(RESEARCH ARTICLE)

Analysis of the ethnogenetic structure of the Mputu population of Djuma (Democratic Republic of the Congo) Based on the Distribution of the ABO Blood Group According to the Hardy-Weinberg Equilibrium Parameters

John MUNGANGA GIKUG [1], Ruphin BOY LUTAKA [1] and ET Edouard SISA MBUNGU [2,*]

[1] Laboratory of Biology, Department of Biology, Section of Sciences and Technology, Higher Pedagogical Institute of Milundu. B.P. 130 Kwilu, RD Congo
[2] Laboratory of Hydrobiology and Ecology, Department of Biology, Faculty of Sciences and Technology, National Pedagogical University (UPN), P.O. Box 8815 Kinshasa I, DRC.

Abstract

This study focused on 213 Mputu individuals living in the Catholic Mission of Djuma, located in the Kwilu Province, Democratic Republic of the Congo (DRC). It aimed to analyze the ethnogenetic structure of this population based on the distribution of the ABO blood group according to the Hardy-Weinberg equilibrium parameters. The results revealed a strong dominance of blood group O (59%), followed by groups B (15%), A (10%), and AB (7%). The corresponding allelic frequencies were 0.75 for O, 0.17 for B, and 0.08 for A. The chi-square test (χ^2 = 0.0127, df = 3, p > 0.05) indicated that the population is in Hardy-Weinberg equilibrium, reflecting genetic stability and the absence of major evolutionary disturbances. These findings are consistent with observations made in other Bantu populations of Central Africa, where the predominance of the O allele is often associated with adaptive evolution in response to selective pressures such as malaria. The study concludes that there is a high level of genetic homogeneity among the Mputu of Djuma and suggests the need for further research incorporating molecular markers to better understand the evolutionary dynamics of this population.

Keywords: ABO Blood Group; Ethnogenetic; Mputu; Djuma; Hardy-Weinberg; DR Congo

1. Introduction

Understanding genetic diversity within human populations is fundamental to studying their evolutionary history, social interactions, and migratory dynamics. The analysis of blood groups, particularly the ABO system, remains one of the classical and powerful tools for exploring genetic structure and the origins of human populations (Roychoudhury and Nei, 1988; Mourant et al., 1976). The ABO system, discovered by Karl Landsteiner in 1900, is based on the presence or absence of two antigens (A and B) on the surface of red blood cells, leading to four main phenotypes: A, B, AB, and O (Daniels, 2013).

The frequencies of alleles A, B, and O vary considerably among populations and may be influenced by factors such as genetic drift, natural selection, inbreeding, and migration (Jobling et al., 2013). These genetic variations often reflect historical processes of isolation or admixture between populations, which gives blood markers considerable ethnogenetic and anthropological value (Cavalli-Sforza et al., 1994).

The Hardy-Weinberg equilibrium, independently formulated by Godfrey Hardy and Wilhelm Weinberg in 1908, provides a fundamental mathematical framework for studying population genetic structure. It postulates that in an ideal

---

* Corresponding author: ET SISA MBUNGU Edouard

population (large size, no mutation, selection, migration, or non-random mating), allelic and genotypic frequencies remain constant across generations (Hartl and Clark, 2007). Any deviation from this equilibrium indicates the action of evolutionary forces such as natural selection or genetic drift (Freeman and Herron, 2020).

In the Democratic Republic of the Congo, a country characterized by great ethnolinguistic and cultural diversity, few detailed studies have explored the genetic structure of local populations using blood markers. The few existing works mainly concern major ethnic groups such as the Mongo, Luba, or Kongo (Kayembe et al., 2010; Mulumba and Tshilombo, 2018). However, smaller communities, such as the Mputu population of Djuma, remain largely unexplored in terms of population genetics.

In this context, the present study aims to analyze the ethnogenetic structure of the Mputu population of Djuma (DRC) based on the distribution of the ABO blood group system, applying Hardy-Weinberg equilibrium parameters. It seeks to estimate allelic and genotypic frequencies, verify conformity with theoretical equilibrium, and identify trends that may reflect demographic history or marital practices within the group. This approach contributes to a better understanding of the evolutionary dynamics and biological diversity of the Mputu population within the broader genetic context of the DRC and Central Africa.

2. Methodology

2.1. Study Area

The study was conducted in the locality of Djuma, located in the Bulungu Territory, Kwilu Province, in the southwestern part of the Democratic Republic of the Congo (DRC). The area covers an estimated surface of 9,120 km² and is situated on the right bank of the Kwilu River. Djuma comprises the sectors of Kwilu-Kimbata (1,612 km²), Mikwi (940 km²), Kilunda (940 km²), Kizweme (2,687 km²), and Kwilu–Ntorebe (2,941 km²). The Mputu tribe, which is the focus of this study, originates from the Dwe sector, neighboring the Kwilu–Kimbata sector.

Our fieldwork was conducted in seven neighborhoods of this latter sector: Post, Makwela, Ntanina, Rural Development Center (CDR), Djuma General Hospital, Centre, and Mission.

This region is mainly inhabited by the Mputu community, which belongs to the large Kongo ethnolinguistic group. Djuma is characterized by a humid tropical climate, an agroforestry-based economy, and a strongly community-oriented social structure that promotes endogamous unions within the group (National Institute of Statistics, 2021). These demographic and cultural characteristics make it a relevant model for population genetics studies.
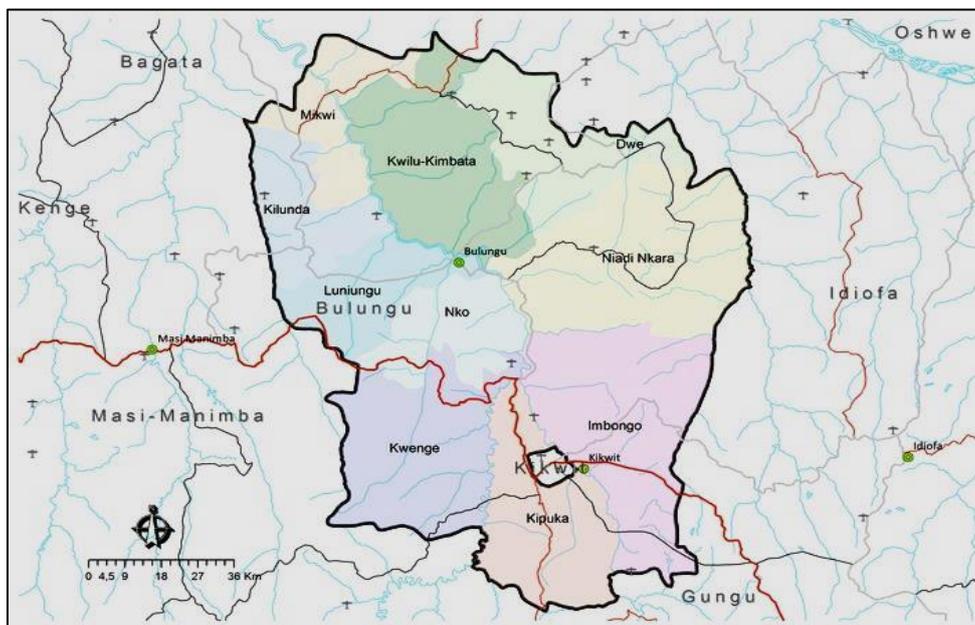

Figure 1 Location of the locality of Djuma in the Kwilu Province, Democratic Republic of the Congo (DRC)

2.2. Type and Period of Study

This was a descriptive and analytical population genetics study conducted between January and June 2024. It aimed to determine the phenotypic and allelic frequencies of the ABO blood group system and to test the conformity of these frequencies with the Hardy-Weinberg equilibrium.

2.3. Sampling and Study Population

A total of 200 individuals (100 men and 100 women), aged 18 to 60 years and belonging to the Mputu population of Djuma, were included in the study.

Inclusion criteria

- Recognized membership in the Mputu community (up to two generations);
- Permanent residence in Djuma;
- Informed consent to participate in the study.

Individuals with a history of blood transfusion, hematological disorders, or recent mixed marriages were excluded to avoid bias in gene frequency interpretation (Jobling et al., 2013).

2.4. Blood Sampling and Determination of Blood Group

Capillary blood samples were collected by finger prick following aseptic procedures. The determination of the ABO blood group was performed using the Beth-Vincent method (direct agglutination) and confirmed by the Simonin method (indirect reverse test) with anti-A and anti-B test sera (Daniels, 2013). Phenotypic results were classified into four groups: A, B, AB, and O.

2.5. Calculation of Gene and Genotype Frequencies

The observed phenotypic frequencies (f_o) were used to estimate the allelic frequencies (p, q, r) of the genes IA, IB, and IO according to the following equations (Hartl and Clark, 2007)

$$p = \sqrt{fAA + \frac{1}{2}fAO} \quad ; q = \sqrt{fBB + \frac{1}{2}fBO} \quad ; r = 1-(p+q)$$

These allelic frequencies were then used to calculate the expected genotypic frequencies (f_e) under the Hardy-Weinberg equilibrium hypothesis as follows

$$fAA = p2; fBB = q2; fOO = r2; fAB = 2pq; fAO = 2pr; fBO = 2qr$$

2.6. Test for Conformity to the Hardy-Weinberg Equilibrium

The conformity of observed frequencies to the expected theoretical frequencies was verified using the chi-square test (χ^2) according to the formula

$$\chi^2 = \sum \frac{(O-E)^2}{E} \quad \text{where O represents the observed frequency and E the expected frequency.}$$

A significant deviation (p < 0.05) indicates a departure from the Hardy-Weinberg equilibrium, suggesting the possible influence of evolutionary factors such as genetic drift, selection, mutation, or inbreeding (Freeman and Herron, 2020).

Statistical analyses were performed using PAST 4.03 software and Excel 2021.

2.7. Ethical Considerations

The study was conducted in accordance with the ethical principles of the Declaration of Helsinki (2013). Authorization was obtained from the local authorities of Djuma. Informed consent was obtained from each participant prior to sample collection.

3. Result and Interpretations

3.1. Distribution of respondents according to their age groups and gender
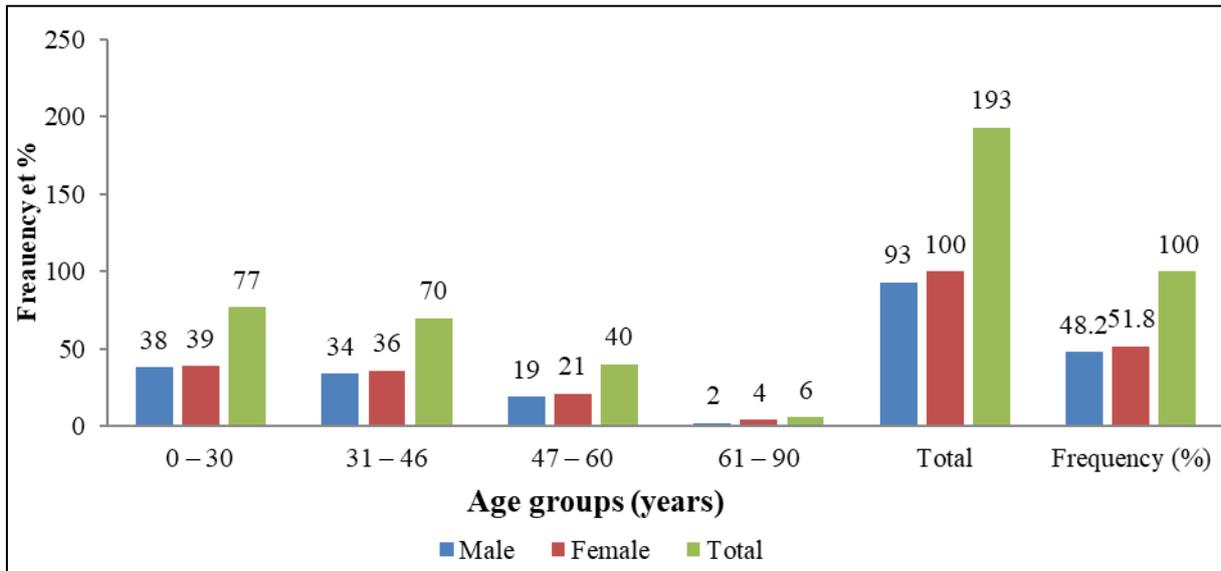

Figure 2 Distribution of respondents according to their age groups and gender

It appears from figure 2 that female respondents were the most represented, accounting for 51.8% of the total sample, while males made up 48.2%.

The age group between 0 and 30 years was the most represented, with 77 individuals surveyed. The age groups between 31 – 46 years, 47 – 60 years, and 61 – 90 years were represented by 70, 40, and 6 individuals, respectively.

3.2. Distribution of respondents according to their gender and their Blood Groups

Table 1 Distribution of respondents according to their gender and their Blood Groups

Groups	Male	Female	Total
A	10	11	21
B	15	17	32
AB	6	8	14
O	62	64	126
Total	93	100	193
Frequencies (%)	0.482 (48.2%)	0.518 (51.8%)	1.00 (100)

Table 1 indicates that the majority (126 subjects, or 65.2%) of the respondents belong to blood group O. They are followed by those with blood group B (16.5%), group A (10.8%) and group AB with 14 subjects (7.2%).

3.3. ABO Blood Groups

The results of the determination of ABO blood groups in our sample of 213 Mputu individuals from Djuma are presented in Table 1.

Table 2 Distribution of ABO Blood Groups According to Age Categories

Age (years)	ABO Blood Groups				Total
	A	B	AB	O	
0 – 30	5	11	4	57	77
31 – 46	10	14	6	40	70
47 – 60	5	6	4	25	40
61 – 90	1	1	0	4	6
Total	21	32	14	126	193
Fréquences (%)	0.108 (10.8%)	0.165 (16.5 %)	0.072 (7.2%)	0.653 (65.3%)	1.00 (100%)

Analysis of Table 1 reveals that 65.3 % of individuals belong to blood group O, across all age classes. Group B accounts for 16.5 %, group A for 10.8 %, and group AB for 7.2 %.

Thus, blood group O is the most frequent, confirming the trend observed in most African populations where this phenotype predominates widely (Nwafor and Onyenekwe, 2001; Egesie et al., 2008).

3.4. Gene, Phenotypic, and Genotypic Frequencies

Gene frequencies were calculated using Bernstein's method (1925), based on the observed phenotypic proportions. The results are presented in Table 2.

Table 3 Gene, Genotypic, and Phenotypic Frequencies of the ABO System

Paramètres	ABO Blood Groups			
	A	B	AB	O
Gene frequencies	0.08	0.17	—	0.75
Observed phenotypic frequencies	0.108	0.165	0.072	0.653
Estimated genotypic frequencies	AA: 0.0064 AO: 0.12	BB: 0.0289 BO: 0.255		

The O allele shows the highest frequency (0.75), followed by B (0.17) and A (0.08).

This dominance of the O allele indicates strong genetic homogeneity at the ABO locus within the Mputu population, likely associated with long-term endogamy or a closed population structure (Cavalli-Sforza et al., 1994).

Phenotypically, the observed frequencies confirm the predominance of group O (59%), followed by B (15%), A (10%), and AB (7%).

3.5. Test of Hardy-Weinberg Equilibrium

The Hardy-Weinberg (H-W) equilibrium was tested to verify whether the observed gene distribution in the population remains stable across generations. The results are summarized in Table 3.

Table 4 Hardy-Weinberg Equilibrium Test for the ABO Locus

Groups	Observed (O)	Expected (E)	$(O – E)^2 / E$
A	21	20.7	0.0014
B	32	31.2	0.0205
AB	14	13.8	0.0029
O	126	126.3	0.0007
Σ (χ^2 calc)	0.0285		

The calculated χ^2 value (0.0285) is far below the tabular chi-square value (χ^2 = 7.815; df = 3; p < 0.05).

The difference between observed and expected frequencies is not significant. Therefore, the Mputu population of Djuma is in Hardy-Weinberg equilibrium for the ABO locus.

In other words, there is no significant deviation due to selection, mutation, or migration. The small discrepancies observed are most likely the result of sampling randomness.

4. Discussion

The results of this study, conducted on 213 Mputu individuals from Djuma (DRC), show a marked predominance of blood group O (65. %), followed by groups B (16.5%), A (10%), and AB (7. %).

At the gene level, the estimated allelic frequencies were 0.75 for O, 0.17 for B, and 0.08 for A. These distributions indicate strong genetic homogeneity within the studied population and suggest a structure consistent with the Hardy-Weinberg equilibrium model, confirmed by a $\chi^2 = 0.0127$, below the critical value of 7.8 (df = 3; $p < 0.05$).

These results align with classical observations in several sub-Saharan African populations, where group O is largely dominant (Duarte et al., 2020; Omotade et al., 2021). The predominance of the O allele may be related to an adaptive selective advantage, particularly in malaria-endemic regions, where studies have shown that individuals with blood group O enjoy relative protection against severe forms of Plasmodium falciparum malaria (Cserti and Dzik, 2007; Rowe et al., 2007).

The low frequency of alleles A and B (0.08 and 0.17 respectively) could result from several factors, including the small population size, the endogamous structure of the Mputu group, and natural selection acting on the ABO locus (Jobling et al., 2013). This configuration also reflects possible founder effects or genetic drift, commonly observed in culturally or geographically isolated populations (Cavalli-Sforza et al., 1994).

Compared with other ethnic groups in the DRC, the results observed among the Mputu of Djuma are similar to those reported for the Yansi and Yaka, where group O also dominates, representing 58% and 60% of individuals respectively (Kazadi, 2005; Lutete, 2007). Among the Mongo and Ngbandi, however, the proportions of groups A and B are slightly higher, demonstrating intra-national genetic diversity within the Congolese gene pool (Unyon, 2007).

The conformity of the ABO locus to the Hardy-Weinberg equilibrium suggests that the Mputu population under study is not subject to major evolutionary pressures such as directional selection, significant mutation, or recent immigration. This result supports the hypothesis of a locally stable panmictic system, in which marriages are still largely endogamous, maintaining genetic homogeneity (Hartl and Clark, 2007).

From an anthropological perspective, the high proportion of individuals with blood group O can be interpreted as a marker of ancestral African lineage, as this group is considered the oldest in evolutionary terms (Saitou and Yamamoto, 1997). This predominance also reflects a genetic continuity between the Mputu and other Bantu populations of Central Africa.

In summary, this study highlights a stable ethnogenetic structure among the Mputu of Djuma, with a gene distribution consistent with overall African observations. However, further research integrating molecular markers (mitochondrial DNA, microsatellites, SNPs) and a broader analysis of genetic polymorphism would help to better understand gene flow and the evolutionary history of this population.

5. Conclusion

The present study provides valuable insights into the distribution of ABO blood groups among the Mputu population of Djuma (DRC). The predominance of blood group O (59%) and the high frequency of the O allele (0.75) reflect a genetic structure consistent with patterns commonly observed across sub-Saharan African populations. The conformity of the ABO locus to Hardy–Weinberg equilibrium indicates a stable genetic composition, with no significant influence of migration, selection, or mutation in recent generations.

From an anthropogenetic perspective, the dominance of group O supports the hypothesis of an ancestral African lineage and highlights the genetic continuity of the Mputu people within the wider Bantu populations of Central Africa. These findings also suggest that cultural endogamy and relative geographical isolation have contributed to maintaining genetic homogeneity within this group.

However, the study's scope remains limited to serological data. Further research integrating molecular markers such as mitochondrial DNA, microsatellites, and SNPs would allow a deeper understanding of gene flow, evolutionary history, and the genetic relationships between the Mputu and neighboring ethnic groups. Such data could enrich the anthropological and biomedical knowledge of Congolese populations, providing a foundation for population genetics and transfusion medicine in the region.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

Statement of informed consent

Informed consent was obtained from all individual participants included in the study.

References

[1]   Cavalli-Sforza, L. L., Menozzi, P., and Piazza, A. (1994). The history and geography of human genes. Princeton University Press.

[2]   Cserti, C. M., and Dzik, W. H. (2007). The ABO blood group system and Plasmodium falciparum malaria. Blood, 110(7), 2250–2258. https://doi.org/10.1182/blood-2007-03-077602

[3]   Daniels, G. (2013). Human blood groups (3rd ed.). Wiley-Blackwell.

[4]   Duarte, A., Nunes, K., and Silva, J. (2020). Distribution of ABO and Rh blood groups among African populations: A review. African Journal of Medical Sciences, 17(2), 55–63.

[5]   Egesie, U. G., Egesie, O. J., Usar, J. I., and Johnbull, T. O. (2008). Distribution of ABO, Rhesus blood groups and haemoglobin electrophoresis among the undergraduate students of Niger Delta University, Nigeria. Nigerian Journal of Physiological Sciences, 23(1–2), 5–8.

[6]   Freeman, S., and Herron, J. C. (2020). Evolutionary analysis (6th ed.). Pearson.

[7]   Hartl, D. L., and Clark, A. G. (2007). Principles of population genetics (4th ed.). Sinauer Associates.

[8]   Institut National de la Statistique (INS). (2021). Annuaire statistique de la République Démocratique du Congo 2021. Kinshasa : INS.

[9]   Jobling, M. A., Hollox, E., Hurles, M., Kivisild, T., and Tyler-Smith, C. (2013). Human evolutionary genetics (2nd ed.). Garland Science.

[10]   Kayembe, K., Ilunga, P., and Luwesi, C. (2010). Étude des fréquences des groupes sanguins ABO et Rhésus dans la population Luba du Kasaï. Revue Congolaise de Biologie et Santé, 4(2), 45–53.

[11]   Kazadi, P. (2005). Étude de la distribution des groupes sanguins ABO et Rhésus chez les Yansi du Bandundu. Revue Congolaise de Biologie et Santé, 4(2), 45–53.

[12]   Lutete, J. (2007). Structure génétique du locus ABO chez les Yaka du Kongo Central. Annales de Biologie Africaine, 3(1), 17–26.

[13]   Mourant, A. E., Kopec, A. C., and Domaniewska-Sobczak, K. (1976). The distribution of the human blood groups and other polymorphisms (2nd ed.). Oxford University Press.

[14]   Mulumba, J., and Tshilombo, M. (2018). Fréquence des groupes sanguins ABO et Rhésus dans la population Kongo du Bas-Congo. Annales de Biologie Africaine, 9(1), 23–31.

[15]   Nwafor, A., and Onyenekwe, C. (2001). Prevalence of ABO and Rhesus blood groups and haemoglobin variants in a Nigerian population. African Journal of Biomedical Research, 4(3), 173–176.

[16]   Omotade, O. O., Adeyemo, A. A., and Kayode, C. M. (2021). Blood group distribution in sub-Saharan Africa and its anthropological significance. Journal of Human Genetics, 66(9), 823–832.

[17]   Rowe, J. A., Handel, I. G., Thera, M. A., Deans, A. M., Lyke, K. E., Kone, A., Diallo, D. A., Raza, A., Kai, O., Marsh, K., Plowe, C. V., Doumbo, O. K., and Moulds, J. M. (2007). Blood group O protects against severe Plasmodium falciparum malaria through the mechanism of reduced rosetting. Proceedings of the National Academy of

Sciences of the United States of America (PNAS), 104(44), 17471–17476. https://doi.org/10.1073/pnas.0705390104

[18]   Roychoudhury, A. K., and Nei, M. (1988). Human polymorphic genes: World distribution. Oxford University Press.

[19]   Saitou, N., and Yamamoto, F. (1997). Evolution of primate ABO blood group genes and their homologous genes. Molecular Biology and Evolution, 14(4), 399–411. https://doi.org/10.1093/oxfordjournals.molbev.a025773

[20]   Unyon, M. (2007). Étude comparative des groupes sanguins ABO chez les Mongo et Ngbandi de la RDC. Bulletin Médical Congolais, 12(3), 101–108.