Dataset on rbcl-based intra-specific diversity of Gongronema latifolium Benth: (Apocynaceae) in South-East Nigeria

Conrad Asotie Omonhinmin*, Chinedu Charles Onuselogu, Enameguono Olomukoro

Department of Biological Sciences Biotechnology Cluster, College of Science and Technology, Covenant University, Canaan land Ota, Ogun State, Nigeria

ABSTRACT

Gongronema latifolium (Apocynaceae) is a versatile plant of nutritional and medicinal value and is widely distributed and endemic to the South-Eastern region of Nigeria. The plant is relatively wild and its natural habitat is threatened by deforestation, excessive exploitation and constant expansion of the urban areas into its endemic space. Hence, there is a need to understand its genetic diversity for breeding and conservation. The data consist of fourteen partial rbcl gene sequences, nucleotide compositions and amino acid profiles of G. latifolium. The data set provides insight on the species genetic diversity and evolution that is important for scientist and breeders alike as well as for conservation efforts of the species.

© 2022 The Author(s). Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/)

* Corresponding author:
E-mail address: conrad.omonhinmin@covenantuniversity.edu.ng (C.A. Omonhinmin).


**Specifications Table**

| Subject                  | Biological Science |
|--------------------------|-------------------|
| Specific subject area    | Agricultural, Genetic diversity, Phylogenetics, Evolution |
| Type of data             | Tables, Figure |
| How data were acquired   | Amplification of the *rbcl* gene through PCR and DNA Sanger sequencing. |
| Data format              | Raw, Analyzed |
| Parameters for data collection | Whether the geographical locations of *G. latifolium* across South-Eastern Nigeria affect intra-specific gene sequence variation in ribulose 1, 5 bisphosphate carboxylase/oxygenase (*rbcl*). |
| Description of data collection | Young leaf samples of *G. latifolium* were collected in South-Eastern Nigeria (Anambra, Ebonyi, Imo, Enugu and Abia) Table 1. All accessions were evaluated using *rbcl* primers and the population diversity, nucleotide and amino acids compositions of the accessions were estimated using DnaSP 4.5. Codon usage bias and the codon usage indices were estimated using CodonW. |
| Data source location     | The data locations are summarized in Table 1. |
| Data accessibility       | The sequence data of the accessions have been deposited in NCBI GenBank data base sequence and has the following accession numbers; MH305573.1, MH305574.1, MH305578.1, MH305579.1, MH305580.1, MH305570.1, MH305571.1, MH305572.1, MH305581.1, MH305582.1, MH305583.1, MH305575.1, MH305576.1, MH305577.1. [https://www.ncbi.nlm.nih.gov/nuccore/?term=Gongronema+latifolium](https://www.ncbi.nlm.nih.gov/nuccore/?term=Gongronema+latifolium) |

**Value of the Data**

- This data provides information of the genetic diversity of *G. latifolium* sequences across South-Eastern Nigeria using information from partial *rbcl* gene sequences, nucleotide polymorphism and amino acids composition.
- The *rbcl* gene sequences can be employed by plant taxonomists to trace the molecular phylogeny, evolution and sub-speciation of *G. latifolium*.
- This data identifies areas of high genetic diversity of *G. latifolium* which can be adopted to create germplasm for species conservation.
- This data presents information on the amino acid composition and codon usage of the species.

1. **Data Description**

*Gongronema latifolium* (Benth.) is classified in the family Apocynaceae and is of considerable nutritional and medicinal importance to the people of West Africa [1]. Despite its nutritional and medicinal uses, the plant is still relatively wild and repeatedly plagued by deforestation, excessive exploitation and constant expansion of the urban areas into rural areas as well as general poor land management practices in the distribution of *G. latifolium* [2]. The management and conservation of *G. latifolium* genetic resources across South-Eastern Nigeria is lacking, yet there is increased demand for its use for herbal formulations and as a leafy vegetable across the West African region and beyond, particularly with the spread of the Igbo cuisine across the region. Therefore, there is a need to understand the current genetic diversity of this species in Nigeria as well as to possibly create an active germplasm for the conservation and breeding of the species. The study presents the first *rbcl* gene sequences of *G. latifolium* from five Nigerian states. Table 1; lists the site collection details and the accessions of fourteen collections of *G. latifolium* as submitted to NCBI GenBank. Table 2; presents information about the accessions, including the % GC and the sequence length. Table 3, records the within collection area (state) genetic diversity of *G. latifolium*, which includes: number of segregating sites; within group mean
### Table 1
Details on Gongronema latifolium accessions as submitted on NCBI GenBank and site collection information.

| S/N | GenBank accession number | Locality       | State | Altitude (m) | LGA             | Latitude NS       | Longitude EW       | Herbarium number (vouchers) |
|-----|-------------------------|----------------|-------|--------------|------------------|-------------------|---------------------|-----------------------------|
| 1   | MH305570.1              | Aba market     | Abia  | 205          | Aba South        | 5° 6' 55.8072" N | 7° 20' 35.1852" E | AbaCH001                    |
| 2   | MH305571.1              | Ohia           | Abia  | 97           | Umuahia South    | 5° 31' 6.708" N  | 7° 27' 17.64" E    | AbaCH002                    |
| 3   | MH305572.1              | Asa            | Abia  | 23           | Ukwa West        | 4° 54' 46" N     | 7° 19' 9" E        | AbaCH003                    |
| 4   | MH305573.1              | Nibo village   | Anambra| 252          | Awka South       | 06° 10' 19" N    | 7° 4' 3" E         | AnaCH001                    |
| 5   | MH305574.1              | Alor Farm      | Anambra| 160          | Idemili South    | 6° 05'N          | 6° 57"E            | AnaCH002                    |
| 6   | MH305575.1              | Onueke market  | Ebonyi| 111          | Ezza South       | 6°20'N           | 8°06"E             | EboCH001                    |
| 7   | MH305576.1              | Nkalagu        | Ebonyi| 126          | Ihielu           | 6° 28' 42" N     | 7° 46' 44" E       | EboCH002                    |
| 8   | MH305577.1              | Eke market     | Ebonyi| 106          | Afikpo           | 5° 53' 2.5008" N | 7° 56' 34.0008" E | EboCH003                    |
| 9   | MH305578.1              | Nsukka         | Enugu  | 430          | Nsukka           | 6° 51'24" N      | 7°23'45" E          | EnuCH001                    |
| 10  | MH305579.1              | Ogbeite main market | Enugu   | 223       | Enugu North     | 9° 2'44" N       | 7° 27' 54" E       | EnuCH002                    |
| 11  | MH305580.1              | Abakpa market  | Enugu  | 223          | Enugu East       | 6° 28' 56.2584" N | 7° 30' 59.4468" E | EnuCH003                    |
| 12  | MH305581.1              | Obowo          | Imo     | 213          | Obowo           | 5° 33' 21.0528" N | 7° 21' 43.3476" E | ImoCH001                    |
| 13  | MH305582.1              | Umu Numu       | Imo     | 252          | Ehime-Mbano      | 5° 39' 55.7784" N | 7° 18' 20.646" E   | ImoCH002                    |
| 14  | MH305583.1              | Eke Okigwe market | Imo   | 158          | Okigwe           | 5° 49' 35.1912" N | 7° 20' 57.3612" E  | ImoCH003                    |

*Voucher specimens in form of leaves and seed as herbarium specimens were deposited in the herbarium repository of the Department of Biological Sciences, Covenant University, Ota, Nigeria.
Table 2
Summary of the rbcL sequences of G. latifolium accessions.

| Accession Number | State      | % GC  | Sequence Length |
|------------------|------------|-------|-----------------|
| MH305570.1       | Abia       | 44.10%| 521             |
| MH305571.1       | Abia       | 44.60%| 514             |
| MH305572.1       | Abia       | 44.20%| 529             |
| MH305573.1       | Anambra    | 44.40%| 532             |
| MH305574.1       | Anambra    | 44.60%| 514             |
| MH305575.1       | Ebonyi     | 44.20%| 523             |
| MH305576.1       | Ebonyi     | 44.70%| 519             |
| MH305577.1       | Ebonyi     | 44.30%| 519             |
| MH305578.1       | Ebonyi     | 44.40%| 525             |
| MH305579.1       | Ebonyi     | 44.70%| 514             |
| MH305580.1       | Enugu      | 44.60%| 514             |
| MH305581.1       | Imo        | 44.10%| 524             |
| MH305582.1       | Imo        | 44.60%| 518             |
| MH305583.1       | Imo        | 44.30%| 519             |

Table 3
Intra-specific diversity of rbcL G. latifolium accessions.

| State  | No. of accessions | No. of segregating sites | Within Group Mean Distance | Nucleotide Diversity       | Average no. Nucleotide Differences k |
|--------|-------------------|--------------------------|----------------------------|---------------------------|-------------------------------------|
| Abia   | 3                 | 9                        | 0.00247                    | 0.01167 ± 0.00550         | 6                                   |
| Anambra| 2                 | 0                        | 0                          | 0                         | 0                                   |
| Ebonyi | 3                 | 9                        | 0.00268                    | 0.01258 ± 0.00593         | 6                                   |
| Enugu  | 3                 | 1                        | 0.000265                   | 0.00130 ± 0.00061         | 0.667                               |
| Imo    | 3                 | 2                        | 0.00053                    | 0.00493 ± 0.00239         | 2.352                               |

distance; nucleotide diversity; and average number of nucleotide differences (k). Table 4, shows the amino acids and nucleotide compositions of the accessions of G. latifolium. Table 5, records the codon usage frequency table for G. latifolium. The genetic diversity of G. latifolium across the accessions is shown in Table 6. The codon usage indices of the accessions are represented in Table 7. Fig. 1 is the map of the collection sites across the study areas.

2. Experimental Design, Materials and Methods

2.1. Plant material

Specimens of Gongronema latifolium were collected in South-Eastern Nigeria, of five states; (Anambra, Abia, Imo, Enugu, and Ebonyi) (Fig. 1). The fresh leaf samples of the accessions were silica gel dried in labelled air-tight bags, and held at −80° prior to molecular analysis at the Bioscience Laboratory, International Institute of Tropical Agriculture (IITA), Ibadan Nigeria.

2.2. Genomic DNA extraction

Genomic DNA was extracted using the CTAB protocol [3].

2.3. Gene amplification and DNA sequencing

A portion of the chloroplast ribulose 1, 5-bisphosphate carboxylase (rbcL) gene was amplified with the rbcL-F (ATGTCACCACAAACAGAGACTAAAGC) and rbcL-R (GTAATACTCAAGTCCACCRCG)
## Table 4
Nucleotide and amino acid compositions for *G. latifolium* accessions.

| Nucleotide/ Amino acid composition | MH305570.1 | MH305571.1 | MH305572.1 | MH305573.1 | MH305574.1 | MH305575.1 | MH305576.1 | MH305577.1 | MH305578.1 | MH305579.1 | MH305580.1 | MH305581.1 | MH305582.1 | MH305583.1 |
|-----------------------------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| T                                 | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.85       |
| C                                 | 22.78       | 22.78       | 22.78       | 22.78       | 22.78       | 22.78       | 22.78       | 22.78       | 22.78       | 22.78       | 22.78       | 22.78       | 22.78       | 22.57       |
| A                                 | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       | 27.64       |
| G                                 | 21.94       | 21.94       | 21.94       | 21.94       | 21.94       | 21.94       | 21.94       | 21.94       | 21.94       | 21.94       | 21.94       | 21.94       | 21.94       | 21.94       |
| Ala                               | 8.23        | 8.23        | 7.99        | 8.23        | 7.99        | 8.23        | 7.99        | 8.23        | 8.23        | 8.23        | 8.23        | 8.23        | 8.23        | 8.23        |
| Cys                               | 127         | 127         | 127         | 127         | 127         | 127         | 127         | 127         | 127         | 127         | 127         | 1.27        | 1.27        | 1.27        |
| Asp                               | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        |
| Glu                               | 7.59        | 7.59        | 7.59        | 7.59        | 7.59        | 7.59        | 7.59        | 7.59        | 7.59        | 7.59        | 7.59        | 7.59        | 7.59        | 7.59        |
| Phe                               | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         |
| Gly                               | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        |
| His                               | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        |
| Ile                               | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        |
| Lys                               | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        |
| Leu                               | 9.49        | 9.49        | 9.49        | 9.49        | 9.49        | 9.49        | 9.49        | 9.49        | 9.49        | 9.49        | 9.49        | 9.49        | 9.49        | 9.49        |
| Met                               | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        | 0.63        |
| Asn                               | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        |
| Pro                               | 8.23        | 8.23        | 8.23        | 8.23        | 8.23        | 8.23        | 8.23        | 8.23        | 8.23        | 8.23        | 8.23        | 8.23        | 8.23        | 8.23        |
| Gln                               | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        | 2.53        |
| Arg                               | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        | 5.06        |
| Ser                               | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         | 3.8         |
| Thr                               | 8.86        | 8.86        | 9.49        | 8.86        | 8.86        | 9.49        | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        | 8.86        |
| Val                               | 6.33        | 6.33        | 6.33        | 6.33        | 6.33        | 6.33        | 6.33        | 6.33        | 6.33        | 6.33        | 6.33        | 6.33        | 6.33        | 6.33        |
| Thr                               | 127         | 127         | 127         | 127         | 127         | 127         | 127         | 127         | 127         | 127         | 127         | 127         | 127         | 127         |
| Tyr                               | 5.7         | 5.7         | 5.7         | 5.7         | 5.7         | 5.7         | 5.7         | 5.7         | 5.7         | 5.7         | 5.7         | 5.7         | 5.7         | 5.7         |
Table 5
Codon Usage of *G. latifolium* accessions.

| Codon   | Count | RSCU*  | Codon   | Count | RSCU  | Codon   | Count | RSCU  | Codon   | Count | RSCU  |
|---------|-------|--------|---------|-------|-------|---------|-------|-------|---------|-------|-------|
| UUU(F)  | 3     | 1      | UCU(S)  | 3     | 3     | UAU(Y)  | 5     | 1.11  | UGU(C)  | 1     | 1     |
| UUC(F)  | 3     | 1      | UCC(S)  | 1     | 1     | UAC(Y)  | 4     | 0.89  | UGC(C)  | 1     | 1     |
| UUA(L)  | 2     | 0.8    | UCA(S)  | 1     | 1     | UAA(∗)  | 0     | 0     | UGA(∗)  | 0     | 0     |
| UUG(L)  | 5.1   | 2.06   | UCG(S)  | 0     | 0     | UAG(∗)  | 0     | 0     | UGG(W)  | 2     | 1     |
| CUC(L)  | 4     | 1.6    | CCA(P)  | 5.8   | 1.78  | CAU(H)  | 1.1   | 2     | CGU(R)  | 3     | 2.25  |
| CUC(L)  | 0     | 0      | CCC(P)  | 3.2   | 0.99  | CAC(H)  | 0     | 0     | CGC(R)  | 1     | 0.75  |
| CUA(L)  | 2     | 0.8    | CCA(P)  | 3     | 0.92  | CAA(Q)  | 3     | 1.5   | CGA(R)  | 3     | 2.25  |
| CUG(L)  | 1.9   | 0.74   | CCG(P)  | 1     | 0.31  | CAG(Q)  | 1     | 0.5   | CGG(R)  | 0     | 0     |
| AUU(I)  | 4     | 1.5    | ACC(T)  | 7.1   | 2.02  | AAA(N)  | 1.1   | 0.56  | AGU(S)  | 0     | 0     |
| AUC(I)  | 4     | 1.5    | ACA(T)  | 3     | 0.85  | AAC(N)  | 2.8   | 1.44  | AGC(S)  | 1     | 1     |
| AUA(I)  | 0     | 0      | ACA(T)  | 3     | 0.85  | AAA(K)  | 8     | 2     | AGA(R)  | 1     | 0.75  |
| AUG(M)  | 1     | 1      | ACC(T)  | 1     | 0.28  | AAC(N)  | 0     | 0     | AGG(R)  | 0     | 0     |
| GUA(V)  | 5     | 2      | GCA(A)  | 5.9   | 1.82  | GAU(D)  | 7     | 1.75  | GGU(G)  | 4     | 1.14  |
| GUC(V)  | 0     | 0      | GCC(A)  | 3     | 0.93  | GAC(D)  | 1     | 0.25  | GGC(C)  | 2     | 0.57  |
| GUA(V)  | 5     | 2      | GCA(A)  | 3     | 0.93  | GAA(E)  | 10    | 1.67  | GGA(G)  | 4.1   | 1.18  |
| GUG(V)  | 0     | 0      | GCG(A)  | 1     | 0.31  | GAG(E)  | 2     | 0.33  | GGG(G)  | 3.9   | 1.1   |

*RSCU: Relatively synonymous codon usage.*
Fig. 1. Species range and collection sites across South-East Nigeria.
primer [4]. The PCR amplicon were sequenced at Inqaba biotechnical Industries (Pty) Ltd, South Africa.

2.4. Data analysis

Sequences were aligned using the Geneious Basic [5] with default settings to obtain the % GC and sequence lengths.

Population diversity indices such as numbers of segregating sites (S), haplotype number (h), haplotype diversity (Hd), nucleotide diversity (π) and average number of pairwise nucleotide differences within the population (K), were estimated using DnaSP 4.5 [6].

The nucleotide and amino acid compositions and the codon usage frequency table of G. latifolium were estimated using DnaSP 4.5.

Codon usage indices were calculated using CodonW as implemented on a public Galaxy server (https://galaxy.pasteur.fr/).

Table 6
Genetic diversity of fourteen G. latifolium accessions.

| Index                                | Value       |
|--------------------------------------|-------------|
| Number of haplotypes                 | 4           |
| Haplotype diversity                  | 0.396 ± 0.159 |
| Nucleotide diversity                 | 0.00493 ± 0.00239 |
| Average no. Nucleotide Differences (k) | 2.352       |
| No. of segregating sites             | 9           |

Table 7
Codon usage indices per accession.

| Accessions   | T3s    | C3s    | A3s    | G3s    | CAI  | CBI  | Fop   | Nc    | GC3s | GC    | L_sym | L_aa  |
|--------------|--------|--------|--------|--------|------|------|-------|-------|------|-------|-------|-------|
| MH305570.1   | 0.4755 | 0.2168 | 0.375  | 0.1562 | 0.267| 0.136| 0.494 | 51.38 | 0.3  | 0.439 | 170   | 173   |
| MH305571.1   | 0.2636 | 0.2713 | 0.304  | 0.4052 | 0.141| -0.057| 0.538 | 61    | 0.532| 0.451 | 154   | 165   |
| MH305572.1   | 0.4658 | 0.2329 | 0.3768 | 0.1462 | 0.262| 0.14 | 0.497 | 50.02 | 0.306| 0.441 | 173   | 176   |
| MH305573.1   | 0.4795 | 0.2192 | 0.3669 | 0.1603 | 0.273| 0.144| 0.5   | 50.69 | 0.305| 0.443 | 174   | 177   |
| MH305574.1   | 0.2636 | 0.2713 | 0.304  | 0.4052 | 0.141| -0.057| 0.338 | 61    | 0.532| 0.451 | 154   | 165   |
| MH305575.1   | 0.4437 | 0.2465 | 0.3957 | 0.1374 | 0.258| 0.118| 0.485 | 49.9  | 0.31 | 0.441 | 171   | 174   |
| MH305576.1   | 0.2595 | 0.2672 | 0.2992 | 0.4153 | 0.142| -0.061| 0.333 | 61    | 0.538| 0.453 | 156   | 167   |
| MH305577.1   | 0.3116 | 0.3478 | 0.3423 | 0.1881 | 0.136| 0.018| 0.426 | 43.27 | 0.453| 0.465 | 148   | 159   |
| MH305578.1   | 0.2652 | 0.2652 | 0.2992 | 0.4153 | 0.141| -0.066| 0.331 | 61    | 0.535| 0.45  | 157   | 168   |
| MH305579.1   | 0.2615 | 0.2692 | 0.3016 | 0.4103 | 0.14 | -0.062| 0.335 | 61    | 0.535| 0.453 | 155   | 165   |
| MH305580.1   | 0.2636 | 0.2713 | 0.304  | 0.4052 | 0.141| -0.057| 0.338 | 61    | 0.532| 0.451 | 154   | 165   |
| MH305581.1   | 0.4722 | 0.2222 | 0.375  | 0.1562 | 0.269| 0.14  | 0.497 | 51.45 | 0.304| 0.439 | 171   | 174   |
| MH305582.1   | 0.2615 | 0.2692 | 0.3016 | 0.4103 | 0.14 | -0.059| 0.335 | 61    | 0.535| 0.452 | 155   | 166   |

CRediT Author Statement

Conrad Asotie Omonhinmin: Conceptualization, Methodology, Supervision; Chinedu Charles Onuselogu: Writing – review & editing, Writing – original draft preparation; Enameguono Olo-mukoro: Sequences submission on GenBank.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests.
Acknowledgments

The authors thank Covenant University, Centre for Research, Innovative and Discovery (CU-CRID) for the publication funding and the various farmers and community leaders that assisted in this work.

References

[1] M.E. Balogun, E.E. Besong, J.N. Obimma, O.S. Mbamalu, S.F. Djobissie, Gongronema latifolium. A phytochemical, nutritional and pharmacological review, J. Physiol Pharmacol Adv. 6 (2016) 811–824.
[2] A.I. Emodi, C.C. Akwue, E.O. Ehebha, Involvement of Farm Households in Bush Buck (Gongronema latifolium) Production in Anambra State, Nigeria, Asian J. Agric. Extension, Econ. Sociol. (2017) 1–9.
[3] F. Beed, I. Ramathani, DNA CA extraction using CTAB and DNA capture kits, in: Paper presented at Regional Training Workshop for Disease Surveillance in 7 countries organized by FAO and IITA in Rwanda, 2010, pp. 1–18.
[4] P. Wongsawad, Y. Peerapornpisal, Molecular identification and phylogenetic relationship of green algae, Spirogyra ellipsospora (Chlorophyta) using ISSR and rbcL markers, Saudi J. Biol. Sci. 21 (5) (2014) 505–510.
[5] M. Kearse, R. Moir, A. Wilson, S. Stones-Havas, M. Cheung, S. Sturrock, S. Buxton, A. Cooper, S. Markowitz, C. Duran, T. Thierer, Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data, Bioinformatics 15 (12) (2012) 1647–1649 28.
[6] J. Rozas, DNA sequence polymorphism analysis using DnaSP, in: Bioinformatics for DNA sequence analysis, Humana Press, 2009, pp. 337–350.