farh	A20		Tilouline	0°08′24.00E″	27°05′.48.00N″	170 m
Manga	A21		Touat Soukt	0°17′00.00E″	27°52′00.00N″	258 m
El Menea	A22		El Habla Tsabit	0°13′06.97E″	28°21′.01.45N″	260 m
Amouche	A23		Deldoul	0°15′34.77E″	29°01′10.40N″	282 m

Table 1. (cont.)

Varieties	Code	Region	Localities	Longitudes	Latitudes	Altitude
Hamra	A9	Tamanrasset	Tamanrasset	5°31′38E″	22°47′13N″	1400 m
Lakhfifa Hamra	A10		Abalessa	4°04′10.36E″	22°11′16.00N″	601 m
Manga1	A11		Abalessa	4°04′10.36E″	22°11′16.00N″	601 m
Manga2	A12		Abalessa	4°04′10.36E″	22°11′16.00N″	601 m
Manga3	A13		Abalessa	4°04′10.36E″	22°11′16.00N″	601 m
Bent M′barak1	A14		Tazrouk	6°15′40.92E″	23°25′17.12N″	1814 m
Bent M′barak2	A15		Tazrouk	6°15′40.92E″	23°25′17.12N″	1814m
Manga2	A16		Tazrouk	6°15′40.92E″	23°25′17.12N″	1814 m
El Hamra	A24		Iglen	4°51′0E″	22°52′59.88N″	1 400 m
Bent M′barak	A25		Tazrouk	6°15′40.92E″	23°25′17.12N″	1814 m
Manga Baydha	A26		Idless	5°56′03.64E″	23°49′03.80N″	1398 m
Labyadh	A27		Tazrouk	6°15′40.92E″	23°25′17.12N″	1814 m
Manga1	A28		Tazrouk	6°15′40.92E″	23°25′17.12N″	1814 m

SSR results were also scored for presence (1) and absence (0) of amplified fragments. A cluster analysis was conducted based on Jaccard's dissimilarity coefficients. The tree topology was constructed based on the neighbor-joining (NJ) method and bootstrapping analysis with 1000 re-samplings using the software program DARwin version 5.0.158 (Perrier and Jacquemoud-Collet 2006). To infer relationships between the different cultivars, the software package Structure 2.3.1 (Pritchard et al. 2000; Falush et al. 2003; Evanno et al. 2005; Hubisz et al. 2009) was employed using Bayesian clustering methods. This process permitted to obtain the most consistent grouping of the twenty-eight studied cultivars and to identify if there are some putative admixed or exchanged genomes. To detect the number of genetically homogeneous groups (K) that best fits the data, ten replicates were performed for each level of K (K = 1 to K = 10) with 5000 iterations and 50,000 burning steps). The estimate of the most likely number of genetic groups K (K = 3) was performed with Structure Harvester following Evanno et al. (2005).

Table 2. Description of tested SSR primers
(https://wheat.pw.usda.gov/cgibin/GG3/report.cgi?class=probe;name)

Primer	Sequences	Motifs	Chromosome location	Alleles size (pb)
WMC 96 F WMC 96 R	TAGCAGCCATGCTTAGCATCAA GTTTCAGTCTTTCACGAACACG	CA	4A	280
WMC 97 F WMC 97 R	GTCCATATATGCAAGGAGTC GTACTCTATCGCAAAACACA	GT	5D	184
WMC 327 F WMC 327 R	TGCGGTACAGGCAAGGCT TAGAACGCCCTCGTCGGA	GT	5A	183
WMC 182 F WMC 182 R	GTATCTCACGAGCATAACACAA GAAAGTGTATGGATCATTAGGC	CT	7A	159
WMC 156 F WMC 156 R	GCCTCTAGGGAGAAAACTAACA TCAAGATCATATCCTCCCCAAC	CA	1B	211
WMC 261 F WMC 261 R	GATGTGCATGTGAATCTCAAAAGTA AAAGAGGGTCACAGAATAACCTAAA	GT	2A	110
WMC 238 F WMC 238 R	TCTTCCTGCTTACCCAAACACA TACTGGGGGATCGTGGATGACA	CA	4B	224
WMC 233 F WMC 233 R	GACGTCAAGAATCTTCGTCGGA ATCTGCTGAGCAGATCGTGGTT	CA	5D	260
WMC 168 F WMC 168 R	AACACAAAAGATCCAACGACAC CAGTATAGAAGGATTTTGAGAG	CT	7A	319
WMC 257 F WMC 257 R	GGCTACACATGCATACCTCT CGTAGTGGGTGAATTTCGGA	GA	2B	329

Results

SSR genetic diversity

The ten selected SSR markers produced a total number of 20 alleles. The number of the amplified alleles varied from one at the locus (WMC97, WMC168) to four for the locus WMC327 with a mean value of two alleles per locus. The allele size ranged from 100 pb (WMC261) to 400 pb (WMC257). Moreover, the allele frequency varied from 0.1 for the allele 230 pb (WMC156) to 1 respectively for the alleles 187 pb, 310 pb (WMC97, WMC168). The PIC values ranged from 0 (WMC97, WMC168) to 0.5 (WMC327, WMC233), averaging at 0.34. The observed heterozygosity (HO) varied from 0 for the primers (WMC97, WMC168) to 0.88 for the primer (WMC233) with an average of 0.55 (Table 3). The repartition of allele frequency according to the two populations (Adrar and Tamanrasset) presented a homogeny distribution and revealed the abundant presence of the alleles 187 pb (WMC97), 215 pb (WMC156) and 200 pb (WMC238). While the alleles 250 pb and 230 pb of the primers (WMC238 and WMC156) presented the lowest frequency < 0.2 (Fig. 1). The AMOVA test revealed that the major part of the total genetic variation occurred within populations (97%) and only 3% occurred among populations (Table 4). In conclusion, these results confirm the highest level of intra-population differentiation of local Saharan bread wheat and high gene flow (Table 1).

Table 3. Genetic parameters obtained from the ten microsatellite markers that were used to evaluate twenty eight investigated Algerian Saharan bread wheat cultivars

Locus	N	Na	Ne	PIC	I	Ho	He
WMC96	21	2.000	1.849	0.46	0.652	0.714	0.459
WMC97	29	1.000	1.000	0	0.000	0.000	0.000
WMC327	29	4.000	1.748	0.43	0.619	0.621	0.428
WMC182	29	2.000	1.998	0.5	0.693	0.966	0.499
WMC156	28	2.000	1.237	0.5	0.340	0.214	0.191
WMC261	29	2.000	1.859	0.2	0.655	0.724	0.462
WMC238	29	2.000	1.488	0.47	0.510	0.414	0.328
WMC233	26	2.000	1.997	0.33	0.692	0.885	0.499
WMC168	24	1.000	1.000	0.5	0.000	0.000	0.000
WMC257	28	2.000	1.645	0	0.581	0.536	0.392

N – number of loci; Na – No. of Different Alleles; Ne – No. of Effective Alleles; Ho – observed heterozygosity; He – excepted heterozygosity; PIC – polymorphism information content; I – Shannon's Information Index; AD – allelic diversity; PAF – principal allele frequency; PI – probability of identity.

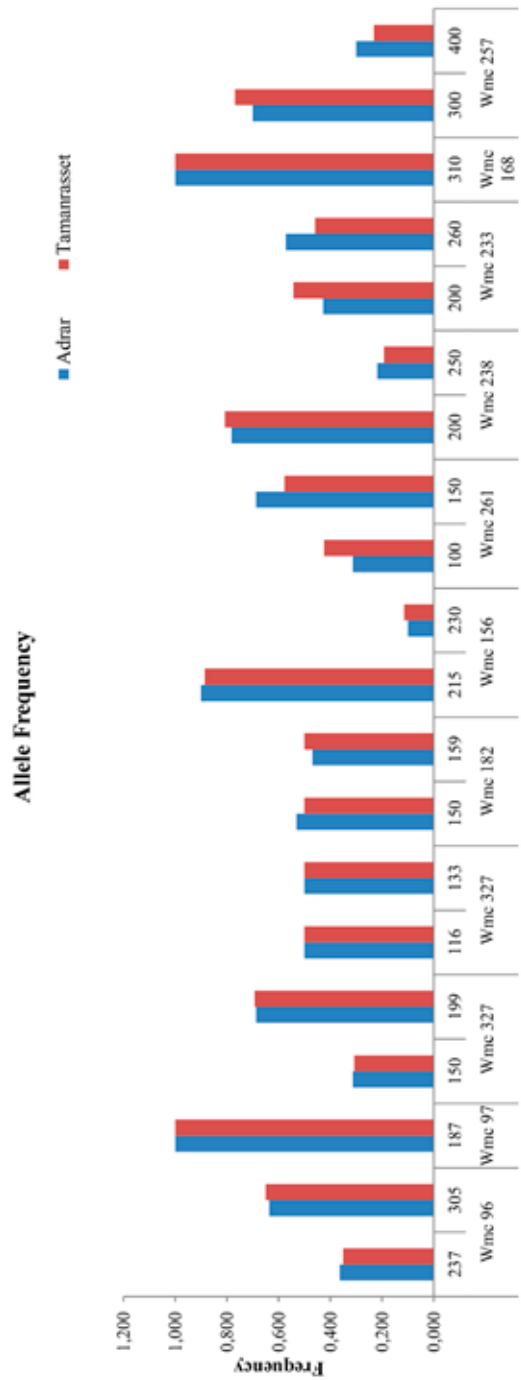

Figure 1. Allelic frequency of the ten tested microsatellites used to evaluate the genetic diversity of twenty-eight Algerian Saharan bread wheat cultivars

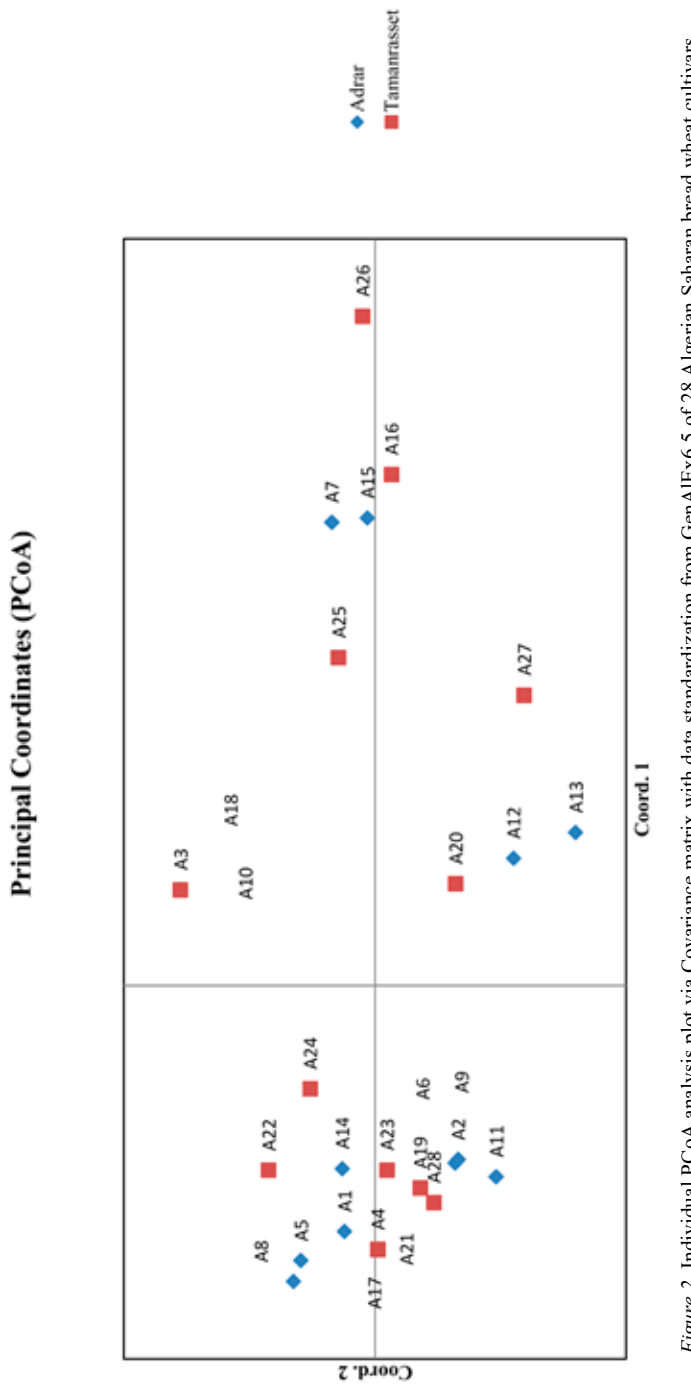

Figure 2. Individual PCoA analysis plot via Covariance matrix with data standardization from GenAlEx6.5 of 28 Algerian Saharan bread wheat cultivars

Table 4. Analysis of the molecular variance results based on ten SSR markers that were observed in twenty-eight Algerian Saharan bread wheat cultivars

Summary AMOVA Table					
Source	df	SS	MS	Est. Var.	%
Among Pops	1	5.649	5.649	0.135	3
Within Pops	27	100.351	3.717	3.717	97
Total	28	106.000		3.851	100

Genetic relationships and differentiation among local Algerian bread wheat cultivars

Genetic diversity levels

The data generated by the SSR study were analyzed using the bootstrapping and NJ method. Neis's genetic test indicated a strong positive correlation between Jaccard and Dice coefficient matrices with r = 0.99 and P = 0.001. Therefore, only the Jaccard coefficient matrix was used in subsequent analyses. All wheat accessions were readily separated

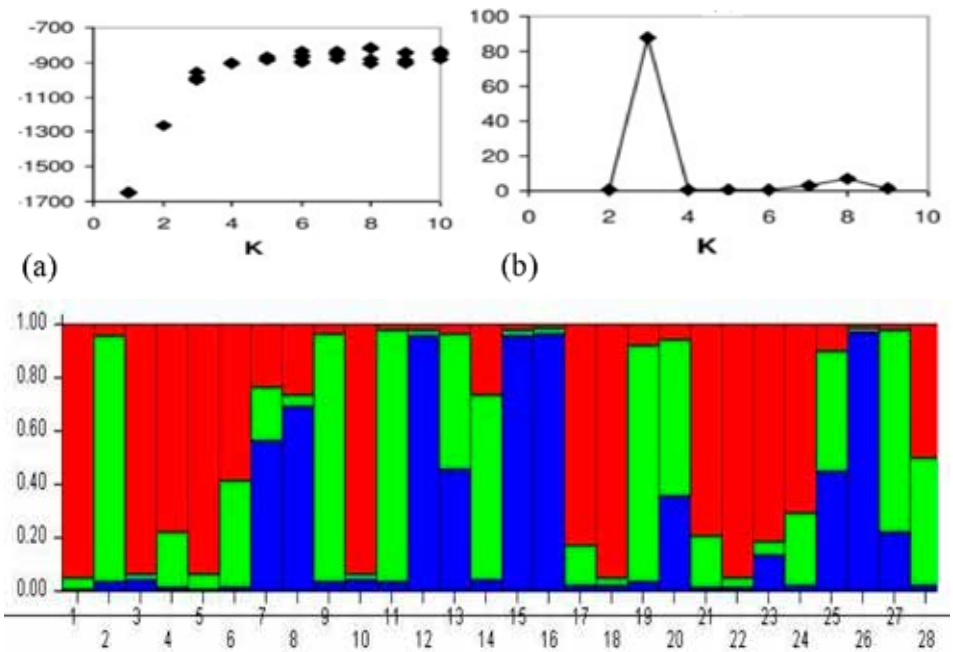

Figure 3. Structure plot generated by Neighbor joining (NJ) clustering technique showing relationships between twenty-eight bread wheat genotypes collected from the Algerian Sahara based on SSR profiling. Each vertical bar represents one soft wheat accession and the colors represent the three groups that were defined by the K value = 3. Genotypes from different clusters are represented with different colors: cluster 1 (red), cluster 2 (green) and cluster 3 (blue). (a) The relationship between the number of cluster (K) and the estimated likelihood of data [LnP(D)]. (b) The relationship between K and ΔK, that is, ΔK reached its maximum when K = 3, suggesting that all genotypes fell into one of the 3 clusters

from each other. The identity value ranged from 0.46 to 1. The highest genetic similarity (GS) (1) was observed between the accessions 'El Menea', 'Belmabroukd5', 'Omrokba', 'Manga1', 'LakhfifaHamra' and 'Belmabrouk', whereas, the lowest GS (0.49) was observed between cultivar 'Bahamoud', 'Omrokba' and 'BahmoudAM. Two large groups and four subgroups were found by cutting the dendrogram at a GS (0.5). There is no correlation between the molecular segregation and the geographical distribution of the tested varieties (Fig. 4). The first subgroup includes the varieties ('El Hamra', 'Sabagha', 'El Menea', 'Bent Mbarek', 'El Farh', 'Bahamoud', 'Omrokba' from Tamantit and Zaoui-

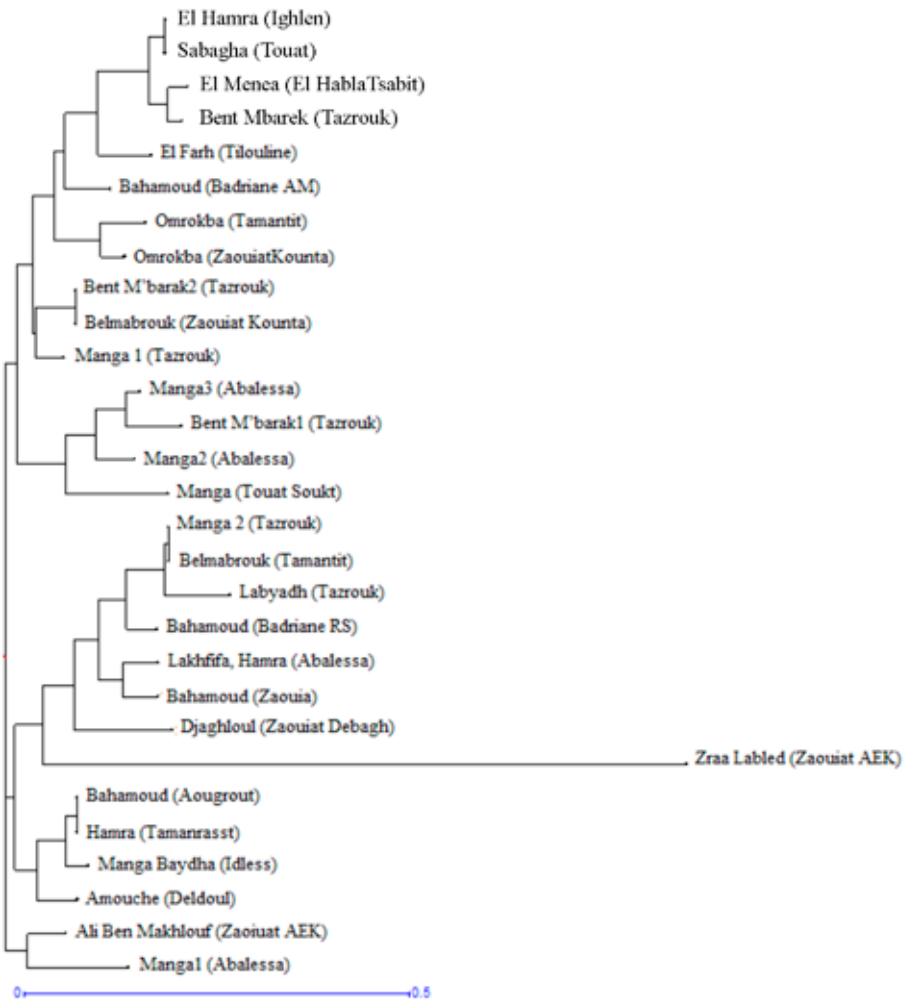

Figure 4. Neighbor-joining tree derived from microsatellite markers with branch lengths reflecting phylogenetic distances based on Jaccard's genetic distances between twenty-eight Algerian Saharan bread wheat cultivars

atKonta, 'Bent Mbarek2', 'Belmabrouk' and 'Manga1'). The second subgroup includes ('Manga3', 'Bent Mbarek1', 'Manga2', 'Manga', 'Bahamoud' and finally 'Manga Baydha). Whereas, the third sub-cluster regroups the accessions ('Zara Labeled', 'Manga2', 'Belmabrouk', 'Labyadh', 'Bahamoud', 'Lakhfifa' or 'Hamra', 'Bahamoud' and 'Djaghloul'). Finally, the fourth subgroup contains the varieties ('Bahamoud', 'El Hamra', 'Manga Bayda' and 'Amouche').

Principal component analysis

The (PCoA) permitted the segregation of the accessions in two major groups and five subgroups according to the first three-axis, which explain 55.08% of the total diversity (Fig. 2). The positive side of axis 1 separates the first two sub-groups, which include principally the varieties found in the oases of 'Adrar' and 'Tamanrasset'. The first subgroup clusters includes eight cultivars ('Belmabrouk', 'Lakhfifa' or 'El Hamra', 'Sabagha', 'El Farh', 'Bent M'barak', 'Manga Baydha' and 'Labyadh') and the second subgroup clusters encompasses five cultivars from ['Djaghloul', 'Manga2' from (Abalessa), 'Manga3', 'Bent M'barak2' and 'Manga2' from (Tazrouk)]. The negative side of axis 1 separates the second group which includes seven cultivars ('Omrokba', 'Bahamoud', 'El Menea', 'Amouche', 'El Hamra' and 'Manga1') and nine cultivars from Adrar and Tamanrasset ('ZraaLabled', 'Bahamoud', 'Omrokba', 'Belmabroukd5', 'Bahmoud AM', 'Ali Ben Makhlouf', 'Hamra', 'Manga1' and 'Bent M'barak1'. The projection of the accessions according to axis 2 segregates the first group into three mains subgroups, the first clusters contains only three cultivars ('Belmabrouk', 'LakhfifaHamra' and 'Sabagha') localized at the positive side of axis1 and axis 2, the second clusters with the cultivars ('Djaghloul', 'Bent M'barak2', 'Manga2', 'Bent M'barak' and 'Manga Baydha') where they are totally superposed with the positive side of the axis1 and the third group includes the cultivars 'Manga2', 'Manga3' and 'El Farh') localized at the positive side of axis 1 and the negative side of axis 2. However, the second major group consists of a single block of bread wheat cultivars.

Structure analysis

To better understand the segregation of the tested bread wheat according to the NJ method and the PCoA analysis, we tried to estimate the most likely number of genetic groups (K) with Structure Harvester (Evanno et al. 2005). It is well known that when K is approaching a true value, L (K) reaches a plateau and has a high variance between runs (Rosenberg et al. 2002). In the present study, the plateau was found at K = 3 (Fig. 3). Therefore, the bread wheat genome was divided by the predominant color into three main groups, red (group 1), green (group 2) and blue (group 3). The red group includes the cultivars ('ZraaLabled', 'Belmabrouk', 'Belmabrouk d5', 'LakhfifaHamra', 'Omrokba', 'Sabagha', 'Manga' and 'ElMenea'). The green group clusters incorporate the cultivars ('Bahamoud' from (Zaouia), 'Hamra', 'Manga1', 'Bahamoud' from (Aougrout) and 'Labyadh') and the blue group comprises the cultivars ('Ali Ben Makhlouf', 'Manga2' from

(Abalessa), 'Bent M'barak2', 'Manga2' from (Tazrouk) and 'Manga Baydha') respectively with a membership values more than 0.8. However, the genetic structure of Algerian Saharan wheat proved the existence of hybrid forms between the accessions of the red and the green groups as ('Bahmoud AM' and 'Manga1') and between the accessions of the red, green and blue groups as ('Djaghloul' and 'Manga1').

Discussion

The first investigation of local bread wheat resources in the oases of Algeria was based on morphological and physiological traits Ducellier (1930). The current inquiry presents the first molecular analysis essay to estimate the genetic variation of the local Saharan bread wheat genotypes in Algeria. SSR markers method was utilized to assess the genetic diversity of this patrimony, and this technique has been widely accepted as useful tools to estimate genetic diversity and divergence within and among populations (FAO 2011).

The data generated by the statistical analysis of the alleles produced by the ten SSR markers revealed an important variation of allele frequency passed from 0.1 to 1 and observed heterozygosity (Ho) ranged from 0 to 0.88 while the polymorphism information content (PIC) shifted from 0 to 0.55. These results are in line with the previous findings of Kara et al. (2016) revealing the low genetic diversity of local Algerian bread wheat landraces based on 16 SSR markers compared to the wild and introduced genotypes. However, the repartition of allele frequency according to the two populations (Adrar and Tamanrasset) disclosed the presence of allele 187 pb (WMC97) in the hole tested cultivars which confirm their resistance to drought. Alhosein and Miyuki (2012), in their analysis of novel QTLs for growth angle of seminal roots in wheat, proved the correlation between the presence of the allele 187 pb of the SSR (WMC97) and the resistance of the wheat accessions to drought. Therefore, the high frequent presence of allele's 187 pb from WMC97 in the studied Saharan Algerian bread wheat proved their high resistance to hydric stress and the urgency to conserve this patrimony, which has become increasingly imperative. The examination of special forms of the Saharan bread wheat has already led us to consider that despite the climatic vicissitudes and the grip of the sands gradually burying the oases, these special forms have remained as relics of the past in the shadows palm trees. These forms would have reached Algeria, thanks to the oases that were previously connected to the outside world only by caravans (Merdas and Yousfi 2005).

The results of the AMOVA analysis prove the high genetic diversity inside populations (H = 97) and otherwise a low diversity among the population (H = 3). Erroux (1963), in his study of oasis bread wheat, showed the richness and diversity of the forms inventoried in the Sahara in each of the two great groups bearded and mute. Connected by intermediaries, it distinguished forms with a whiteor red spike, with glumes or hairy hairless and provided either red or white grains. The low genetic variability observed between local populations of bread wheat can be explained by natural selection over several years and a selective selection by farmers in the region directed to the same strategies, which makes the varieties genetically closely (genetic convergence). Indeed, natural selection, generally due to climatic hazards and environmental stress, leads to the creation of suitable

germplasm and consequently a reduction in genetic variability through the disappearance of unsuitable genotypes. Salehi et al. (2018), in his study, proved that the genetic diversity of wild wheat based on SSR markers revealed a high intra-population polymorphism. This phenomenon is accentuated in autogamous species where cross-pollination is low compared to allogamous species where cross-pollination is mandatory. In wheat species, cross-pollination is in the order of 0 to 0.06 (Enjalbert and David 2000) which results in a low contribution of external genes and consequently a fall in genetic variability and creation of genetically close populations or meta-populations.

The statistical geometric distribution of the tested varieties based on PCoA, NJ method and structure analysis confirmed the existence of four major bread wheat classes in the Algerian Sahara and the absence of correlation between the SSR polymorphism and the geographical distribution of these cultivars. Erroux (1963) distinguishes on the bases of the morphological parameters four groups of bread wheat. Wheat with distinctly Saharan fancies characterized by short, broad, bulging glumes with an angled beak. The second class includes Saharan wheat with a speltoid form, which is a group of intermediate wheat between common and spelled-type wheat from Europe with forms of transition to bread wheat. Bellatreche et al. (2017); Merdas and Yousfi (2005) and Ducellier (1930) approached this class to a series of forms to particular characters that stand out by a rigid spike and marked hull glum. The third class incorporates bread wheat with a highly compact spike as the varieties 'Fartass', 'Tabelballa' and 'El khelou'. Finally, the fourth group encompasses Saharan wheat with attenuated characters suggested as forms from outside sources coming from the northern territories, or Niger and Chad (Merdas and Yousfi 2005). Therefore, it will be interesting to extend this study to other Saharan regions, integrating other aspects such as agronomical analysis and varietal behavior. This will allow the knowledge of these resources for a backup and a better valuation.

Thus, the creation of the genetic fingerprint database of the local bread wheat varieties is paramount to predict the performance of the succeeding generation and to study their genetic diversity, relationships, and heritage mechanisms. The genetic pool of this species constitutes a precious treasure to cope with the negative effects of climate change on the human diet, especially that the Saharan wheat genetic resources may constitute a real base to improve the resistance of this species to drought stress. The current study presents the first molecular investigation of the Saharan bread wheat in Algeria. Our research substantiates the results of the previous morphological analysis and approves the existence of three different groups besides a cluster of hybrid forms with an admixed genetic profile. This characterization work, of descriptive type, based on the molecular study will constitute a platform of selection program of the most productive varieties under conditions of thermal and drought stress.

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