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PHARMACOGNOSTIC PROFILES AND DNA BARCODING OF THE STEMBARK OF *IRVINGIA GABONENSIS* (AUBRY-LECOMTE EX O'RORKE) BAIL. (IRVINGIACEAE): A FORENSIC PHARMACOGNOSY DATA

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ABSTRACT: *Irvingiagabonensis* is a plant popularly used for both medicinal and dietary purposes. The plant have been used to treat various diseases like diabetes, inflammation, alopecia, fever and ulcers. The study was aimed at evaluating some pharmacognostic fingerprints and molecular DNA barcoding of the stem bark. The pharmacognostic fingerprint analysis of the stem bark was carried out using standard procedures while the molecular DNA barcoding was done using automated DNA extraction and barcoding by the polymerase chain reaction machine. The organoleptic evaluation showed that the greyish brown stem bark of *I. gabonensis* has a strong bitter taste, acrid odour and slightly coarse to the touch. Chemomicroscopic evaluations reveal the presence of cellulose, suberin, lignin, mucilage, prismatic calcium oxalate crystals and tannins. The transverse section of the stem bark showed bicollateral vascular bundle, beaded hexagonal shaped cork cells, fibre sclereids with wide cell lumen, non-striated eccentric oval shaped aggregate starch grains, and wide pith as observed under the scanning electron microscope. The moisture content was 5.13 ± 0.11 w/w %, total ash was 18.58 ± 0.23 w/w %, water soluble and acid insoluble ash were 13.96 ± 0.66 w/v % and 8.02 ± 0.17 w/v % respectively. All the values were within the acceptable ranges. Molecular studies using ribulose biphosphate carboxylase Large chain (rbcL) primers produced consensus DNA that shared alignment and phylogeny with *I. gabonensis* in the Genbank. Our study showed that *I. gabonensis* contain important pharmacognostic fingerprints that can distintguish it from closely related species, and help to check adulteration of drug from the stem bark.

INTRODUCTION: Traditional medicine system continues to play an essential role in health care, with about 80% of the world population relying mainly on traditional medicine as the primary source of health care¹.

It has been well documented that higher plants and their extracts have been used in the treatment of several diseases in traditional African medicine as an age-old practice these plants have been useful in the development of new drugs and continue to play an important role in the drug discovery process therefore there is need to standardize these products²⁻³. There is a renewed interest in drugs of natural origin due to their easy availability, accessibility and little or no side effects⁴, coupled with a growing interest in correlating the phytochemical



constituents of a medicinal plant with its pharmacological activity⁵. The Family Irvingiaceae comprises ten species of tropical trees found in Africa, Southeast Asia to western Malaysia. These species usually grow in regions with altitudes from 200 to 500 m with annual rainfall from 1200 to 1500 mm and at temperatures ranging from 20 to 38 °C⁶.

They are glabrous trees; wood is extremely hard; leaves sometimes papillate underneath mucilage cells in leaf and stem epidermis having secretory canals containing mucilage in leaves and stems. The leaves are alternate, simple, entire, petiolate, pinnately veined, coriaceous; stipules very large, unequal, intrapetiolar, encircling the terminal bud, early caducous and leaving a very distinct scar. Inflorescences are paniculate, axillary or terminal. The flowers are small, hermaphroditic, regular, pedicels articulated; the sepals are five in number, small and imbricate.

The petals are also five in number, free, imbricate, exceeding the sepals, the stamens are ten in number, which are distinct exceeding the petals and inserted below the large intrastaminal nectary disk. The filaments are plicately folded in bud, the anthers are subbasifixed. The ovary is superior, locular with one ovule per locule. The style is terminal and short. The stigma is punctiform. The fruit is a drupe with one or more pyrenes or a broadly winged samara. The seeds have large embryos, while the cotyledons are flattened and cordate, and the endosperm is fatty. The genera include *Desbordesia*, *Klainedoxa* and *Irvingia*⁷.

Irvingia is a genus of African and Southeast Asian trees of the Irvingiaceae family, sometimes known as wild African mango or bush mango. They produce edible mango-like fruits and are prized for their fat and protein-rich nuts. The species are vastly distributed with *Irvingia smithii* (central Africa), *Irvingia gabonensis* (west and central Africa), *Irvingiagrandifolia* (central Africa), *Irvingia excels* (central Africa), *Irvingia malayana* (Southeast Asia), *Irvingia robur* (west and central Africa), *Irvingiatenuinucleata* (west and central Africa) and *Irvingia tenuinucleata* (west and central Africa) being the seven (7) species⁸⁻⁹. *Irvingia gabonensis* is widely cultivated in West African countries including southwest and

southeast Nigeria, southern Cameroon, Côte d'Ivoire, Ghana, Togo, and Benin, to produce its edible fruit whose seed is used in the preparation of local delicious viscous soup for swallowing yam and cassava puddings Oladunjoye and Awani-Aguma¹⁰. Fat extracted from its seeds is commonly known as dika fat and majorly consists of C₁₂ and C₁₄ fatty acids, alongside smaller quantities of C₁₀, C₁₆, and C₁₈, glycerides and proteins.

Irvingia gabonensis seeds are also a good source of nutrients including a variety of vitamins and minerals such as sodium, calcium, magnesium, phosphorus, and iron. It is also a rich source of flavonoids (quercetin and kaempferol), ellagic acid, mono-, di-, and tri-O-methyl-ellagic acids, and their glycosides which are potent antioxidants¹¹.

Phytochemical analysis of its seeds showed that it contains tannins, alkaloids, flavonoids, cardiac glycosides, steroids, carbohydrates, volatile oils, and terpenoids and its proximate moisture 1.4 ± 0.11%, ash 6.8 ± 0.12%, crude lipid 7.9 ± 0.01%, crude fibre 21.6 ± 0.45%, and crude protein 5.6 ± 0.20% (Mahunu et al., 2019; Olorundare et al., 2020). Pure compounds already isolated from the seed extract include methyl 2-[2-formyl-5-hydroxymethyl)-1 H-pyrrolyl]-propanoate, kaempferol-3-O-β-D-6" (p-coumaroyl) glucopyranoside and lupeol (3β-lup-20(29)-en-3-ol). Meanwhile, the antioxidant property of *Irvingia gabonensis* seed extract has been largely attributed to its high lupeol content¹².

Plant molecular barcoding is a technique used in identifying and classifying plant species based on their DNA sequences. It involves the use of short, standardized DNA sequences, usually from specific genes, as "barcodes" to uniquely identify plant species. The most commonly used DNA sequences for plant molecular barcoding are those from the chloroplast genome, specifically the regions known as ribulose biphosphate carboxylate large gene (*rbcL*) and Maturase K gene (*mat K*). These regions are highly conserved, meaning they are similar across plant species, but also contain enough variation to differentiate between different plant species¹³. The process of plant molecular barcoding typically involves several steps. First, plant tissue is collected and DNA is extracted from

the sample. The *rbcL* and *mat K* regions of the chloroplast genome are then amplified using polymerase chain reaction (PCR), a process that selectively amplifies specific DNA sequences. The PCR products are then sequenced, and the resulting DNA sequences are compared to a reference database of known plant barcodes to identify the plant species¹⁴.

Plant molecular barcoding has several advantages over traditional methods of plant identification, such as morphology-based identification. DNA sequences are less subject to variation due to environmental factors, making molecular barcoding more reliable and accurate. Additionally, DNA sequences can be easily stored and shared in databases, facilitating the creation of a comprehensive library of plant barcodes for future use¹⁵.

Irvingia gabonensis is known to contain a variety of bioactive compounds with potential health benefits. However, there are concerns about the sustainability of harvesting the bark of this tree for medicinal use, as well as the potential for misidentification and adulteration of different samples of bark. By using DNA barcoding techniques, researchers can accurately identify different samples of *Irvingia gabonensis* stem bark and distinguish them from other plant species. This can help to ensure that the bark is being harvested sustainably and that consumers are getting the genuine product. It can also help to prevent the sale of adulterated or counterfeit products¹⁶.

Several methods can be used for DNA barcoding of *Irvingia gabonensis* stem bark, including PCR amplification of specific regions of the DNA and sequencing of the amplified DNA. Once the DNA sequences have been obtained, they can be compared to a reference database of known sequences to identify the species.

DNA barcoding of *Irvingia gabonensis* stem bark can provide a valuable tool for ensuring the authenticity and sustainability of this important medicinal resource. It has the potential to improve the quality and safety of traditional medicines and commercial products, as well as aid in forensic investigations¹⁷. However, to the best of our knowledge, there is no report on the

pharmacognostic fingerprints and DNA barcoding of the stem bark of *I. gabonensis*. Therefore, the present study was aimed at identifying some pharmacognostic profiles of stem bark and providing its DNA barcoding for easy taxonomic identification from closely related species which will help in assessing adulteration of medicinal and economic products from the stem bark of the plant.

MATERIALS AND METHODS:

Chemicals, Reagents, and Equipment: Molecular and analytical tools such as cetyltrimethylammonium bromide buffer (CTAB), Proteinase-K, RNase A, 95% ethanol, isopropanol, DNA polymerase (Taq polymerase), deoxyribonucleoside triphosphates (dNTPs), PCR primers (*rbcL* II), DNA polymerase (e.g., Taq polymerase), sequencing primers (specific to the barcoding region of interest), fluorescent dyes, PCR machine (Eppendorf master-cycler nexus X2 thermal cycler), UV-vis spectrophotometer (NANODROP 2000c Thermo-Scientific, UK), gel electrophoresis system (Maxi-Broad-H), centrifuge (Eppendorf 5702), refrigerator and freezer (Haier Thermocool Refrigerator HR-130 AS –Silver/Haier Thermocool Chest Freezer HTF 150HAS R6 Silver), Vortex mixer (LABOID L 20), UV transilluminator Visualizer (Enduro-temp V1) and DNA extraction kits **Table 1**.

TABLE 1: DNA EXTRACTION KIT SPECIFICATIONS USED

Component	Product procured (mL)	Volume used (mL)
Lysis buffer L	1 x 30, 2 x 60	30
Binding buffer I	1 x 7, 1 x 25	7
Solution WN	1 x 18, 1 x 55	18
Wash solution A	2 x 38	38
Elution buffer B	1 x 30	15
RNase A	5 vials (5 x 80 µL)	1 vial (80 µL)
Spin columns	1 x 250	50
Filter columns	1 x 250	50
Collection tubes	1 x 500	100
Elution tubes	1 x 250	50
Product insert	1 x 1	1

Collection, Identification, and Preparation of Plant Materials: Fresh stem barks of *I. gabonensis* were collected from a forest in the Iragbiji community, Osun State, Nigeria, in October 2018. The plant was identified by a taxonomist Mr Namadi Sunusi of the Department of Botany, Ahmadu Bello University, Zaria.

A voucher specimen number ABU06926 was deposited for the plant at the herbarium of the Department of Botany for referencing. The stembarks were allowed to dry under shade for two weeks and prepared accordingly following standard procedures.

Macroscopic examination of *I. gabonensis*

Stembark: Macroscopic observations were carried out on the whole dried stembark of the plant, and these entail colour, odour, taste, texture, shape and fracture¹⁸.

Microscopic analysis of *I. gabonensis* Stembark:

To remove obscuring materials, the powdered stembark of *I. gabonensis* was cleared with a 70% chloralhydrate solution and boiled in a water bath for 30 min. The cleared sample was mounted on a microscopic slide with dilute glycerol and observed under the microscope (40x), for the presence of pharmacognostic fingerprints of the powdered stembarks. Suitable photographs were taken and recorded¹⁹.

Scanning Electron Microscopy of the Leaf of *I. gabonensis*:

The detailed internal structure (transverse section) of the leaf was observed using a Phenom desktop scanning electron microscope (PhenomWorld, USA) at 8000x magnification to reveal some pharmacognostic features.

Chemo-microscopic Analysis on *I. gabonensis*

Stembark: This was carried out on powdered stembark of *I. gabonensis*. Briefly, the finely crushed stembark was cleared using 70% chloral hydrate solution to remove obscuring materials. It was then heated for 30 min in a water bath. Using two drops of dilute glycerol, the cleared sample was then placed on a microscope slide, and the presence of several cell inclusions and cell wall components was observed using various detecting reagents¹⁹⁻²⁰.

Determination of Physicochemical Parameters of *I. gabonensis* Powdered Stembark:

The physicochemical parameters such as moisture content, ash value, total ash, extractive values, acid insoluble, water-soluble ash values, swelling and foaming indices were determined following standard procedures. For each parameter, a total of ten replicate readings were taken, and results were recorded as mean \pm SE.

DNA Barcoding of *I. gabonensis* Stembark:

DNA barcoding of *I. gabonensis* was carried out according to the methods by Kress *et al.*,¹⁵ and de Oliveira *et al.*,²¹. Various steps were involved following protocols previously described. DNA extraction was carried out using the DNA kit (NORGEN BIOTEK[®] Plant DNA isolation kit, USA).

DNA Extraction Procedure:

Lysate Preparation: Less than 100 mg of plant tissue was placed into a mortar and ground into a powder. The ground material was then transferred into a DNase-free 1.7 mL- micro-centrifuge tube with 500 μ L of lysis buffer L, and 1 μ L of RNase A. was added. This was incubated at 65⁰ C for 10 min with occasional mixing of the lysate 3 times during incubation by inverting the tube. 100 μ L of binding buffer 1 was then added, mixed thoroughly and incubated for 5 min on ice.

The filter column (clear O-ring) with one of the provided collection tubes was then assembled, and the lysate was pipetted into the filter column and spun for 2 min at 20,000 x g (~14,000 RPM). The clear supernatant from the flow-through was then transferred into a DNAase-free micro-centrifuge tube using a pipette. An equal volume of 70% ethanol was added to the lysate collected (100 μ L of ethanol was added to every 100 μ L of lysate), and vortex to mixed²¹.

Binding to Column: A spin column (grey O-ring) with a collection tube was assembled, and then up to 650 μ L of the clarified lysate with ethanol onto the spin column and centrifuge for 1 min at 10,000 x g (~10,000 RPM). The flow-through was discarded, and then the spin column with the collection tube was reassembled.

Column Wash: 500 μ L of solution WN was added to the column and centrifuge for 1 min at 20,000 x g (~14,000 RPM). The flow-through was discarded and the spin column with its collection tube was reassembled. 500 μ L of Wash solution A was added to the column and centrifuge for 1 min at 20,000 x g (~14,000 RPM).

The flow-through was then discarded and the spin column with its collection tube was reassembled, and the process repeated. The column was spun for

2 min at 20,000 x g (~14,000 RPM) to thoroughly dry the resin, and the collection tube was discarded.

DNA Elution: The column was placed into a fresh 1.7 mL elution tube, and 100 µL of elution buffer B was added to the column and incubated for 1 min at room temperature, then centrifuged for 1-2 min at 10,000 x g (~10,000 RPM).

DNA Quantification: The extracted DNA was then analysed using a UV-vis spectrophotometer (NANODROP 2000c), and the concentration of DNA was then obtained.

DNA Storage: The purified genomic DNA extracted was then stored in a DNA sample bottle at 2-8 °C in a refrigerator.

DNA Amplification: The polymerase chain reaction (PCR) master mix containing the *I. gabonensis* DNA, the forward primer, reverse primer, deoxynucleotide triphosphates (dNTPs) mix, taq polymerase, buffer solution with DNA polymerase and magnesium chloride (MgCl₂) solution was placed in a PCR tube and vortex gently to ensure homogeneity.

The rbcL II primer was used in this mix. The PCR tubes were then placed into the thermal cycler, ensuring they were securely sealed; then the appropriate heating block was set on the PCR machine. After the thermal cycling process was completed, the tubes were removed and run on agarose gel with a DNA ladder to estimate the size of the amplified product ²¹.

Agarose Gel Electrophoresis: This procedure was used to separate and analyze the DNA obtained from thermocycler ¹⁵.

Briefly, 2 g of agarose powder was weighed and added to a beaker containing 200 mL volume of TAE/TBE buffer, to make (1% w/v) the mix was then gently heated on a hot plate until the agarose was completely dissolved. 0.5 µg/mL ethidium bromide was the added to the warm agarose solution.

The solution was mixed well and poured into the gel casting tray, a space was left for the comb and was allowed to cool and solidify. The DNA sample and DNA ladder were then mixed with

bromophenol blue which is the loading dye and then kept ready. The comb was carefully removed from the solidified gel and placed into the gel electrophoresis apparatus filled with TAE/TBE buffer, ensuring the wells were on the cathode side. Using a micropipette, the DNA sample and ladder were carefully placed into separate wells.

The electrophoresis was run at 90V for 45 min. After this, the gel was removed and placed on a UV transilluminator where the separated DNA fragments were visualized and recorded ²¹.

DNA Sequencing and Analysis: The purified DNA fragment obtained was then sequenced; where the sequence obtained was trimmed and cleaned to remove any low-quality or ambiguous bases. The consensus sequences were then subjected to sequence analysis using bioinformatics tools; comparing with reference sequences available in public DNA barcode databases GenBank and BOLD (Barcode of Life Data Systems).

Statistical Analysis: Data obtained from the physicochemical analysis were expressed as mean ± SE (n = 10).

RESULTS:

Macroscopic Parameters of *I. gabonensis*

Powdered Stembark: The organoleptic evaluation of *I. gabonensis* stembark showed a brown to greyish colour powder with a slightly acrid odour and strong bitter taste as well as coarse texture

Table 2.

TABLE 2: ORGANOLEPTIC PARAMETERS OF *I. GABONENSIS* POWDERED STEMBARK

Test	Observation
Colour	Greyish-brown
Odour	Acrid
Taste	Strong bitter
Texture	Coarse

Microscopic Examination of *I. gabonensis*

Stembark: The scanning electron microscopy of the leaf revealed the presence of a few numbers of paracytic stomata on the adaxial surface (upper) than on the abaxial surface (lower) which is typical of most terrestrial plants among the angiosperms

Fig. 1.

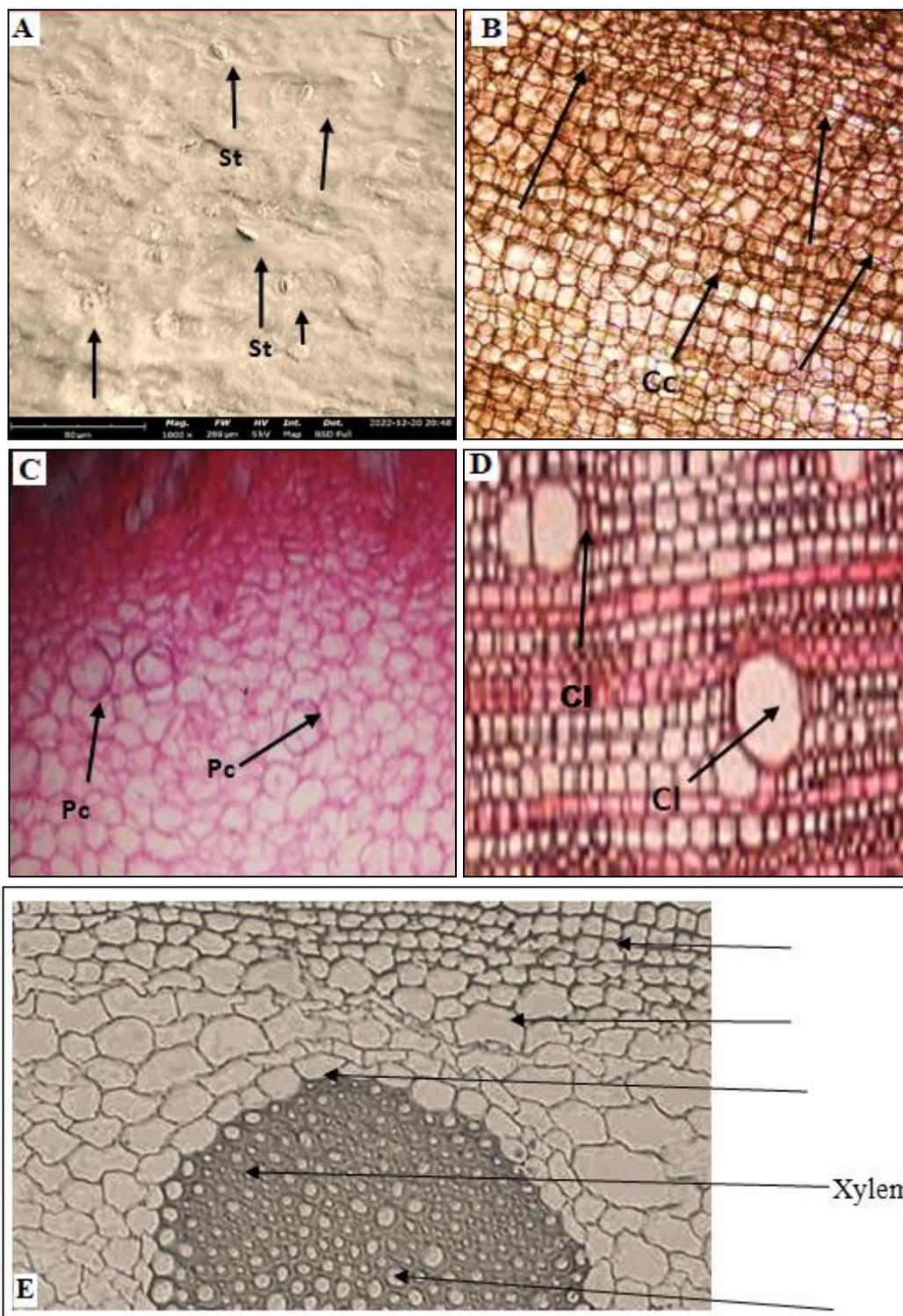


FIG. 1: SCANNING ELECTRON MICROSCOPY OF A LONGITUDINAL SECTION THROUGH *I. GABONENSIS* SHOWING PARACYTIC STOMATA (ARROWS); 8000X (A), BEADED CORK CELLS (B), PARENCHYMATOUS CELLS; PC STAINED WITH SAFRANIN (C), FIBRE SCLEREIDS WITH WIDE CELL LUMEN; CL (D), AND TRANSVERSE SECTION OF STEMBARK WITH WIDE PITH (E) AS VIEWED USING THE SCANNING BIOLOGICAL MICROSCOPE, 3000X. A FEW STOMATA WERE OBSERVED ON THE UPPER SURFACE OF THE LEAF TYPICAL OF TERRESTRIAL ANGIOSPERMS (A).

Chemomicroscopical Evaluation of the Powdered Stembark of *I. gabonensis*: Chemomicroscopical evaluation of the powdered stembark of *I. gabonensis* revealed the presence of cellulose cell

wall, lignified cell wall, tannins, starch, calcium oxalate, suberin and mucilage **Table 3.**

TABLE 3: CHEMOMICROSCOPICAL FEATURES OF *I. GABONENSIS* STEMBARK POWDER

Constituents	Inference
Starch	+
Lignin	+
Tannins	+
Calcium oxalate	+
Calcium carbonate	-
Cellulose	+
Suberin	+
Gums and Mucilage	+

+: present and -: absent.

Evaluation of Physicochemical Parameters of *I. gabonensis* the Stembark: The total ash was $18.58 \pm 0.23\%$ w/w, acid-insoluble ash was $8.02 \pm 0.17\%$ w/w and water- soluble ash was $13.96 \pm 0.66\%$ w/w, to the physicochemical parameters. The ethanol-soluble extractives were $18.20 \pm 0.28\%$ w/v and $28.60 \pm 0.12\%$ w/v water-soluble extractives. The moisture content was 5.13 ± 0.11 .

The plant's swelling index was 4.55 ± 0.32 mL. The plant's foaming index was calculated as $142.9 \pm 0.61\%$ w/v **Table 4.**

TABLE 4: PHYSICOCHEMICAL PARAMETERS OF *I. GABONENSIS* STEMBARK POWDER

Parameters	Values (%w/w or w/v) \pm SE
Moisture content	5.13 ± 0.11
Total ash	18.58 ± 0.23
Acid insoluble ash	8.02 ± 0.17
Water soluble ash	13.96 ± 0.66
Ethanol extractive	18.20 ± 0.28
Water extractive	28.60 ± 0.12
Swelling index	4.55 ± 0.32 mL
Foaming index	142.9 ± 0.61

Data were expressed as means \pm SE (n = 10).

DNA Molecular Barcoding Analysis: Results of the gel electrophoresis after visualization show a clear band concerning the ladder as presented in **Fig. 2.**

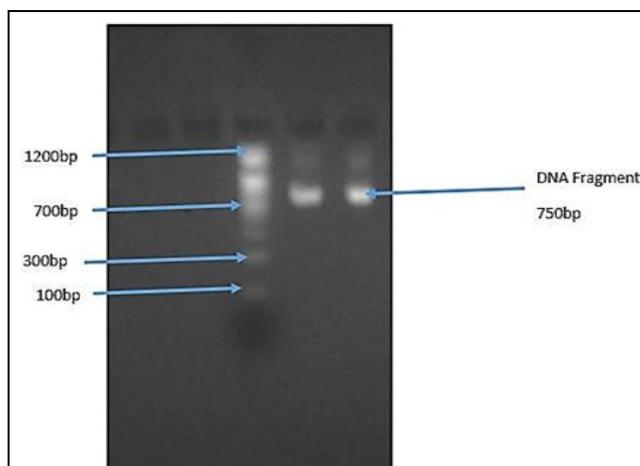


FIG. 2: ELECTROPHORESIS GEL STAINED WITH BROMOPHENOL BLUE UNDER UV TRANSILLUMINATOR COMPARED WITH A 1200BP LADDER

Sequencing and Analysis of DNA Fragments: **Fig. 3(A)** below shows the consensus DNA after the sequencing process. This sequence was obtained after the purified fragment was trimmed and cleaned to remove any low-quality or ambiguous bases. The consensus DNA obtained was analysed with bioinformatics tools; the DNA was compared with reference sequences available in public DNA barcode databases NCBI and blasted. **Fig. 3(B)** and **(C)** show that the consensus DNA sequence has an alignment like that of *I. gabonensis*. Similarly, **Fig. 3(D)** shows the consensus DNA's phylogenic relationships.

AGCAAGTGTGGATTCAAAGCTGGTGTAA
AGATTATAAATTACTTATTATACTCCTGACT

ATGAAACCAAAGATACTGATATCTTGGCAG
ATTCCGAGTAACTCCTCAACCTGGAGTTCC
GCCTGAGGAAGCAGGGGCGCGTTGCTTCTA
CTGGGACATGGACAACTGTGTGGACCGGGA
CTTACCTAGTCTTGATCGTTATAAGGGAAG
ATGCTACCATCCCGTTGCGGTGGAGAAGAA
AATCAATATATTGCTTATGTAGCTTATCCTT
TCCTGAACTAAATGTTTACTTCCATTGTGGG
TAATGTATCGGGTTGGCAAAGTCTACGCGC
CCTGCGTTTGGAGGATTTGCGAATCCCTGC
CTACTGCTTATACTAAAACCTTCCAAGGTCC
GCCTCATGGCATTCAAGATGAACAAGTACG
GTCGCCCTATTGGGCTGACTATAACCTA
AATTGGGTTTATCCGCTAAGAATTACGGTA
AGTTTATGAATGTCTCCGCGGTGGGCTTGA
TTTTACGAAAGATGATGAGATGTGGGTACG

TGAATTCCCAACCATTATGCGTTGGAGAG
ACCGTATTTTGTGCCGAAGCGCTTTTAA

GCACAGGCCGAAACAGGTGAAAGACA
TTATTTGAAT GCTACTCGTC

(A)

Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments

Download | Select columns | Show 100

select all 100 sequences selected

GenBank | Graphics | Distance tree of results | MSA Viewer

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> Ivingia gabonensis voucher PM5258 ribulose-1,5-bisphosphate carboxylase/oxygenase large s...	Ivingia gabon...	734	734	99%	0.0	87.12%	706	KC628322.1
<input checked="" type="checkbox"/> Desbordesia glaucescens voucher PM5464 ribulose-1,5-bisphosphate carboxylase/oxygenase l...	Desbordesia g...	728	728	99%	0.0	86.98%	706	KC628662.1
<input checked="" type="checkbox"/> Ivingia malayana chloroplast rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase la...	Ivingia malay...	728	728	99%	0.0	86.98%	1331	AB233892.1
<input checked="" type="checkbox"/> Ivingia gabonensis voucher PM5099 ribulose-1,5-bisphosphate carboxylase/oxygenase large s...	Ivingia gabon...	726	726	98%	0.0	87.05%	702	KC628208.1
<input checked="" type="checkbox"/> Desbordesia glaucescens voucher PM4968 ribulose-1,5-bisphosphate carboxylase/oxygenase l...	Desbordesia g...	725	725	99%	0.0	86.84%	706	KC628066.1
<input checked="" type="checkbox"/> Klainedoxa gabonensis voucher MO-398653 plastid complete genome	Klainedoxa ga...	723	723	99%	0.0	86.84%	160118	NC_044475.1
<input checked="" type="checkbox"/> Ivingia malayana ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene...	Ivingia malay...	723	723	99%	0.0	86.84%	1425	JX664054.1
<input checked="" type="checkbox"/> Desbordesia glaucescens ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) gene parti...	Desbordesia g...	721	721	98%	0.0	86.99%	1398	AY663631.1

(B)

<input checked="" type="checkbox"/> Klainedoxa gabonensis ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) gene, partial...	Klainedoxa ga...	710	710	98%	0.0	86.71%	1398	AY663630.1
<input checked="" type="checkbox"/> Suregada glomerata ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) ge...	Suregada glo...	601	601	99%	1e-167	83.80%	1407	AY794896.1
<input checked="" type="checkbox"/> Securinea capuronii ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) gene, partial cd...	Securinea ca...	595	595	99%	5e-166	83.66%	1408	AY663621.1
<input checked="" type="checkbox"/> Cleistanthus pemieri ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) gene, partial cds...	Cleistanthus p...	590	590	99%	2e-164	83.52%	1408	AY663578.1
<input checked="" type="checkbox"/> Idesia polycarpa chloroplast complete genome	Idesia polycarpa	586	586	96%	3e-163	83.91%	156077	MN057562.1
<input checked="" type="checkbox"/> Bennettiodendron leprosipens chloroplast complete genome	Bennettiodend...	586	586	96%	3e-163	83.91%	157330	MK301202.1
<input checked="" type="checkbox"/> Idesia polycarpa chloroplast rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase lar...	Idesia polycarpa	586	586	96%	3e-163	83.91%	1331	AB233935.1
<input checked="" type="checkbox"/> Gomphia serrata chloroplast rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase lar...	Campylosper...	579	579	99%	5e-161	83.24%	1331	AB233907.1
<input checked="" type="checkbox"/> Amanoa strobilacea ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) gene, partial cds...	Amanoa strobi...	575	575	96%	7e-160	83.62%	1408	AY663562.1
<input checked="" type="checkbox"/> Ouratea sp. CCD-2012 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) g...	Ouratea sp. C...	573	573	99%	2e-159	83.10%	1425	JX664061.1
<input checked="" type="checkbox"/> Cleistanthus oblongifolius ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) gene, parti...	Cleistanthus o...	573	573	99%	2e-159	83.10%	1408	AY663577.1
<input checked="" type="checkbox"/> Ouratea hexasperma isolate NE826 ribulose-1,5-bisphosphate carboxylase/oxygenase large su...	Ouratea hexas...	569	569	96%	3e-158	83.48%	704	MT304330.1
<input checked="" type="checkbox"/> Dialypetalanthus fuscescens ribulose-1,5-bisphosphate carboxylase (rbcL) gene, partial cds, chl...	Dialypetalanth...	569	569	96%	3e-158	83.33%	1380	AF206761.1
<input checked="" type="checkbox"/> Idesia polycarpa TF<JPN>-TW023363 chloroplast rbcL gene for ribulose-1,5-bisphosphate carb...	Idesia polycarpa	568	568	93%	1e-157	83.82%	666	LC691920.1
<input checked="" type="checkbox"/> Campylospermum sulcatum voucher PM5492 ribulose-1,5-bisphosphate carboxylase/oxygenase...	Campylosper...	568	568	99%	1e-157	82.96%	706	KC628103.1
<input checked="" type="checkbox"/> Campylospermum flavum voucher PM5440 ribulose-1,5-bisphosphate carboxylase/oxygenase la...	Campylosper...	568	568	99%	1e-157	82.96%	706	KC628026.1
<input checked="" type="checkbox"/> Pseudolachnostylis maprouneifolia ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) g...	Pseudolachno...	566	566	98%	4e-157	83.08%	1398	AY663614.1
<input checked="" type="checkbox"/> Campylospermum flavum voucher PM5251 ribulose-1,5-bisphosphate carboxylase/oxygenase la...	Campylosper...	564	564	96%	1e-156	83.33%	703	KC628443.1
<input checked="" type="checkbox"/> Idesia polycarpa TF<JPN>-TW021583 chloroplast rbcL gene for ribulose-1,5-bisphosphate carb...	Idesia polycarpa	562	562	93%	5e-156	83.75%	661	LC692465.1

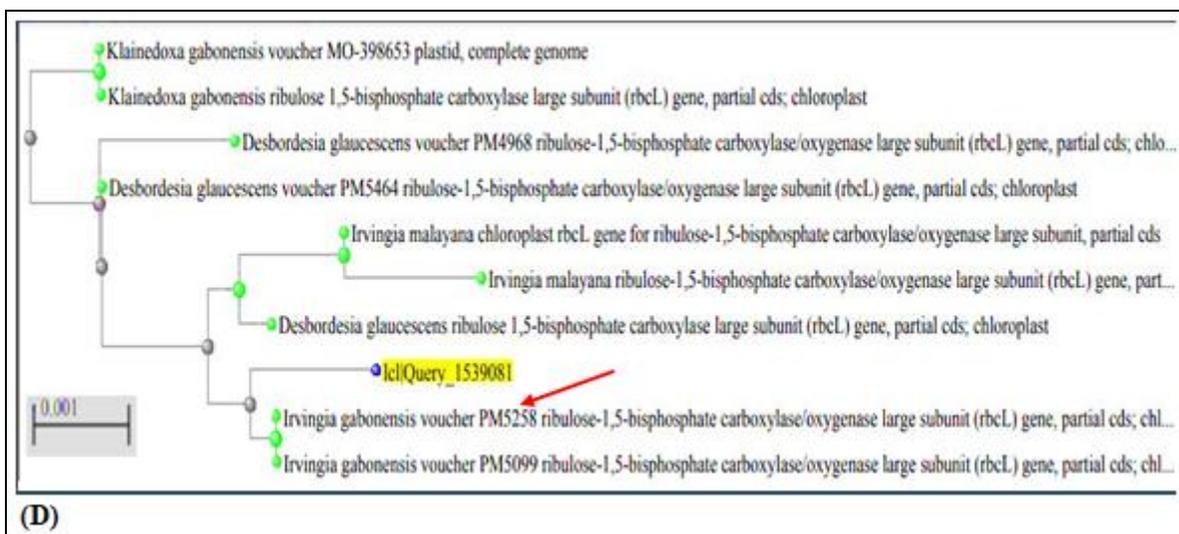
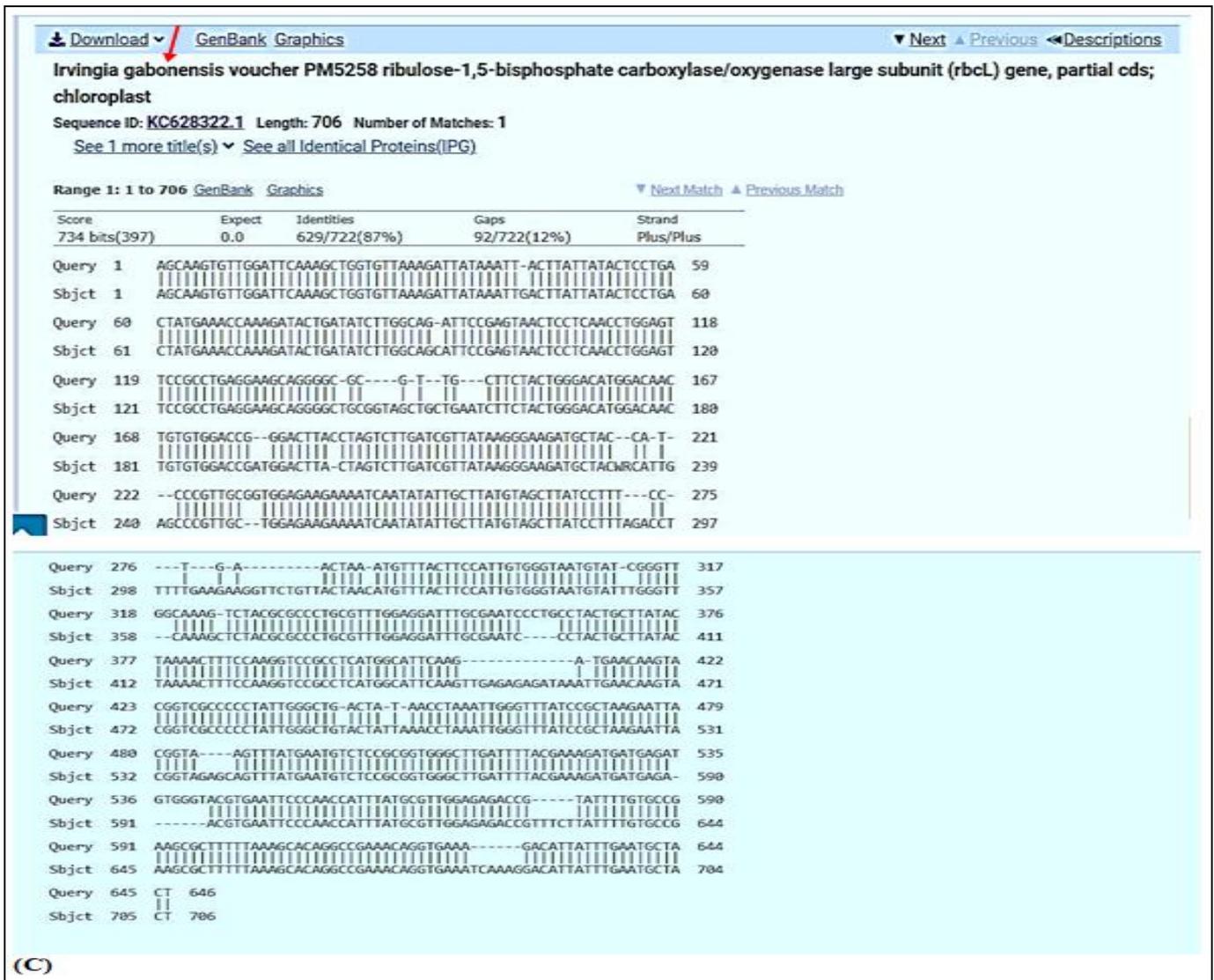


FIG. 3: CONSENSUS DNA OBTAINED FROM SEQUENCING OF THE DNA FRAGMENTS BY THE PCR MACHINE(A), CONSENSUS DNA MATCHING WITH *I. GABONENSIS* SPECIES IN THE GENBANK (B), CONSENSUS DNA ALIGNMENT WITH SPECIES OF *I. GABONENSIS* PRESENT IN THE GENBANK GRAPHICS (C), AND PHYLOGENY TREE SHOWING THE TAXONOMIC RELATIONSHIP BETWEEN *IRVINGIA SPECIES* AND THE CONSENSUS DNA FRAGMENTS(D). THE RED ARROW INDICATES THE TAXON OF *I. GABONENSIS* FROM THE GENBANK.

DISCUSSION: Macroscopical evaluation of the stem bark of *I. gabonensis* reveals a greyish-brown colouration. The stem bark is known for its distinctive greyish-brown colouration. This colouration is a result of tannins and flavonoids that are present in the plant, which was observed and reported by Ojo²². Tannins are a type of plant compound that is often responsible for the astringency or bitterness of certain foods²³. The organoleptic evaluation of the stem bark of *I. gabonensis* showed that the bark is greyish-brown in colour. The colour of the stem bark is usually associated with the age of the plant, as it matures naturally takes up a brownish coloration²⁴⁻²⁵. Environmental conditions are also implicated in the colour of the stem bark as described by Savage and Vellend²⁶. Other factors such as the composition of minerals in the soil have also proven to be significant as a determinant of the colour of the stem bark²⁷.

This research has also discovered that the odour of the stem bark of *I. gabonensis* is acid, this was also described in a research conducted in 2020 by Egwunatum, and co-workers²⁸, to study the effect of variegated forest soil amendments on the germination and early growth of *I. gabonensis* where the odour of the stem bark was one of the parameters evaluated and was concluded to be acid. Otitolaiye et al.²⁹, in research conducted to evaluate the phytochemical activity and in-vitro antioxidant potential of aqueous and ethanol extracts of *I. gabonensis* stem bark, reported the odour as bitter. The odour of *I. gabonensis* stem bark can be associated with the presence of resins in the cells³⁰.

A study conducted by Godayol et al.³¹, which aims to study odour-causing organic compounds in wastewater treatment plants, reported that the presence of certain phenols and aldehydes in the stem bark which they postulated is responsible for its odour. Kola-Mustapha et al.³², reported that environmental conditions play a significant contribution to the odour that is associated with stem barks. The texture of *I. gabonensis* as determined by this research is coarse, this was also the conclusion drawn by Nuhu and co-workers in 2020³³, in research that aimed to establish the macroscopic profile of *I. gabonensis* in Wistar rats. Cell division that is influenced by the environment

can affect the texture of the stem bark Funada et al.³⁴. A tough fibrous sclerenchyma can also be implicated in the texture of the stem bark, this was described in research conducted by Zhang, and co-workers³⁵. The chemomicroscopic analysis of the stem bark of *I. gabonensis* revealed the presence of cellulose, suberin and lignin, this is consistent with research conducted by Nuhu et al.³³ while investigating the safety profile of *I. gabonensis* root bark extract. Mgbemena, and co-workers in 2019³⁶, studying the chemical composition, proximate and phytochemical analysis of the peels, seed coat, leaves and seeds of *I. gabonensis*, reported the presence of cellulose, suberin and lignin in their chemomicroscopic analysis.

Cellulose typically adds to the structural support of the plant hence its presence is integral for strength and rigidity Pauly et al.³⁷, this discovery was made while studying the molecular domains of the cellulose/xyloglucan network in the cell walls of higher plants. Cellulose also serves as a barrier against pathogens that could damage tissues involved in the transportation of water and minerals Souza et al.³⁸. Therefore cellulose plays a significant role in regulating water and nutrient exchange in the plant, this is made possible through small pores present in them that assist in the movement Franca et al.³⁹. Suberin which was present in the stem bark is a waxy hydrophobic substance that helps to prevent water loss in the plant especially when environmental conditions are not favourable de Silva et al.²¹. Suberin also protects from pathogens and extends the lifespan of the plant Shukla and Barberon⁴⁰. Like cellulose, suberin found in the stem bark plays an important role in regulating the movement of water and nutrients in and out of plant tissues. Baxter et al.⁴¹.

A moisture content of 5.13% for the stem bark of *I. gabonensis* indicates that 5.13% of the weight of the bark is water. Moisture content is an important parameter in the processing and storage of plant materials. A high moisture content can lead to microbial growth and spoilage, while a low moisture content can result in brittleness and loss of quality. The ideal moisture content for the stem bark of *I. gabonensis* would depend on the intended use of the material. For medicinal use, a moisture content of 5.13% is relatively low and indicates that the bark has been properly dried and stored.

This low moisture content helps to preserve the active compounds in the bark and ensures its effectiveness. All these and other pharmacognostic fingerprints evaluated in this study perform various functions in plants and are used in the pharmaceutical industry for quality assurance.

The obtained DNA sequence of 650 base pairs after sequencing was subjected to a BLAST (Basic Local Alignment Search Tool) analysis. BLAST is a widely used bioinformatics tool that compares the query sequence against a vast database of known sequences to find similarities. The BLAST analysis has shown that the 650-base pair sequence from *I. gabonensis* aligns significantly with an entry in the GenBank database. This suggests that the sequence obtained from the organism shares similarities with a previously documented sequence in GenBank. The fact that the sequenced DNA aligns with a known sequence in the GenBank database supports the accuracy and validity of the sequencing process. It indicates that the DNA sample extracted from *I. gabonensis* is consistent with genetic information previously documented for this species. While the alignment with an existing sequence is a positive indication, further analysis may be required to fully characterize the genetic makeup of *I. gabonensis*. This will involve sequencing comparison with additional sequences, and functional analysis of specific genes or regions.

CONCLUSIONS: Our study comprehensively evaluated various pharmacognostic parameters and DNA barcoding of *I. gabonensis* stem bark, shedding light on its botanical and genetic characteristics to provide accurate taxonomic identification. Through detailed analysis, essential parameters such as moisture content, acid-insoluble ash, and total ash among others were determined, providing crucial insights into the plant's quality and purity. Moreover, the successful extraction and sequencing of a DNA fragment from the chloroplast gene further enriched our understanding of the genetic makeup of *I. gabonensis*. The deposition of this DNA sequence in GenBank enhances accessibility for future studies and facilitates accurate species identification and authentication. By integrating traditional pharmacognostic methods with modern molecular techniques, this research contributes valuable data to the field of Pharmacognosy and genetic resource

conservation. Moving forward, the findings from this study serve as a foundation for further research into the medicinal and genetic potential of *I. gabonensis*.

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CONFLICT OF INTEREST: We have none.

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