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Assessment of the genetic diversity of onion cultivars (*Allium cepa*, Amaryllidaceae) collected in southern Benin

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Abstract: Onion is one of the widely consumed vegetables in most food preparations. The present study aims to evaluate the genetic diversity of onion cultivars in southern Benin in 2023. DNA isolation of the fourteen (14) morphotypes collected was carried out using the CTAB protocol and amplified by PCR using five RAPD markers. The observed polymorphism rate was 100%. A total of 35 alleles were scored with an average of 7 per locus. The Polymorphism Information Content (PIC) of loci varies from 0.734 to 0.806 with an average of 0.784. The loci OPA08 (Na = 8 alleles, PIC = 0.806) was the most polymorphic and the most discriminating. OPB08 (Na = 6 alleles, PIC = 0.734) was the least polymorphic and the discriminating loci. The rate of rare alleles was Ra = 31.42%. The lowest genetic distance (D = 0.09) was observed between PVOV and PVAL but the highest (D = 0.94) was between FPAL and BQOV genotypes. The dendrogram classified the morphotypes into four genetic groups with a dissimilarity coefficient of 40% confirmed by the Principal Coordinate Analysis. These results are globally significant for the definition of strategies for the improvement, conservation and sustainable use of onion genetic resources in Benin.

Keywords: *Allium cepa*, Genetic differentiation, RAPD marker, Genetic group, Benin.

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Introduction

The onion (*Allium cepa* L.) is a herbaceous monocotyledon belonging to the family Amaryllidaceae and the genus Allium, one of the largest genera composed of 750 species including the shallot (*Allium cepa* L. var. *aggregatum* G. Don), multiplying onion (*Allium fistulosum* L.), garlic (*Allium sativum* L.) and leek (*Allium ampeloprasum* L. var. *porrum*.) (Fritsch and Friesen, 2002). Onion is a diploid bulb vegetable with a chromosome number of 2n = 2x = 16 with a largest genome size of 15290 Mbps/1C (King et al., 1998). It is a culture with asexual propagation and presenting a great morphological diversity in terms of weight, presence of scales, color and shape of bulbs and leaves, height of the plant, color of flowers, fertility and bulbil development (Pooler and Simon, 1993; Akter et al., 2015). The onion is a vegetable plant native to Central Asia, much appreciated by most populations around the world for its fresh, slightly spicy taste and its milder, more generous flavor which increases with cooking. It is widely consumed throughout the year in the majority of food preparations. Because of these curative properties, onion is used to relieve patients of certain illnesses such as: digestive disorders, hyperglycemia, heart disease, certain forms of cancer, rheumatism and cough (Birlouez, 2020). Sought after for its many uses, the domestication of the onion has been accompanied over time by a selection of cultivars with significant bulb development during the first year of cultivation. Known to the Egyptians, Romans and Greeks, this species was first exploited as a medicinal plant before becoming a condiment or vegetable (Doyle and Doyle, 1987).

Among the most cultivated vegetables in the world, the onion is ranked second, preceded by the tomato and is produced at different latitudes between 10°S and 65°N (Foury and Schweisguth, 1992; Ricciardi et al., 2020). Given its importance, the onion is cultivated in more than 140 countries for an annual global production estimated at 93,226,400 tons (Sakatai et al., 2019). In 2020, according to FAO statistics, the five main onion producing countries are India (26,738,000 tons), China (23,723,552 tons), the United States of America (3,821,044 tons), Egypt (3,155,649 tons) and Algeria (1,665,671 tons). In Sub-Saharan Africa, Nigeria and Niger are the two leading onion producing countries with annual production of 1,382,044 tons and 1,310,444 tons respectively (FAO, 2021).

In Benin, onion cultivation is mainly done in the north in the Alibori department but also in the south of the country in the Littoral, Atlantique, Mono and Couffo departments (Assogba-Komlan et al., 2006; Sikirou et al., 2011; Bello et al., 2012). Although the onion production sector is faced with numerous constraints including pressure from pests causing low levels of yield, this speculation contributes to the creation of more than 600,000 direct jobs and constitutes an important source of employment in urban, peri-urban environments and especially the banks of rivers and/or valleys in certain areas (Baco et al., 2005; Sikirou et al., 2011). Onion production in 2020 in Benin is 77,362 tons for a yield of 128,062 hg/ha (FAO, 2021). This production is very low to cover the consumption need for this vegetable in Benin. Thus, to satisfy its customers, the Beninese market is flooded with a multitude of local onion varieties coming from West African producing countries but mainly from Niger, which ranks 7th in the world as an onion producing country with a production of 1,310,444 tons after Nigeria with 1,382,044 tons of onion produced (Assogba-Komlan et al., 2006; FAO, 2021).

There is a variability and heterogeneity of shapes and colors of onion bulbs marketed in Benin which would be due to natural inter and intra specific crossings. Which creates the existence of homonymy and synonymy in onion cultivars in Benin. It is therefore urgent to carry out a genetic characterization study of onion cultivars consumed in Benin in order to remove not only this homonymy and synonymy but also to establish improvement strategies in order to boost the yield of this major crop. Thus, the National Institute of Agricultural Research of Benin (INRAB) carried out agro-morphological characterization studies which consisted of collecting onion cultivars and organizing them into collections based on agro-morphological descriptors or characters of the species. These studies made it possible to identify six (06) varieties of onion cultivated in Benin. These are: Amani Violet, Tana Red, Texas Grano 502, Galmi White, Ares and Malanville Violet (Mensah et al., 2019).

Given the influence of environmental factors on descriptors, it is essential to characterize onion cultivars at the molecular level using nucleic acid markers. Thanks to the advent of new molecular techniques which have followed one another, studies of the genetic diversity of onions based on several types of molecular markers giving greater polymorphism and numerous rare allelic forms have therefore made it possible to construct different intra-specific classifications. Nucleic acid markers (RAPD, RFLP, AFLP, SSR, etc.) have been widely used for the molecular genetic characterization of the species throughout the world (Baldwin et al., 2012), (Khosa et al., 2013), (Ricciardi et al., 2020). The use of RAPD (Random Amplified Polymorphic DNA) markers would allow the development of unique DNA profiles of onion genotypes due to a high level of polymorphism, its wide distribution in the genome and its ability to provide greater information genetics (Wilkie et al., 1993).

Unfortunately, studies on the evaluation of genetic diversity based on onion nucleic acid markers are rare and almost non-existent in Benin. It is therefore essential to know the genetic diversity of onion cultivars that the beninese market abounds with. The objective of this study is to evaluate the genetic diversity of onion cultivars (*Allium cepa*, Amaryllidaceae) in southern Benin.

Materials and Methods

Sampling plant material

The plant material consists of 14 onion morphotypes selected from a collection of 104 accessions sampled during a survey in several markets in the Atlantic and Littoral departments in southern Benin. These morphotypes were selected based on the shape and color of the bulb (Table 1, Figure 1).

Biological material

Young onion leaves represent the biological material used in this genetic characterization study. So, the onion bulbs were potted in a greenhouse in order to have young leaves from which the DNA is extracted. Polyethylene bags filled with potting soil were used to sow these bulbs. Each pot was labeled according to the morphotype it contained and watered twice a day as needed before and after germination. Around ten days after the germination of the onion bulbs, the young leaves were removed using sterile scissors, then wrapped in aluminum foil and labeled (write the morphotype code and the date of the sampling). Young leaves are used in because cell division (interphase and mitosis) is occurring and more intense at their level, which allows many more new cells to be obtained and therefore a high concentration of DNA extract. Once in the laboratory, the samples were stored in a refrigerator at a temperature of 4°C.

DNA isolation

The Laboratory of Molecular Genetics and Genome Analysis (LGMAG) of the Department of Genetics and Biotechnologies of the University of Abomey-Calavi (Benin) served as a framework for the molecular analyses. The protocol used for the extraction of genomic DNA from onion morphotypes is that using CTAB (Doyle and Doyle, 1987). Thus, 0.5 g of young leaf of each onion morphotype was weighed and then ground in a porcelain mortar with 1 ml of 2X CTAB solution. The ground material was then poured into a 2 ml Eppendorf tube then 50 µl of 20% sodium dodecyl sulfate (SDS) were added then the mixture was homogenized and incubated at 65°C for 1 hour. After 60 min, 800 µl of Chloroform Isoamyl Alcohol (CIA) in the proportions 24/1 were added to the cooled mixture then centrifuged at 10,000 rpm for 15 min. The upper aqueous phase containing the DNA is collected in a new 1.5 ml tube to which 800 µl of cold isopropanol was added and together was incubated at -20°C for 30 min. After incubation, the mixture was homogenized by inversion to precipitate the DNA. Centrifugation at 10,000 rpm for 10 min was done and the supernatant poured; 500 µl of 70% ethanol were added to the DNA pellet and centrifugation at 10,000 rpm for 5 min was done to purify the DNA. The DNA pellet is then dried and then taken up in 100 µl of Tris EDTA.

Verification of the DNA extract was carried out by electrophoresis on a 1% agarose gel. A mixture of 2 µl of DNA extract and 8 µl of 2X loading blue were deposited in the wells of the gel and migrated at 100V for 15 min with 1X TBE buffer. After migration, the gel was stained with ethidium bromide (0.1%BET) for 15 min then rinsed with

distilled water for a few minutes. Then the gel was visualized with a UV transilluminator.

RAPD markers

Five (05) RAPD markers (OPA02, OPA08, OPB05, OPN08 and OPB08) selected were used to evaluate the genetic diversity of the cultivars collected (Wilkie et al., 1993). The most polymorphic and discriminative markers (revealed in other research on the species) were selected to screen the collection of morphotypes using a thermal cycler. The reaction medium for the PCR is made to a final volume of 25 µL consisting of: 2.5 µL of PCR Buffer, 0.75 µL of MgCl2, 1 µL of dNTP, 7 µL of primer (primers), 0.25 µl of Taq polymerase, 10.5 µL of H2O and 3µl of DNA (Wilkie et al., 1993). The thermal cycler used for the amplification was the Peltier-Effect Cycling type (PTC 100TM) with an amplification program consisting of an initiation at 94°C for 5 min and 41 reaction cycles. Each cycle consists of denaturation at 94°C for 30 seconds, annealing of the primers at 37-44°C for 30 seconds and elongation carried out at 72°C for 1 min and was finished with a final extension at 72°C for 7 min (Wilkie et al., 1993).

The PCR products were separated by electrophoresis on a 3% agarose gel run at 80 V for 45 min to 1 h with 1X TBE buffer. The gel was stained with 0.1% BET for 15 min then rinsed with distilled water for 5 min. The bands were visualized on screen using a Trans UV illuminator (Figure 2).

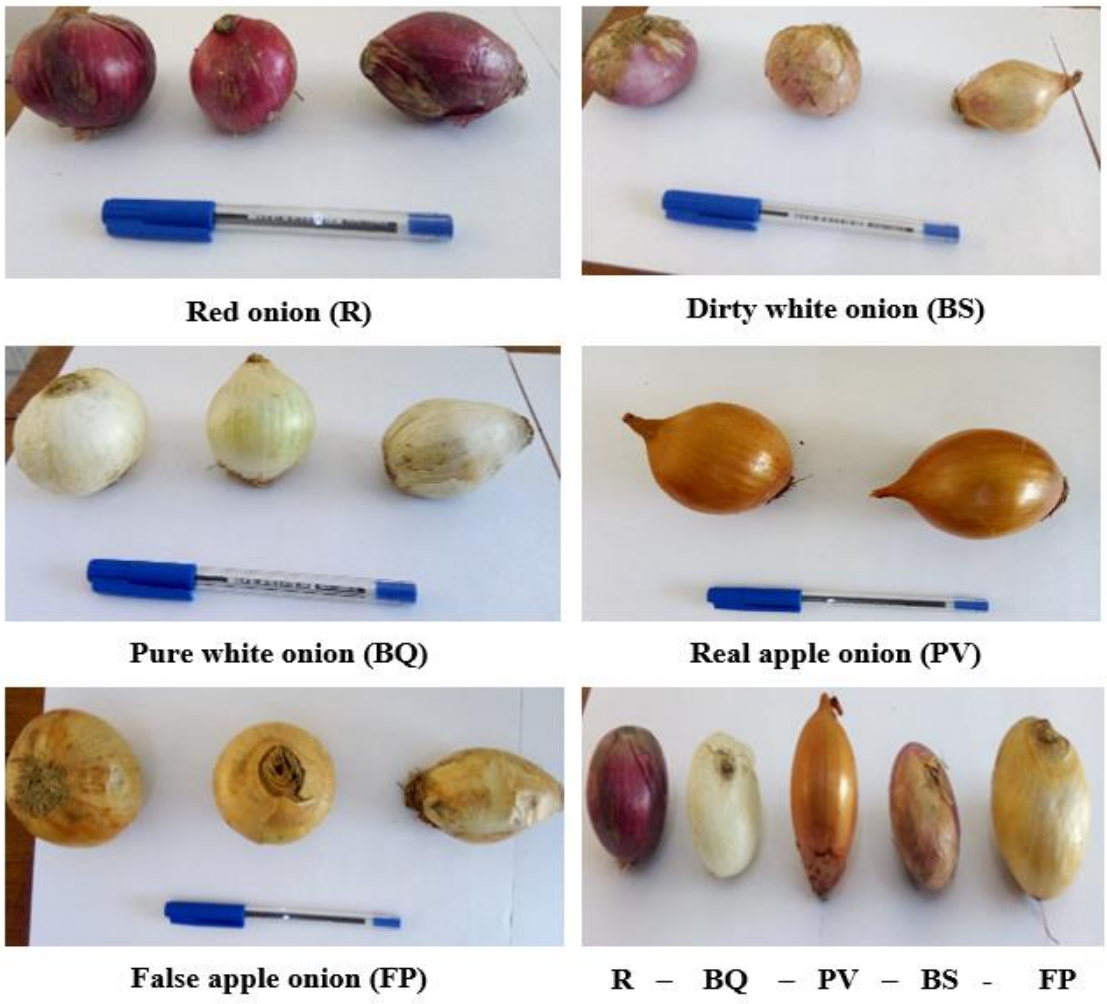

Figure 1. Onion morphotypes.

Table 1. Characteristics of selected onion morphotypes.

Cultivars names	Meaning of names	Shape of cultivars	Morphotypes code
Ayo massa vovo	Red onion	Elongated	RAL
		Flattened	RAP
		Ovoid	ROV
Ayo massa pomme	Real apple onion	Elongated	PVAL
		Ovoid	PVOV
Ayo massa pomme wégo	False apple onion	Elongated	FPAL
		Flattened	FPAP
		Ovoid	FPOV
Ayo massa wéwé tété	Pure white onion	Elongated	BQAL
		Flattened	BQAP
		Ovoid	BQOV
Ayo massa wéwé	Dirty white onion	Elongated	BSAL
		Flattened	BSAP
		Ovoid	BSOV

Data analysis

The bands obtained at each locus were recorded as allelic compositions. The absence and presence of bands are coded 0 and 1 respectively. The data obtained are recorded in an Excel sheet and constitute the analysis matrix. Genetic diversity parameters such as the polymorphism rate (P), allelic richness (Ra), the rate of rare alleles (Ar) and the Information Content of the polymorphism, PIC (Polymorphism Information Content) are estimated. The polymorphism rate is calculated by the number of polymorphic markers out of the total number of markers used. Allelic richness represents the number of alleles per locus. An allele is qualified as rare when its frequency (fi) is less than or equal to five (05) percent (fi ≤ 5%). The PIC values are calculated according to the formula: PIC = 1- Σ fi^2 with fi, the frequency of each allele (Agbo et al., 2021). The PIC value varies from 0 (monomorphic and non-discriminating locus) to 1 (highly discriminating loci, with several alleles each in low and equal frequency). Based on the binary matrix (0/1), genetic distances from (Nei, 1972) are calculated between pairs of morphotypes. To access the structure within the collection, a dendrogram is constructed according to the UPGMA method (Unweighted Pair-Group Method using the Arithmetic average) following the SAHN procedure (Sequential Agglomerative Hierarchical Nested method) of the NTSYS software version 2.11a (Rohlf 2000). In addition, to confirm the possible groupings of the cultivars analyzed, the DCENTER and EIGEN procedures of this software are used to carry out a Principal Coordinate Analysis (PCoA) based on the matrix of genetic coordinates in order to better appreciate the genetic differentiation between the groups obtained.

Table 2. Genetic parameters of the onion RAPD Primers used (Wilkie et al. 1993).

Primers	Primer sequence	PIC	Ra	Ar
OPA02	TGCCGAGCTG	0.795	7	2
OPA08	GTGACGTAGG	0.806	8	2
OPB05	TGCGCCCTTC	0.780	7	2
OPB08	GTCCACACGG	0.734	6	3
OPN08	ACCTCAGCTC	0.805	7	2
Mean	-	0.784	7	-

Results

Polymorphism and genetic variability

All of the RAPD markers used turned out to be polymorphic, i.e. a polymorphism rate of 100%. In total, 35 alleles were noted with an average of 7 per marker. The information content of the

polymorphism (PIC) ranges from 0.734 to 0.806 with an average of 0.784. The most polymorphic marker is the OPA08 marker with 8 alleles and the least polymorphic is the OPB08 marker with 6 alleles. The most discriminating marker is OPA08 with a PIC of 0.806 while the least discriminating is OPB08 with a PIC of 0.734. The rate of rare alleles is 31.42% (11 rare alleles out of 35) (Table 2).

Genetic structure of the collection

In order to evaluate the genetic structuring of onion morphotypes, a genetic distance matrix based on dissimilarity was constructed (Table 3). The lowest genetic distance (D = 0.09) is observed between the PVOV and PVAL morphotypes. On the other hand, the highest genetic distance (D = 0.94) is observed between the cultivars FPAL and BQOV on the one hand and between ROV and PVAL on the other hand. Dendrogram obtained from the cluster analysis of the 14 morphotypes, using the average distance algorithm (UPGMA SAHN method analysis), revealed four genetic groups with a dissimilarity coefficient proposed by the analysis procedure of 40% (Figure 3). The first group is made up of 2 morphotypes namely: PVAL and PVOV which are onion morphotypes qualified as true apples. The second group only includes quality white morphotypes such as BQAP, BQOV and BQAL.

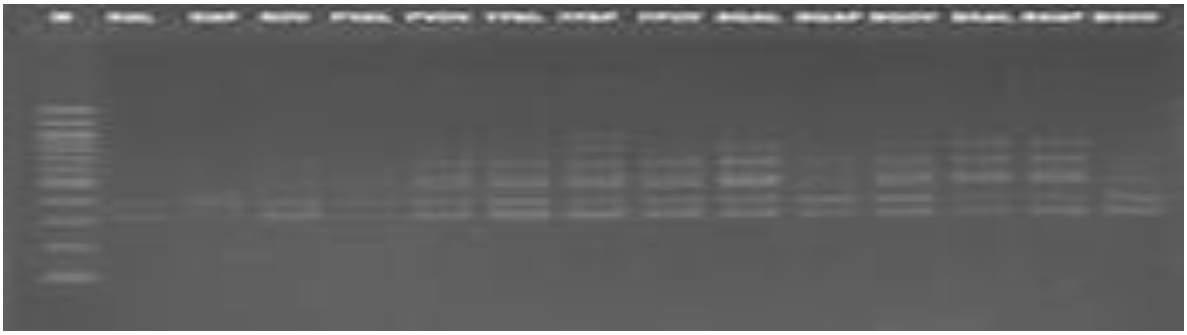

Figure 2. Polymorphic bands within the gel profile generated by the OPN08 marker used in the study. The codes correspond to the initials of the onion morphotypes and M: Size Marker.

Table 3. Genetic distance dissimilarity matrix of Nei (1972) estimated between different onion morphotypes.

	PVAL	ROV	BQAP	RAL	RAP	BQOV	BQAL	PVOV	BSAL	FPAP	FPAL	BSOV	FPOV	BSAP
PVAL	0.00													
ROV	0.94	0.00												
BQAP	0.40	0.52	0.00											
RAL	0.43	0.25	0.38	0.00										
RAP	0.35	0.42	0.48	0.22	0.00									
BQOV	0.43	0.69	0.20	0.42	0.51	0.00								
BQAL	0.37	0.59	0.24	0.29	0.37	0.37	0.00							
PVOV	0.09	0.82	0.53	0.46	0.46	0.37	0.50	0.00						
BSAL	0.41	0.51	0.59	0.32	0.58	0.51	0.54	0.27	0.00					
FPAP	0.50	0.51	0.72	0.25	0.49	0.63	0.54	0.53	0.21	0.00				
FPAL	0.64	0.66	0.91	0.52	0.52	0.94	0.69	0.66	0.41	0.32	0.00			
BSOV	0.27	0.54	0.50	0.28	0.28	0.54	0.37	0.38	0.24	0.24	0.35	0.00		
FPOV	0.35	0.58	0.65	0.36	0.43	0.69	0.52	0.37	0.25	0.18	0.35	0.21	0.00	
BSAP	0.71	0.62	0.73	0.34	0.54	0.77	0.40	0.90	0.43	0.23	0.36	0.36	0.41	0.00

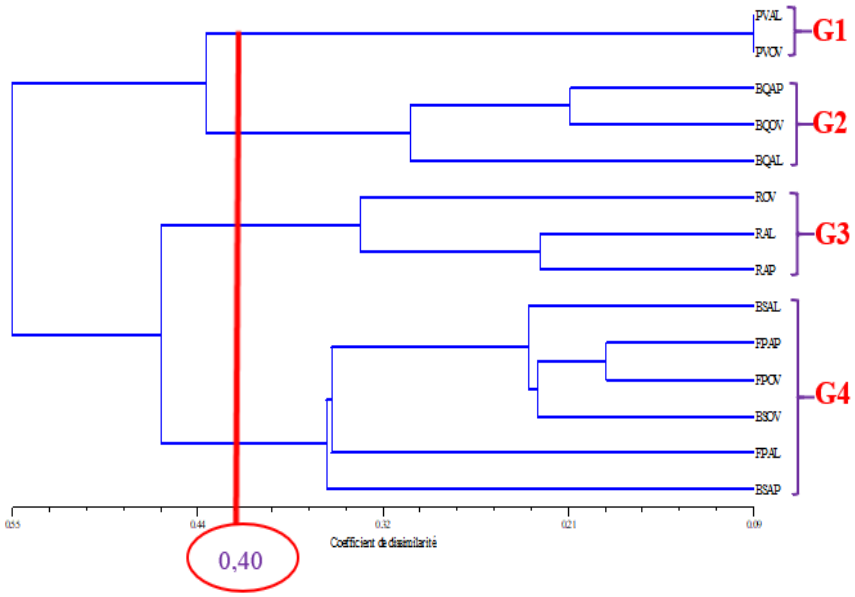

Figure 3. Dendrogram of onion morphotypes.

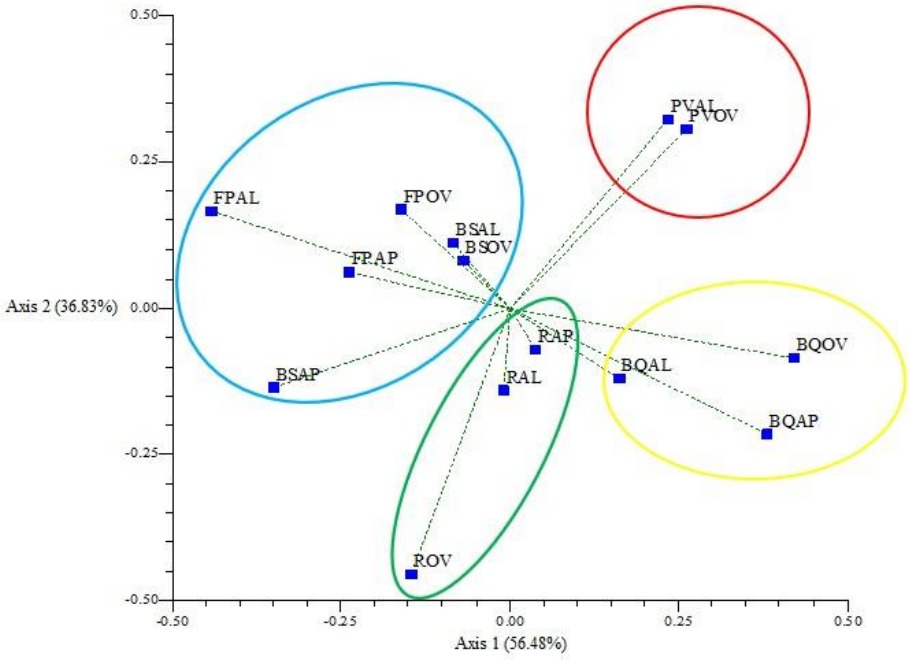

Figure 4. Principal Coordinate Analysis (PCoA) of onion morphotypes. The third group is made up only of Red morphotypes such as ROV, RAL and RAP. Finally, the fourth group is composed of a mixture of morphotypes of simple white onions and false apples such as BSAP, BSOV, BSAL, FPAP, FPAL, FPOV. This classification of the 14 morphotypes into four groups is confirmed by Principal Coordinate Analysis (PCoA). The first two axes express 93.31% of the total variation with 56.48% for axis 1 and 36.83% for axis 2.

Discussion

The onion is an agricultural crop of great importance in West Africa, the subject of intensive trade between countries. The onion sector constitutes for the majority of producers in this region a means of meeting daily needs. But several poorly performing local varieties are produced in these different countries, particularly in Benin. The varietal selection of a species involves its characterization with genetic markers which provide information on the genetic diversity of the species by referring to genome differences ranging from the rearrangement of a single base pair to an entire chromosome (Hamrick and Godt, 1996). Rouamba et al. (1994) report that the color and shape of onion bulbs are the main morphological descriptors that help differentiate African varieties. Variations in genome interactions with the environment reveal notable changes in plant diversity (Huang and Han, 2014). It should be noted that genetic diversity is a fundamental strategy in improving cultivars in terms of productivity and also for the conservation of agricultural crops (Sudha et al., 2019). Twenty-eight (28) morphological markers (descriptors) were identified from characters of onion bulbs, leaves, stems, flowers and seeds (Rabiou et al., 2015). Although these markers are easily observed by eye, they have the disadvantage of being dominant, influenced by the environment and often dependent on the stage of development of the plant (Cramer and Havey, 1999). However, nucleic acid markers (RAPD, RFLP, AFLP, SSR, etc.) directly resulting from existing polymorphism at the DNA level are very useful to differentiate the different varieties of onion, to distinguish the species from other cultivated species and spontaneous species of the genus *Allium* and to analyze the levels of introgression between the onion and other species of the genus (Rabiou et al., 2015). RAPD markers, although dominant, are widely used for the molecular genetic characterization of onion genetic resources (Sudha et al., 2019). This wide use is justified by the specificity, dominance, relatively high discriminating power, wide distribution (present along the genome) and multi-allelicism of RAPD markers. The results of the present study confirm this effectiveness of these markers by the high rate of polymorphism obtained (100%) and the high value of the average PIC (0.784).

The RAPD markers were able to group the collection of onions studied on the basis of molecular traits close to the color of the bulbs but not their shapes. Similar results were obtained by (McCallum et al., 2008)and (Khar et al., 2011)on the molecular characterization of onion with microsatellite markers. (Sudha et al., 2019)obtained 2 genotypic groups with 16 RAPD and SSR primers on a collection of nine (09) onion cultivars. This could mean that the shape of the onions (rounded, elongated or flattened) is not of genotypic origin but depends on environmental factors (climatic and edaphic). Indeed, the color of the onion bulb is mainly governed by a set of genes with Mendelian inheritance (Rieman, 1931). According to El-Shafie and Davis (1967), the white color of the bulb can be attributed either to an incompletely dominant color inhibitor gene (II), which suppresses all coloring, or to a recessive gene (rr) leading to the colorless mutants appearing in red varieties, yellow or brown. This could explain the predominance of white morphotypes. Kim et al. (2004) indicate the existence of another independent allele (P) which controls the purple color of the bulbs. According to Fossen et al. (1996), the presence of flavonoid compounds from the anthocyanin family produces colors in the bulb varying from red to purple. It should be noted that the genetic groups obtained in this study include cultivars belonging to different local varieties. These morphotypes would be synonyms.

The literature has documented the existence of six (06) varieties of onion cultivated in Benin (Mensah et al., 2019). These varieties found in southern Benin come from local crops and also imports. The four (04) genetic groups obtained in the present work corroborate these different varieties, apart from the cultivars qualified as true apple. In fact, this group of morphotypes is a genetically modified variety imported by traders. The genetic group of red onion morphotypes corresponds to the varieties Rouge de Tana, Violet d'Amani, Violet de Malanville and Ares; the white quality group represents onions of the Blanc de Galmi variety; the heterogeneous group consisting of simple white morphotypes and false apples corresponds to the Texas Grano 502 varieties. These cultivars bearing different local

names but which belong to the same genotypic class could be synonyms. Indeed, according to the work of (Boukary et al., 2012) and those conducted by Rabiou et al. (2015) in Niger, certain synonyms of onion names designate different ecotypes, but these ecotype names vary depending on the language of the producer; the same ecotype can have different vernacular names from one site to another. This synonymy is therefore lifted by this marker.

Also, we note the massive use of improved onion varieties in Africa and in particular in Benin which could lead to the loss of the genetic diversity of this very important crop. The presence in Benin of numerous imported varieties resulted in the relatively high rate of rare alleles (31.42%) obtained in the present study of the characterization of the onion collection which is explained by gene flow during exchanges. onion seed companies and the strong heterogeneity of onion cultivars present in southern Benin.

To avoid this decline in genetic structure, it is essential to take measures to conserve the germplasm of the species (Rouamba et al., 2001). It is in this sense that FAO through RADHORT (African Horticulture Development Network) and IPGRI (International Plant Genetic Resources Institute), now Bioversity International, had set up networks to coordinate the collection, conservation and use of wild species, improved varieties, farmer varieties and ecotypes of onion in Africa (Currah, 2002).

Conclusion

This summary study has highlighted a significant level of diversity of onion cultivars in southern Benin. The molecular genetic characterization of onion cultivars with RAPD markers made it possible to determine the genetic structure of the 14 onion morphotypes in four (04) genotypic groups. These results show that the local variety names given by traders and producers do not reflect perfect identity of the genotype of the cultivars. These results are generally significant for the definition of strategies for the improvement, conservation and sustainable use of onion genetic resources in Benin.

Supplementary Materials

No supplementary material is available for this article.

Author Contributions

Conceptualization, methodology, formal analysis, writing—original draft preparation, R.I.A.; read the protocol and improved the manuscript drafted, A.A.M. and D.M.; collection and sampling, R.I.A. and L.K.; molecular analysis, R.I.A., P.S. and GA; validation, writing—review and editing, R.I.A., G.L.D. and C.A. All authors have read and approved the final manuscript.

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Conflicts of Interest Statements

The authors declare that they have no conflict of interest.

References

Agbo, R.I., Missihoun, A., Montcho, D., Dagba, R., Sédah, P., and Agbangla, C. (2021). Spatial scale patterns of genetic diversity and gene flow in populations of sweet detar (*Detarium microcarpum* Guill. & Perr.; Fabaceae). *Annu Res Rev Biol* 37(5).

Akter, M., Biswas, A., Siddique, S., Hossain, S., and Ivy, N. (2015). Estimation of genetic diversity in onion (*Allium cepa* L.). *The Agriculturists* 13(1): 26-34.

Assogba-Komlan, F., Sikirou, R., Singbo, A., and Azagba, J. (2006). *Mieux conduire la culture de l'oignon sous regime pluvial au Sud du Bénin. Référentiel technico-économique (RTE).* Bénin.

Baco, M., Bello, S., and Assogba-Komlan, F. (2005). Etude socio-économique de la production et de la commercialisation de l'oignon dans l'Alibori. *Bull de la Recherche Agron du Bénin* 47: 26-37.

Baldwin, S., Pither-Joyce, M., Wright, K., Chen, L., and McCallum, J. (2012). Development of robust genomic simple sequence repeat markers for estimation of genetic diversity within and among bulb onion (*Allium cepa* L.) populations. *Mol Breed* 30: 1401-1411.

Bello, S., Amadji, G., Gbehounou, G., Aho, N., and Ahanchede, A. (2012). Influence de la densité de repiquage sur l'enherbement et la production d'oignon au Nord-est du Bénin. *J Animal Plant Sci* 15(1): 2074-2082.

Birlouez, É. (2020). Petite et grande histoire des légumes. *Petite et grande histoire des légumes*: 1-176.

Boukary, H., Roumba, A., Adam, T., Barage, M., and Saadou, M. (2012). Interaction between onion ecotypes variability and agroclimatics factors in Niger. *Tropicultura* 30(4): 209-215.

Cramer, C.S., and Havey, M.J. (1999). Morphological, biochemical, and molecular markers in onion. *HortScience* 34(4): 589-593.

Currah, L. (2002). 16 Onions in the tropics: cultivars and country reports. *Allium crop science: Rec Adv* 2(17): 379.

Doyle, J.J., and Doyle, J.L. (1987). A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochem Bull* 19: 11-15.

El-Shafie, M., and Davis, G.N. (1967). Inheritance of bulb color in the onion (*Allium cepa* L.). *Vegetable Crops of Russia*.

FAO, F. (2021). Agriculture Organization of the United Nations. FAOSTAT–food and agriculture data: http://www. FAO. org/faostat/en/# data/FBS, Rome (Headquarters). *Accessed online*.

Fossen, T., Andersen, Ø.M., Øvstedal, D.O., Pedersen, A.T., and Raknes, Å. (1996). Characteristic anthocyanin pattern from onions and other *Allium* spp. *J Food Sci* 61(4): 703-706.

Foury, C., and Schweisguth, B. (1992). Onion. *Amélioration des espèces végétales cultivées: Objectifs et Critères de Sélection.*: 406-473.

Fritsch, R., and Friesen, N. (2002). Evolution, domestication and taxonomy. *Allium crop science: Rec Adv*: 5-30.

Hamrick, J., and Godt, M.W. (1996). Effects of life history traits on genetic diversity in plant species. *Philosophical Transactions of the Royal Society of London. Series B: Biological Sciences* 351(1345): 1291-1298.

Huang, X., and Han, B. (2014). Natural variations and genome-wide association studies in crop plants. *Annu Rev Plant Biol* 65: 531-551.

Khar, A., Lawande, K., and Negi, K. (2011). Microsatellite marker based analysis of genetic diversity in short day tropical Indian onion and cross amplification in related *Allium* spp. *Genet Resour Crop Evol* 58: 741-752.

Khosa, J., Dhatt, A., Negi, K., and Singh, K. (2013). Characterization of Allium germplasm using bulb onion derived SSR markers. *Crop Improv* 40(1): 69-73.

Kim, S., Binzel, M.L., Yoo, K.S., Park, S., and Pike, L.M. (2004). Pink (P), a new locus responsible for a pink trait in onions (*Allium cepa*) resulting from natural mutations of anthocyanidin synthase. *Mol Genet Genomics* 272(1): 18-27.

King, J., Bradeen, J., Bark, O., McCallum, J., and Havey, M. (1998). A low-density genetic map of onion reveals a role for tandem duplication in the evolution of an extremely large diploid genome. *Theor Appl Genet* 96: 52-62.

McCallum, J., Thomson, S., Pither-Joyce, M., Kenel, F., Clarke, A., and Havey, M.J. (2008). Genetic diversity analysis and single-nucleotide polymorphism marker development in cultivated bulb onion based on expressed sequence tag–simple sequence repeat markers. *J Am Soc Hort Sci* 133(6): 810-818.

Mensah, A.C.G., Sikirou, R., Assogba-Komlan, F., Yarou, B.B., Midingoyi, S.K., Honfoga, J., Dossoumou, M.E., Kpéra, G.N., and Djinadou, A.K.A. (2019). *Mieux produire l'oignon au Bénin. Référentiel technico-economique (RTE). MAEP/INRAB/FIDA/ProCar/PADMAR/World Vegetable Center/Bénin.* Bénin.

Nei, M. (1972). Genetic distance between populations. *Midl. Nat.* 106(949): 283-292.

Pooler, M., and Simon, P. (1993). Characterization and classification of isozyme and morphological variation in a diverse collection of garlic clones. *Euphytica* 68: 121-130.

Rabiou, A., Bakasso, Y., Adam, T., Saadou, M., and Baudoin, J.-P. (2015). Biologie, diversité et outils pour l'analyse de la diversité génétique de l'oignon, *Allium cepa* L.(synthèse bibliographique). *Biotech, Agro, Société et Envir* 19(2).

Ricciardi, L., Mazzeo, R., Marcotrigiano, A.R., Rainaldi, G., Iovieno, P., Zonno, V., Pavan, S., and Lotti, C. (2020). Assessment of genetic diversity of the "acquaviva red onion"(*Allium cepa* L.) apulian landrace. *Plants* 9(2): 260.

Rieman, G.H. (1931). Genetic Factors for Pigmentation in the Onion and their Relation to Disease Resistance.

Rohlf , F. (2000). NTSYS-pc: numerical taxonomy and multivariate analysis system, version 2.1. *New York: Exeter Software*.

Rouamba, A., Sandmeier, M., Sarr, A., and Ricroch, A. (2001). Allozyme variation within and among populations of onion (*Allium cepa* L.) from West Africa. *Theor Appl Genet* 103: 855-861.

Rouamba, A., Sarr, A., and Ricroch, A. (1994). Dynamic management of genetic resources of *Allium cepa* L.(onion) in West Africa. *Acta Hortic* 443: 185-190.

Sakatai, D.P., Chendjou, R., Bassala, J.-P.O., Sobda, G., Kamga, R., and Hamidou, A. (2019). Caractérisation de cinq variétés d'oignons (*Allium cepa* L.) à partir des paramètres physiques de la maturation des bulbes en vue d'optimiser leur production à l'Extrême-Nord Cameroun. *Afr Sci* 15(1): 314-331.

Sikirou, R., Hoteigni, J., Godonou, I., James, B., Grehounou, G., and Assogba-Komlan, F. (2011). Performance of varieties of Gboma (*Solanum macrocarpon*) under disease pressure with organic amendment in Southern Benin. *Annal Des Sci Agro* 15(2): 205-216.

Sudha, G.S., Ramesh, P., Sekhar, A.C., Krishna, T.S., Bramhachari, P., and Riazunnisa, K. (2019). Genetic diversity analysis of selected onion (*Allium cepa* L.) germplasm using specific RAPD and ISSR polymorphism markers. *Biocatal Agric Biotechnol* 17: 110-118.

Wilkie, S.E., Isaac, P.G., and Slater, R.J. (1993). Random amplified polymorphic DNA (RAPD) markers for genetic analysis in Allium. *Theor Appl Genet* 86: 497-504.

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مقاله پژوهشی

ارزیابی تنوع ژنتیکی ارقام پیاز (*Allium cepa*، Amaryllidaceae) جمع‌آوری شده در جنوب بنین

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چکیده: پیاز یکی از سبزیجات پرمصرف در مواد غذایی بشمار می‌رود. مطالعه حاضر با هدف بررسی تنوع ژنتیکی ارقام پیاز در جنوب بنین در سال ۲۰۲۳ انجام شد. استخراج DNA ۱۴ مورفوتیپ جمع‌آوری‌شده با استفاده از پروتکل CTAB انجام شد و با استفاده از پنج آغازگر RAPD در PCR تکثیر شد. میزان پلی‌مورفیسم مشاهده شده ۱۰۰٪ بود. در مجموع ۳۵ آلل با میانگین ۷ در هر جایگاه امتیازدهی گردید. محتوای اطلاعات چندشکلی(PIC) جایگاه‌ها از ۰،۷۳۴ تا ۰.۸۰۶ با میانگین ۰.۷۸۴ متغیر بود. آغازگر OPA08 (Na = PIC = 8 0.80)، بیشترین چندشکلی و تمایز را نشان داد. آغازگر OPB08 (Na = 6 آلل، PIC = 0.734) دارای کمترین چندشکلی و جایگاه متمایزکننده بود. میزان آلل‌های نادر Ra = 31.42 درصد بود. کمترین فاصله ژنتیکی (D = 0.09) بین ژنوتیپ‌های PVOV و PVAL مشاهده شده، در حالی‌که بیشترین فاصله (D = 0.94) بین ژنوتیپ‌های FPAL و BQOV بود. دندروگرام مورفوتیپ‌ها را به چهار گروه ژنتیکی با ضریب عدم تشابه ۴۰٪ خوشه‌بندی نمود که نتایج توسط تجزیه و تحلیل مختصات اصلی نیز تایید گردید. بطورکلی نتایج این تحقیق می‌تواند برای تعریف استراتژی‌هایی به منظور بهبود، حفاظت و استفاده پایدار از منابع ژنتیکی پیاز در کشور بنین مورد استفاده قرار گیرد.

کلمات کلیدی: *Allium cepa*، تمایز ژنتیکی، نشانگر RAPD، گروه ژنتیکی، بنین.

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