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Genetic Characterization of Three Strains of *Gallus domesticus* Linnaeus, 1758 in Nigeria using Random Amplified Polymorphic DNA (RAPD) and Microsatellite DNA Markers

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ABSTRACT

This study was carried out to characterize three strains of Nigerian indigenous chickens, *Gallus domesticus* using molecular markers; Microsatellite (SSR) and Random Amplified Polymorphic DNA (RAPD). This was with a view to determining the amount of genetic diversity in the chicken populations as well as differentiating the strains genetically which has implications for their conservation and effective management. A total of thirty chickens; ten each belonging to normal feather, frizzle feather and naked neck strain were characterized by five RAPD and five microsatellite DNA primers. Indices of genetic diversity and differentiation within and among the populations were estimated using Genalex software. Result from both the RAPD and microsatellite data suggest that the three chicken strains had relatively low genetic diversity as indicated in their Ho values which ranged from 0.301 to 0.523. Dendrogram based on the microsatellite data showed a clear separation among the studied chicken strains. This might be due to the fact that these local chicken strains originated from different background and bred for different purposes. Our result suggests that the studied *G. domesticus* strains needs conservation intervention in order to preserve the uniqueness of their genetic identity and also monitor their long-term health and persistence. **KEYWORDS**: Genetic Diversity, Conservation, Strain, Differentiation, Heterozygosity

INTRODUCTION

The indigenous chicken (*Gallus domesticus*) which belongs to the family Phasianidae, order Galliformes is widely believed to have evolved from the wild red jungle fowl, *Gallus gallus* from south-east Asia (1). *G. domesticus* is distributed widely in Nigeria and are raised by several households especially in rural areas; constituting about 80% of the 120 million poultry type raised in Nigeria (2). Indigenous chickens are strong and hardy; they adapt easily to changes in environment and they have the ability to fend for their own food by exploiting different food source in their immediate environment ranging from plants to grains, cooked food and even small arthropods and lizards. They also have the ability to hatch on their own and they possess appreciable immunity against endemic diseases. *G. domesticus* flesh is a choice meat for majority of Nigerians because of its sweet taste, high nutrition and leanness. It is also considered a special delicacy for occasions and its sales generate huge profit which serves as a good source of income at both subsistence and commercial scale (3).

Previous descriptions of local chickens in Nigeria are based on morphological characterization of various chicken types such as normal feather, naked neck, frizzle feather, featherless wing and rose comb (4). Multivariate analysis was used to morphologically characterize three strains namely: frizzle feather, normal feather and naked neck (5). Meanwhile, in recent past; the use of molecular markers has been adopted to genetically characterize several strains of the indigenous chicken which include normal and frizzled feathered strain, naked neck strain, dwarf type and those with colour variants such as black, white, brown, mottled etc. (6). The indigenous chickens have also been characterized based on location as various ecotypes of the indigenous chicken in different ecological zones of Nigeria have been reported (7). Similarly, two ecotypes from rain forest and savannah zones of Nigeria were reported and characterized as Yoruba and Fulani ecotypes respectively (8). Three different strains characterized in South-Eastern states of Nigeria were identified as Nsukka, Owerri and Awgu types (9). The normal feathered strain of *G. domesticus* has been reported as the most common, having the highest abundance in different agro ecological zones. The naked neck and frizzled feathered strains are scarce and may eventually become endangered if conservation efforts are not adequately channeled towards them. This can be achieved by estimating and monitoring their genetic diversity while

Corresponding Author: Tofunmi Elizabeth Oladimeji, Department of Zoology, Obafemi Awolowo University, Ile-Ife, Nigeria. Email: tofunmioladimeji9@gmail.com; +2348033092964 Citation: Ajoke Rafiat. Oseni, Michael Olufemi Awodiran, Tofunmi Elizabeth Oladimeji 2021, Genetic Characterization of Three Strains of *Gallus domesticus* Linnaeus, 1758 in Nigeria using Random Amplified Polymorphic DNA (RAPD) and Microsatellite DNA Markers; Journal of Basic and Applied Scientific Research, 11(5)1-9.

attempting to know how genetically differentiated the strains are. Genetic diversity is the variation in DNA sequences from individual members of a given species (10). It is necessary for the long-term health of populations and persistence of species as it helps individual organisms to adapt and cope with environmental changes. When a population of a species is sufficiently diverse, some individuals would possess alleles that would be able to withstand pressure, survive, reproduce and contribute to the gene pool of the next generation, thus preventing extinction of such a population. Loss of genetic diversity is known to reduce the potential of populations to evolve (11). Genetic diversity among individuals leads to differentiation at the population level, species level and other higher taxonomic groups (12).

Random Amplified Polymorphic DNA (RAPD) marker and microsatellite markers are suitable genetic markers that have been widely used in characterizing strains/populations of different species of chickens. The sustainable management, utilization and conservation of domestic animals require its genetic characterization. The genetic characterization of *G. domesticus* strains is of utmost importance in the bid to improve their production and the conservation of their genetic diversity in order to forestall their extinction. This study therefore seeks to determine the genetic diversity and differentiation pattern among three strains (Frizzle feathered, FRF; Normal feathered, NF and Naked neck, NNK) of *Gallus domesticus* using RAPD and microsatellite markers.

MATERIALS AND METHODS

Animal Collection, DNA Extraction and Polymerase Chain Reaction (PCR)

A total of thirty Gallus domesticus individuals, ten from each strain viz: frizzle feathered (FRF); normal feathered (NF) and naked neck (NNK) were collected from the Teaching and Research Farm Directorate, Federal University of Agriculture (FUNAAB), Alabata and OGADEP (Ogun State Agricultural Development Project), Abeokuta, Nigeria. The three chicken strains which have been previously described by (7) were characterized by five RAPD primers and five microsatellite primers (Table 1&2). All applicable international, national and institutional ethical standards for the care and use of animals were followed. Blood samples were collected from the veins of each of the chicken in a process known as brachial venipuncture. Genomic DNA was extracted from the blood samples using Qiagen DNA easy blood and tissue kit while the quantity and quality of the DNA was measured on Nanodrop Spectrophotometer. Isolated DNA was amplified following standard PCR protocol as described by (13, 14). The PCR reaction mixture was carried out with a 25 µl final volume containing 1 µl template DNA, 2.5 µl of 10 x Buffer, 1 µl of 25 mM dNTPs, 2 µl of each pair of forward and reverse primer, 0.2 µl of (5 U/µl) Taq DNA polymerase, 2.2 µl of 25 mm/mol Mg2+ and 16.1 µl nuclease-free water. Amplification on the thermal cycler was run with the following program: initial denaturation at 95°C for 5 mins, denaturation at 94°C for 60 sec, annealing for 30 sec, and extension at 72°C for 60 sec and final extension at 72°C for 10 mins. The annealing temperatures of the primers used were adjusted through optimization using a temperature gradient. The PCR products were run on 2% agarose gel electrophoresis and detected under UV light with the aid of a trans-illuminator.

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Primer Codes	Sequence					
OPA18	CAGGCCTTC					
OPB08	TGCCGACTG					
OPB14	AGTCAGCCAC					
OPB18	AATCGGGCTG					
OPB20	AGGGGTCTTG					

Table 1: List of Operon Random Primers Used

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Locus	Annealing Temperature ([®] C)	Forward and Reverse Primer Sequence (5′- 3′)
MCW0018	55	TCCCTAGGCAAACCTGCTTAC AAGACCCCACAACTTGACTTG
MCW0029	68	CATGCAATTCAGGACCGTGCA GTGGACACCCATTTGTACCCTATG
MCW0032	55	AAGTTCCTTGTACAATTGTTA CATTACTAGTACAATCAAGATGG
MCW0036	55	CCTCATGTGAAGCATCTTTTCATA TGTCTTCAGTAGGACTGTGATAC
MCW0040	50	ACCGAAATTGAGCAGAAGTTA ACTCAAAAATGTGTAGAATATAG

Table 2: List of Microsatellite Primers Used for the Study

Statistical Analysis

Band sizing was performed using a 100 base pair DNA ladder (Norgen PCR Sizer) loaded along side the PCR products. For microsatellite DNA analysis, DNA fragments were scored manually and the sizes were estimated using semi-log plot. The RAPD bands were scored as binary data using GelQuest software. The similarity coefficients were calculated across all pair while the binary values were transferred into NTSYS software for analysis of genetic similarities. The data generated were analysed using the GenAlEx Software, version 6.5 (15). Microsatellite data were analysed with Microsatellite Analyser (MSA) version 4.05 (16) and GenAlex 6.5 software (15, 17). The following indices of genetic diversity were assessed for each population: mean number of alleles (Na), number of effective alleles (Ne), Shannons' information index (I), observed and expected heterozygosity (Ho and He) and percentage of polymorphic loci (P). Analysis of hierarchical F statistics which includes Fis (the inbreeding coefficient within individuals relative to the subpopulation); Fit= the inbreeding coefficient within individuals relative to the total and Fst (the inbreeding coefficient within subpopulations relative to the total) were assessed over all populations for each locus. Pairwise population genetic differentiation (Fst) was used to analyze the degree of genetic differentiation between population pairs. Gene flow (Nm) was estimated from Nm = 0.25 (1-Fst)/Fst (18). Neighbour-joining method and analysis of molecular variance (19) were used to construct phylogenetic trees for the three chicken populations. Test for conformity to Hardy-Weinberg equilibrium was assessed at each locus for all the populations studied. The significance of the deviation was evaluated with a Chi-Square test following the method of (20).

RESULTS

RAPD results

A total of 35 bands were produced with 100% polymorphism across the three chicken populations (strains). The electrophoresis gel photographs for two of the primers (OPB 08 and OPB 14) are shown on Figures 1 and 2. Mean expected heterozygosity (H_E) across the three populations of *Gallus domesticus* was 0.378 ± 0.015 , 0.396 ± 0.014 and 0.398 ± 0.017 for the normal feathered, frizzle feathered and naked neck populations respectively (Table 3). The mean number of alleles (A_N) across the three population, effective number of alleles (A_E) and Shannon index information (I) are shown on table 3. Analysis of molecular variance (AMOVA) showed that 100% of the total molecular variance was within the population and there was no variation (0%) among the populations.

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Figure 1: Gel electrophoresis for RAPD marker OPB 08



Figure 2: Gel electrophoresis for RAPD marker OPB 14

- I ADIC J. DASIC III UICALUIS UI GEHELIC VAHAUUH ACIUSS LIIC SAIIDIEU I UDUIALUUIS HUIH INALD AHAIVSI	Table 3:	Basic Indicators	of Genetic `	Variation acros	s the Samı	pled Por	pulations from	RAPD Analysis
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Population	Polymorphic Loci	Mean no of Alleles (A _N)	Effective no of Alleles (AE)	Shannon Information Index(I)	Expected Heterozygosity (He)	Unbiased Expected Heterozygosity (UHe)
NF	100	2.00	1.637±0.037	0.561±0.017	0.378±0.015	0.398±0.016
NNK	100	2.00	1.684±0.037	0.582±0.015	0.396±0.014	0.417±0.014
FRF	100	2.00	1.689±0.039	$0.582{\pm}0.020$	0.398±0.017	0.419±0.018
MEAN	100	2.00	1.670±0.033	0.575±0.015	0.391±0.014	0.411 ± 0.014

NF =Normal Feathered, FRF = Frizzled Feathered, NNK = Naked Neck

Microsatellite Result

A total of 25 alleles were scored in the microsatellite analysis with the sizes ranging from 210 base pairs to 1500 base pairs while 95% success was recorded upon amplification. Electrophoresis gel plate for two of the microsatellite primers are represented on Figures 3 and 4. Allelic diversity ranges from two to eight alleles per microsatellite locus. The overall heterozygosity for all samples at all the five microsatellite loci was 30% and no locus was monomorphic. The mean number of alleles (Na) per population, the effective number of alleles (NE) contributing to the population, Shannon information index (I), observed and expected heterozygosities as well as percentage of polymorphic loci are shown on table 4. Analysis of molecular variance (AMOVA) showed that 83% and 17% of the total molecular variance was within and among the populations respectively. The highest genetic identity (1.1036) was recorded between frizzle feathered and naked neck population (table 5). The phylogenetic consensus tree constructed using Nei's unbiased genetic distance (Figure 5) grouped all the three strains into two clusters. The dendrogram showed that frizzle feathered and naked necked populations clustered together and was separated from normal feathered. Thus, indicating that the frizzle feathered and naked necked populations are more similar genetically than the normal feathered population based on the microsatellite DNA analysis.



Figure 3: Gel electrophoresis for SSR marker MW0029



Figure 4: Gel electrophoresis for SSR marker MW0040

microsatellite loci									
Population	Mean number of alleles (An)	Effective number of alleles (AE)	Shannon's Information index (I)	Observed Heterozygosity (Ho)	Expected Heterozygosity (He)				
NF	3.600±0.510	2.616±0.396	1.031±0.159	0.301±0.055	0.634±0.104				
NNK	4.400±0.678	2.877±0.442	1.138±0.211	0.317±0.062	0.590±0.077				
FRF	4.000±0.632	3.143±0.509	1.172±0.181	0.523±0.152	0.574±0.073				

Table 4: Genetic Diversity Information for the three populations of Gallus domesticus estimated from five microsatellite loci

NF= Normal feathered, FRF= Frizzle feathered, NNK= Naked neck

Table 5: Pairwise Population of Nei's unbiased genetic distance (above diagonal) and genetic identity

(below diagonal)						
Population	NF	FRF	NNK			
NF	***	0.4683	0.3912			
FRF	0.7586	***	0.3317			
NNK	0.9384	1.1036	***			

NF= Normal feathered, FRF= Frizzle feathered, NNK= Naked neck





Figure 5: Dendrogram based on Nei's (1972) showing genetic distances between the three populations of *Gallus domesticus*.

1 represents Frizzled feathered, 2 represents Naked Neck while 3 represents Normal feathered.

Genetic structure

Microsatellite analysis revealed a high level of genetic differentiation within populations/strains. The coefficient of hierarchical Fst estimated among the three strains had an average value of 0.364 (Table 6). The overall gene flow (Nm) among the populations was 0.442, which gave an estimate of the average number of migrants between all studied populations per generation. The observed value shows that gene exchange between the populations is low. Test for departure from Hardy- Weinberg (H-W) equilibrium showed significant deviation (P<0.001) for at least one locus per population (Table 7). The deviations were attributed to deficit of heterozygotes in the populations. Fit which is the overall inbreeding coefficient of an individual relative to the whole set of populations had a mean value of 0.473 (Table 6). This shows that the three population have deficiency of heterozygotes. Also, Fis which is the inbreeding coefficient of an individual relative to its own population had an average value of 0.562. This also shows that there is inbreeding within populations and a regular heterozygote deficiency.

Locus	Fis	Fit	Fst	Nm
MCW0018	0.7638	0.8506	0.3676	0.4300
MCW0029	-0.0169	0.3258	0.3371	0.4917
MCW0032	0.3502	-0.6247	0.4225	0.3417
MCW0036	0.8507	0.9042	0.3578	0.4487
MCW0040	0.8611	0.9077	0.3354	0.4954
Mean	0.5618	0.4727	0.3641	0.4415

Table 6: Analysis of Genetic differentiation and estimates of gene flow over all Populations for Each Locus

Fis = inbreeding coefficient at population level

Fit = Inbreeding coefficient at total sample level Fst = Proportion of differentiation

Nm = Gene flow

Nm = Gene flow

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Populations	Locus	Df	ChiSq	Probability	Significane
NF	MCW0018	1	10.000	0.002	**
NF	MCW0029	6	10.044	0.123	ns
NF	MCW0032	15	13.333	0.577	ns
NF	MCW0036	10	21.667	0.017	*
NF	MCW0040	10	30.000	0.001	***
NF	MCW0018	1	10.000	0.002	**
FRF	MCW0029	3	9.184	0.027	*
FRF	MCW0032	6	10.111	0.120	ns
FRF	MCW0036	10	17.357	0.067	ns
FRF	MCW0040	6	10.111	0.120	ns
NNK	MCW0018	1	9.000	0.003	**
NNK	MCW0029	6	21.000	0.002	**
NNK	MCW0032	15	12.833	0.615	ns
NNK	MCW0036	6	8.750	0.188	ns
NNK	MCW0040	6	7.389	0.286	ns

Table 7: Test of Conformity to Hardy – Weinberg Equilibrium

ns = not significant, *P<0.05, **P<0.01, ***P<0.001

DISCUSSION

The results of this study showed that all the RAPD and microsatellite markers used were highly polymorphic, thus establishing the usefulness of this markers in chicken's genome analysis (21). Genetic characterization using microsatellites, yield reliable estimates of variability among chicken populations, as demonstrated in several studies (22, 23, 24). In this study, microsatellite marker was able to characterize the populations more efficiently than the RAPD marker due to its high rate of mutation which brings about high standing allelic diversity. Microsatellite variability enables a clearer differentiation, even between closely related breeds, and provide more evidence of the predicted divergence (25, 26). The low heterozygosity values recorded in this study from both RAPD and microsatellite analysis is an indication that inbreeding is evident at the population level in the three strains of G. domesticus examined. Studies have reported negative correlation between mean heterozygosity from multiple loci in non-coding DNA regions and inbreeding depression in wild populations; as individuals that are inbred are relatively homozygous through out the genome unless there is a recent mutation (27, 28). Inbreeding usually leads to reduced fitness, a phenomenon referred to as inbreeding depression. Inbreeding increases the chance that an individual will be homozygous for segregating harmful recessive alleles which is the major factor responsible for inbreeding depression in populations (29). The heterozygosity values obtained in this study are comparable to those recorded in breeds of G. domesticus from Iran, India, Ethiopia, and Brazil in earlier reports (23, 24, 30). Significant average Fst value (0.36) recorded among the three strains indicates that the strains are genetically differentiated; thus, suggesting that each of the strains be treated separately for conservation and management. This will help to preserve the uniqueness of their genetic identity and reduce potential threat to their long-term health and persistence. The test of departure from Hardy-Weinberg equilibrium showed that none of the studied populations of G. domesticus is at random mating as they all deviated significantly from H-W equilibrium (P < 0.001) at not less than two, out of the five microsatellite DNA loci examined. This also accounts for the positive inbreeding values observed in the chicken populations. The significant deviation of the populations from H-W equilibrium at several loci is also an indication that the populations are under the influence of evolutionary forces such as mutation, migration, genetic drift, and selection; therefore, the populations can be said to be evolving.

Citation: Ajoke Rafiat. Oseni, Michael Olufemi Awodiran, Tofunmi Elizabeth Oladimeji 2021, Genetic Characterization of Three Strains of *Gallus domesticus* Linnaeus, 1758 in Nigeria using Random Amplified Polymorphic DNA (RAPD) and Microsatellite DNA Markers; Journal of Basic and Applied Scientific Research, 11(5)1-9.

CONCLUSION

The study concluded that the three *G. domesticus* strains/populations need conservation intervention in order to ensure their increased productivity and sustainable yield. Also, each of the strains should be treated with separate management and conservation approach in order to preserve the uniqueness of their genetic identity and forestall probable extinction in the nearest future.

Competing Interest

The authors declare that they have no conflicts of interests.

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Comparative Study of Annual Precipitation between Oran Aerodrome (Algeria) and Marseille Marignane (France) Stations Located in the Mediterranean Basin

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ABSTRACT

Over the past decade, the issue of climate change has been recognized as one of the major development issues at the local, regional and even international levels, alongside sustainable development, conservation and sustainable development of the protection of the environment. In fact, the current trend is to consider that climate change responses are an integral part of sustainable resource management decision-making. In the catchment area, it is recognized that measures are needed to improve the ability to adapt to rainfall variability and extreme events (floods and droughts). Drought can be considered at different scales: monthly, seasonal and annual. It becomes dangerous as soon as it persists two or three successive years. So, we also chose to study the persistence of drought on an annual and seasonal scale. In our work consists in doing the annual rainfall survey of the region of Oran Aerodrome and comparing with that of the region of Marseille Marignane in the period (2000-2017). To try to elucidate this problem, it is essential to analyze beforehand the term precipitation. We will try to answer some worrying and fundamental questions, among others:

How does the rainfall of two Mediterranean shores in space be evaluated?

Is there a decrease in rainfall during this last decade?

In this perspective, we contribute to studying rainfall by using statistical processing. For our work, we have chosen a methodology that is characterized as follows:

1. Collection of rainfall data and creation of a databank on the computer.

2. Preprocessing data:

- Wilcoxon test
- > Normal fit test
- Coefficient of variation test
- Chi-square test

KEYWORDS: Hydrology, Climatology, Precipitation, Statistics, Marseille, Oran.

1. INTRODUCTION

The analysis of climate data consists of carrying out a statistical analysis of the data [4]. So as to show to quantify the spatio temporal variability of the climate.

This variability can be studied on the basis of the analysis of long time series, continuous and homogeneous, of climatic or agro-climatic variables over a period of 18 years [8], the current reference being the period 2000-2017 according to the two climatologically stations will be located in the Mediterranean basin, namely Oran aerodrome (Algeria) and Marseille Marignane (France).

2. MATERIALS AND METHODS

Precipitation in the Mediterranean basin has been specifically studied by the author [5]. For this purpose based on the database

To study and analyze the fluctuation in rainfall in the Mediterranean basin

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2.1. Collection of data

The monthly precipitation values were collected from the climate information station (France) and the national meteorological office (Oran) [7]. These values represent monthly totals taken from the original documents of the stations in our study.

2.2. Choice of study period

For our work, we have chosen the period available according to the weather stations.

Table. 1: Presentation of rainfall stations

Station	Geographical coordinates	Year of study
Oran Aérodrome	35°41'55,555'' N 0°38'30" Ouest	2000-2017
Marseille Marignane	43°17'49Nord, 5°22'51"Est	2000-2017



Figure .1: Location of study areas

3. RESULTS AND DISCUSSIONS

3.1 Checking the homogeneity of the data

Any climatic or hydrological study [3] is based on the exploitation of data series collected over longer or shorter periods, continuous or discontinuous. The statistical methods of analysis of these series require homogeneity of their components, it is therefore necessary, before any use of the rainfall variables, to control their quality by the use of statistical and graphic tools, in order to reduce systematic errors which could affect them [2].

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3.3.1. Wilcoxon test

It is a non-parametric test which uses the series of ranks of observations, instead of the series of their values. The Wilcoxon test is based on the following principle: If the sample X comes from the same population Y, the sample XUY (union of X and Y) is also derived from it.

We proceed as follows:

Let be a series of observations of length N from which two samples X and Y are drawn:

N1 and N2 are respectively the sizes of these samples, with N = N1 + N2 and N1 \leq N2

We then classify the values of our series in ascending order. Thereafter, we will only be interested in the rank of each of the elements of the two samples in this series. If a value is repeated several times, we associate it with the corresponding mean rank.

We then calculate the sum Wx of the ranks of the elements of the first sample in the common series: $Wx = \sum rank x$

Wilcoxon has shown that, in the case where the two samples X and Y constitute a homogeneous series, the quantity Wx is between two limits Wmax and Wmin given by the following formulas:

$$\mathbf{W}_{\min} = \frac{(N_1 + N_2 + 1)N_1 - 1}{2} - Z_{1-\alpha/2} \sqrt{\frac{1}{12}N_1N_2(N_1 + N_2 + 1)}$$
$$\mathbf{W}_{\max} = (N_1 + N_2 + 1)N_1 - W_{\min}$$

 $Z_{1-\alpha/2}$: Represents the value of the reduced centered variable of the normal distribution corresponding to a (at the 95% confidence level, we have = 1.96)

We will use the Wilcoxon test to verify the homogeneity of rainfall data from the four stations at the 5% significance level.

3.3.1.1. Application of the Wilcoxon method on the Marseille Marignane station

x	У	Rank	(x)U(y)	origin	Rank	(x)U(y)	origin	
630	645,6	1	276,8	Х	11	530,1	Y	
358	843,3	2	292,2	Y	12	542	Y	
788,8	610,1	3	311,7	Y	13	610,1	Y	
523,4	509,8	4	315,8	Х	14	630	Х	
292,2	441,3	5	346,3	Y	15	645,6	Y	
434,4	542	6	358	Х	16	661,6	Y	
315,8	661,6	7	434,4	Х	17	788,8	Х	
276,8	530,1	8	441,3	Y	18	843,3	Y	
	346,3	9	509,8	Y				
	311,7	10	523,4	Х				

Table. 2 : Appl	lication of the	Wilcoxon method	l on the M	[arseille M	arignane statio	n

On a: $N_1=8$, $N_2=10$ Wmin = 53,45 Wmax=98,55 Wx=59

we check the inequality: Wmin<Wx<Wmax

that is to say 5 3, 45< 59<98, 55

> The inequality is therefore verified, the series is homogeneous

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3.3.1.3. Application of the Wilcoxon method on the Oran Aerodrome Station.

Х	Y	Rank	(X)U(Y)	Origin	Rank	(X)U(Y)	Origin
390	239	1	167	Y	11	496	Y
763	167	2	239	Y	12	547	Y
617	253	3	253	Y	13	617	Х
691	299	4	267	Х	14	678	Y
699	378	5	299	Y	15	691	Х
451	326	6	325	Х	16	699	Х
325	547	7	326	Y	17	763	Х
267	496	8	378	Y	18	790	Y
	678	9	390	Х			
	790	10	451	Х			

Tab. 3: Application of the Wilcoxon method on the Oran Aerodrome Station.

On a: $N_1=8$, $N_2=10$ Wmin = 53,45 Wmax=98, 55 Wx=90

we check the inequality: Wmin<Wx<Wmax that is to say 53, 45<90<98, 55

The inequality is therefore verified, the series is homogeneous

3.3.2. Adjustment by Normal law

The collected data can undergo several statistical treatments in order to check the reliability and the precision of the latter. Among its treatments we can cite the study of data homogeneity using the double mass method and linear regression among others [6].

This approach requires reference stations adjacent to our study stations. The lack of these leads us to set aside this aspect and to try to treat data series by employing an adjustment method that of the Normal law which alone can summarize the reliability of each series.

3.3.2.1. Theory of adjustment to the Normal law

The Normal law (the symmetrical bell curve around the mean) is a theoretical function commonly used in statistics as an approximation of sampling distributions, in general, the Normal law provides a good model for a random variable when:

1- There is a strong tendency for the variable to take a central value.

2- The positive and negative deviations from this central value are of equal probability.

3- The frequency of deviations decreases rapidly as the deviations increase.

The function of the Normal law is determined by the following formula:

 $\mathbf{F}(\boldsymbol{x}) = \frac{1}{\sqrt{2\pi}} \int_{-a}^{u} l^{-u^2/2}$

_

Where U is the reduced variable of GAUSS

$$U = \frac{X - X}{\delta x}$$
$$\overline{X} = \frac{1}{N} \sum_{i=1}^{n} X_{i} \qquad , \qquad \delta x = \sqrt{\frac{\sum (X_{i} - x)^{2}}{N}}$$

With :

x : random variable

 $\overline{\mathbf{x}}$: the mean of the random variable $\delta \mathbf{x}$: Standard deviation of the random variable

a) Marseille Marignane station:

1 able .4: Table of annual rannal frequency in Marselle Marignane.					
observed value	effective n	cumulative effective	Frequency Fi= n /N+1 (%)		
276,8	1	1	5,26		
292,2	1	2	10,52		
311,7	1	3	15,78		
315,8	1	4	21,05		
346,3	1	5	26,31		
358	1	6	31,57		
434,4	1	7	36,84		
441,3	1	8	42,1		
509,8	1	9	47,47		
523,4	1	10	52,63		
530,1	1	11	57,89		
542	1	12	63,15		
610,1	1	13	68,42		
630	1	14	73,68		
645,6	1	15	78,94		
661,6	1	16	84,21		
788,8	1	17	89,47		
843,3	1	18	94,73		

Table 4. Table of annual rainfall frequency in Marseille Marianane





Figure 1: Plot of the Normal law of Marseille Marignane station

3.3.2.2. Analysis of normal law plots

The analysis of figure 1, shows us that the distributions observed in the station form a clear structure around different lines. We notice that the distribution aligns to the right while others deviate more or less. In order to confirm whether there is any normality of the different distributions we will submit them to the chi-square test.

b) Oran Aerodrome station:

Table, 5. Trequency table of annual rannan at Oran Actourome.						
observed value	effective n	cumulative effective	Frequency Fi= n /N+1 (%)			
167	1	1	5,26			
239	1	2	10,52			
253	1	3	15,78			
267	1	4	21,05			
299	1	5	26,31			
325	1	6	31,57			
326	1	7	36,84			
378	1	8	42,1			
390	1	9	47,47			
451	1	10	52,63			
496	1	11	57,89			
547	1	12	63,15			
617	1	13	68,42			
678	1	14	73,68			
691	1	15	78,94			
699	1	16	84,21			
763	1	17	89,47			
790	1	18	94.73			

Table. 5: Frequency table of annual rainfall at Oran Aerodrome.

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Figure .2: Plot of the Normal law of the Oran Aérodrome station

3.3.2.2. Analysis of normal law plots

Figure analysis. 2, shows us that the distributions observed in each of the stations form a clear structure around different lines. We notice that some distributions are aligned on the lines while others deviate more or less.

In order to confirm whether there is any normality of the different distributions we will submit them to the chi-square test.

3.3.3. Chi-square test

Before performing the chi-square test we will first try to determine the coefficient of variation (Cv) which will tell us if all the conditions are met to perform the chi-square test, i.e. the coefficient of variation must be less than 0.5 for each station

a) Calculation of the coefficient of variation (Cv)

It is the ratio of the standard deviation to the mean. The coefficient of variation numerically indicates the importance of the degree of variability of rainfall averages in the series [1] as well as the dispersion in number of values around the mean, the larger this number, the greater the dispersion, it also allows us to better understand the variability of rainfall and the irregularity of rainfall.

As the coefficient of variation is less than 0.5 for the four stations, we can calculate the chi-square.

Table. 6: Calculation of the coefficient of variation							
Station Average p(mm) Standard deviation δ Cv= δ /P							
Marseille Marignane	503,4	170,57	0,33				
Oran Aérodrome	465,33	200,04	0,42				

b) Chi-square test theory

If ni represents the number of samples observed and npi the number of theoretical samples, calculated as a function of a certain distribution hypothesis, the tables of the chi-square distribution law allowing for various adequacy thresholds to obtain the value of the chi-square test not to be exceeded as a function of the number of degrees of freedom in the sample.

ddl= K-1

With ddl: number of degrees of freedom

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K: number of class

This is a test that checks whether the differences between the distribution of the sample series and the distribution of the theoretical law are due to mere chance or if the sample follows a law other than the one used.

The application of the test consists in comparing the observed size (ni) with the theoretical size (npi) obtained for each class, by applying the law we then have:

$$\chi^2 = \sum_{i=1}^p \frac{(ni-npi)}{npi}$$

Or the theoretical class size: $nni = \frac{n}{2}$

With k: the number of classes n: observed number of class k = 4

Table .7 Chi-square lest for the Marsene Marignane station						
Class K	Class limits	Observed effective (ni)	Theoretical effective (npi)	$\frac{(ni-npi)^2}{npi}$		
1	276,8-315,8	4	4,5	0,05		
2	346,3-441,3	4	4,5	0,05		
3	509,8-542	4	4,5	0,05		
4	610,1-843,3	6	4,5	0,5		
Total		N=18	Npi=18	$\chi^2 = 0,65$		

Table .7 Chi-square test for the Marseille Marignane station

I able 8: Chi-square test for the Oran A
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Class K	Class limits	Observed effective (ni)	Theoretical effective (npi)	${(ni-npi)^2\over npi}$
1	167-267	4	4,5	0,05
2	299-378	4	4,5	0,05
3	390-547	4	4,5	0,05
4	617-790	6	4,5	0,5
Totals		N=18	Npi=18	$\chi^2 = 0.65$

Table 9: Result of the test of χ^2 of the annual precipitation of the four stations.

		Oran Aérodrome	Marseille Marignane
χ^2 calculated		0,65	0,65
Ddl		3	3
χ^2 tabulated	7,815		
Observation	Good fit		

c. Chi-square test result

 χ^2 calculated = 0.65

The number of degrees of freedom dof = k - 1 = 4 - 1 = 3

For a risk $\alpha = 5\% \chi^2$ tabulated = 7.815> χ^2 calculated = 0.65; therefore the fit to the normal distribution is acceptable.

4. CONCLUSION

The analysis of the different graphs of the plot of the normal law showed us that the series can be distributed normally. In order to confirm this possibility of normal distribution we proceeded to the chi-square test which revealed to us that the adequacy to a normal distribution is possible.

So we can use our data in perceptual terms by determining the different parameters a namely the rainfall periods for a given recurrence period more precisely the calculation of the dry and wet modulus for the periods of ten, fifty and a hundred years then a study of the annual variations and monthly rainfall amounts for the various stations in the study region.

ABDELKADER, 2021

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Data bank

Data source: International Climatology Agency (www.infoclimat.fr/climatologie) and National Meteorological Office (Algeria).

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