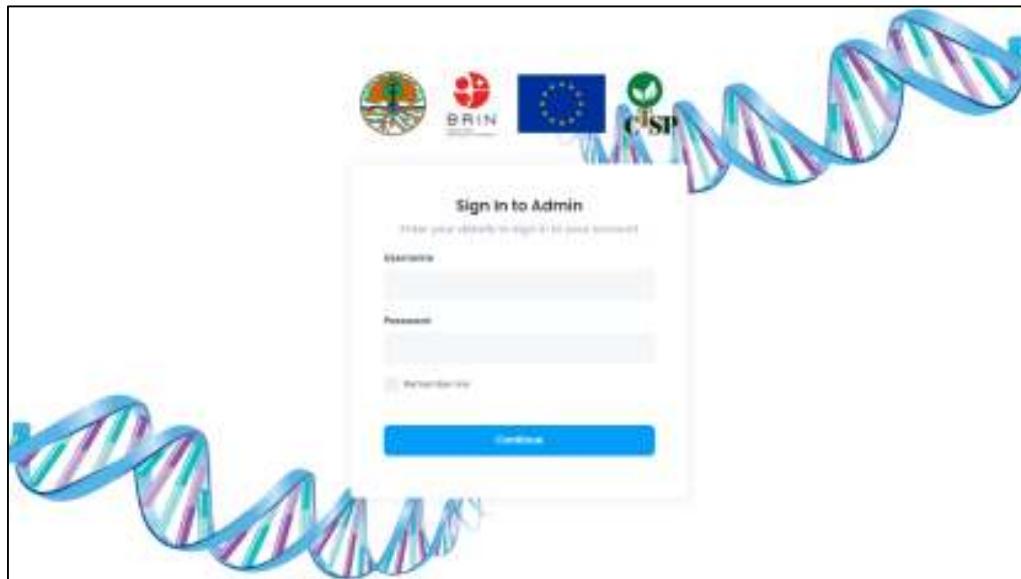




A Report on the Development of the *Dalbergia latifolia* Database in Indonesia



KS Yulita and I Kamal

Jakarta, Indonesia

September 2022

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Program	: CITES Tree Species Programme Web Page: https://cites-tsp.org/
Financial Support	: The European Union and the CITES Tree Species Programme
Implementing Agency	: Directorate of Biodiversity Conservation of Species and Genetics, Ministry of Environment and Forestry, and the National Research and Innovation Agency, Indonesia
Authors	: KS Yulita and I Kamal
Indonesia Project Team and Contributors to the Report:	
HH Rachmat, T Setyawati, W Wardani, RA Fambayun, A Subiakto, TD Atikah, BA Pratama, FG Dwiyanti, F Nopiansyah, Susila, N Arrofaha, and S Nurjanah	
Cover	: Upper photo — sign-in page of the DNA database Lower photo — data summary page of the DNA database Photo by I Kamal
Citation	: KS Yulita and I Kamal. 2022. A Report on the Development of the <i>Dalbergia latifolia</i> Database in Indonesia. Directorate of Biodiversity Conservation Species and Genetics, Ministry of Environment and Forestry, and the National Research and Innovation Agency, Indonesia
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ACKNOWLEDGMENTS

The CTSP Indonesian Team wishes to acknowledge the European Union for funding this project and the CITES Secretariat for coordinating the project. During this project, from preparation to post-project implementation, we owed our respect and gratitude to Mr. Thang Hooi Chiew as the Regional Coordinator for Asia and to Dr. Milena Sosa Schmidt as the CITES Tree Species Programme Coordinator and Regional Coordinator for Central and South America and the Caribbean. We also acknowledge the support of Dr. Haruko Okusu and Ms. Sofie H. Flensburg from the CITES Secretariat.

We are grateful to Mrs. Indra Exploitasia , Director of Biodiversity Conservation of Species and Genetics, Ministry of Environment and Forestry, and her staff, Dr. Kirsfianti L. Ginoga , former Director of Forest Research and Development Center, which is currently the Center for Standardization of Sustainable Forest Management Instruments, Dr. Atit Kanti , former Head of Research Center for Biology, Dr. Anang Setiawan , Head of Research Center for Ecology and Ethnobiology , and Dr. Bayu Adjie , Head of Research Center for Biosystematics and Evolution, National Research and Innovation Agency, for their support and assistance in this project.

On behalf of the project team,

Dr. Kusumadewi Sri Yulita
Project Team Leader

ACRONYMS AND ABBREVIATIONS

BRIN	National Research and Innovation Agency (<i>Badan Riset dan Inovasi Nasional</i>)
CITES	Convention on International Trade in Endangered Species of Wild Fauna and Flora
CTSP	CITES Tree Species Programme
D.	<i>Dalbergia</i>
DNA	Deoxyribonucleic Acid
HTML5	Hyper Text Markup Language Version 5
i.e.	that is
KKHSG	Direktorat of Biodiversity Conservation of Species and Genetics (<i>Direktorat Konservasi Keanekaragaman Hayati Spesies dan Genetik</i>)
MOEF	Ministry of Environment and Forestry (<i>Kementerian Lingkungan Hidup dan Kehutanan</i>)
NDF	Non-detriment Findings
PDF	Portable Document Format
Perhutani	State-Owned Forestry Company (<i>Perusahaan Hutan Negara Indonesia</i>)
PHP	Hypertext Preprocessor
SNPs	Single Nucleotide Polymorphisms

EXECUTIVE SUMMARY

The wood of *Dalbergia latifolia* is one of the most expensive wood products on the market. The highly traded *D. latifolia* has created illegal trade and illegal woods from timber theft and to reduce the illegal trade in *D. latifolia* the DNA database was developed. The DNA database of *D. latifolia* is to store and organize information on *D. latifolia*. The information contains ecological data, location, and DNA data from *D. latifolia*. The information on *D. latifolia* was obtained from several visited sites while the DNA data were obtained from laboratory activities involving the isolation of the genetic materials from samples collection, and molecular analysis of the data. The DNA data from *D. latifolia* are very important data for *D. latifolia*.

The DNA database is web-based so users can access it at <http://103.8.238.15/sonokeling/login>. Other than storing the information, the database also functions as a tool for timber tracking. The DNA data from sample collection and molecular analysis can be used to support timber tracking and to trace the origin of the woods and wood products of *D. latifolia*. Besides using it as a forensic tool, the genetic data in the *D. latifolia* database can be used to identify *D. latifolia* at the population and species levels. In addition, the DNA database of *D. latifolia* can be further developed to upgrade its ability to meet future needs.

1. Background

The *Dalbergia latifolia* (rosewood) is one of the most expensive types of wood not only because the quality of the wood is very strong, but also because of its good appearance of the wood. The demand for *D. latifolia* wood is quite high and the price is high too, causing a large amount of harvest in its range of distribution. The *D. latifolia* has been included in Appendix II of CITES since 2017, which means that this species is considered endangered while the trade in this species continues without proper rules and regulations. Consequently, there must be adjustments made to the national laws and supporting documents for local and international trade, which should accommodate CITES trading instruments. This regulation applies to trade in all types of rosewood, both in the form of logs, sawn timber, and finished products.

The lack of adequate data regarding the natural distribution and availability of rosewood supply and trade in the domestic market, as well as to ensure the sustainable management of *D. latifolia*, the Directorate of Biodiversity Conservation of Species and Genetics (KKHSG), the Ministry of Environment and Forestry (MOEF), and the Research Organization for Life Sciences and Environment of the National Research and Innovation Agency (BRIN), through the CITES Tree Species Programme (CTSP), had conducted a comprehensive study on *D. latifolia* in Java and West Nusa Tenggara. One of the outputs of this project was to develop a DNA database as a storage and data management system for the information and data collected during the course of the project.

During the implementation of the CTSP project, Indonesia had collected a large amount of information, including soil types, locality details and coordinates, DNA materials, DNA sequences, cultivated materials, and market supply chains. Such data need to be stored and managed in a system so that they can easily be retrieved by the users. The database system was initially developed as a tool for tracking the traceability of *D. latifolia* based on DNA sequence data. The DNA sequence data obtained from this project would be used as reference data for genetic analysis and forensic purposes.

2. Objective

One of the objectives of the project was to develop a database system based on DNA sequences linked to all the information collected from each specimen. It is expected that the database would be used as a forensic tool for tracing the origin of the woods or wood products of *D. latifolia* from Java and West Nusa Tenggara in Indonesia.

3. Development Process

The *D. latifolia* database is web-based and as such, it would need to be connected to the internet network to access it. The database application was developed by a web developer in consultation with the authors of this report. The agreed system for the developed database was for the developers to use the PHP programming language for the back end and using the HTML5 and Javascript programming languages for the front end.

The design of the DNA database application system started with the initial communication between the database developer and the users to identify the user needs. The results of the initial communication with users of this database application were that the database has to function as a storage for the *D. latifolia* samples collected from the various locations in Java and West Nusa Tenggara. The main aim was to identify the genetic variation of each sample collected from a specific location/population and to use the information to determine the origin of the samples. Data and application operational requirements are in **Figure 1**.

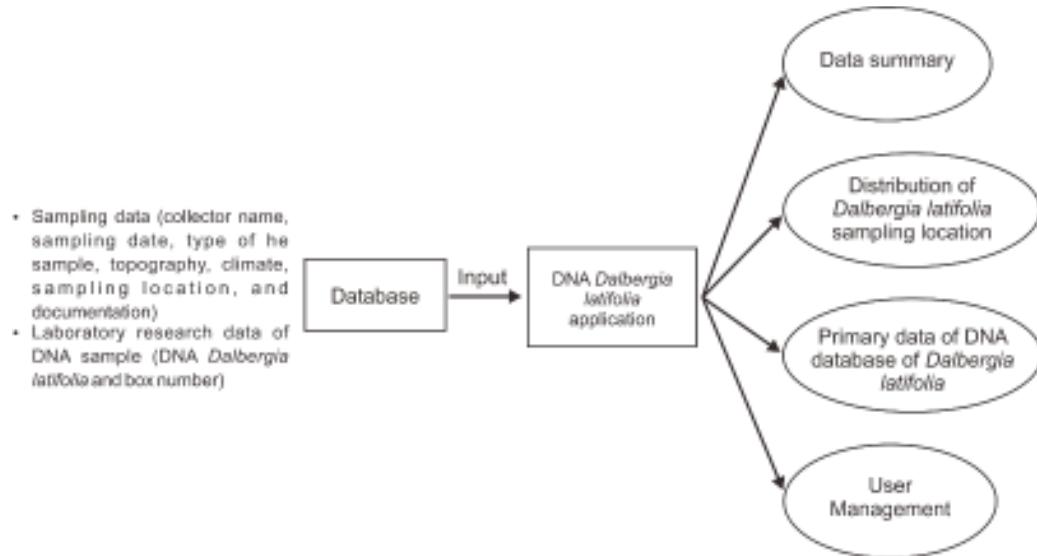


Figure 1. Flow chart diagram from data input to data display of the database application

This database application had been disseminated in a one-day workshop held on 31 May 2022 to interested stakeholders. Some of the important points raised during the workshop discussion were (i) currently, the DNA database is not very beneficial but will be helpful for a future chain of custody process, particularly during the occurrence of illegal trade and cutting in a particular area; (ii) additional samples are needed to provide more data and a genetic haplotype map since the distribution of *D. latifolia* in Indonesia is also present in other areas, i.e., Sumatra, Kalimantan and East Nusa Tenggara; (iii) a secure and capable server is indispensable to integrating and storing the collected data; and (iv) guidelines for developing the DNA database platform should be compiled to accommodate future improvements or updates.

4. Description of the Database

The *D. latifolia* DNA database is useful as a reference for *D. latifolia* in Indonesia in tracking and tracing the origins of *D. latifolia* in Java and West Nusa Tenggara, analyzing forensic data on timber theft in an area, and providing valuable information for genetic diversity and traceability of *D. latifolia* study in Indonesia. Considering the importance of the benefits of the *D. latifolia* DNA database, in the future, it is necessary to develop the database by adding information and collection of *D. latifolia* other than those in Java and West Nusa Tenggara.

The targeted principal beneficiaries of the DNA database *D. latifolia* are (i) researchers; (ii) forest managers; (iii) policy-makers; (iv) customs officers; (v) the state-owned forestry company, Perhutani; and (vi) the general public.

Several recommendations agreed upon by the participants of the workshop on the dissemination of the development of a DNA database that was held on 31 May 2022 were as follows:

- (i) Coordination between MOEF and BRIN is needed to decide on the server that will be used to store the database data.
- (ii) Web developers must provide all documentation of the stages in preparing a developed database application to facilitate further development without obstacles in updating data.
- (iii) This database will be in the public domain with limited data that can be accessed, and all the data will be stored and become the joint property of MOEF and BRIN.
- (iv) Chain-of-custody techniques and DNA databases that have been developed will be used as reference data for the identification of DNA population fingerprints at the provincial and district levels, and the final haplotype map will continue to be developed. Specific data for each district and province in Java and West Nusa Tenggara is expected to be obtained.

The *D. latifolia* database was developed to store *D. latifolia* sample data in the form of complete information on the samples taken starting with the sample name, sampling date, coordinate location and sampling area, soil data, and sample photographs, as well as storing the genetic data from *D. latifolia* in a DNA sequence. The complete information on *D. latifolia* was derived from field sampling data. Samples from the field in the form of leaves, wood, fruits, or flowers were specifically taken as genetic samples, and then the genetic materials of *D. latifolia* were isolated from the genetic samples and followed by molecular analysis. Five chloroplast DNA regions were selected for use in the genetic analysis of *D. latifolia*, namely, petD, CLP, *trnL* intron, rpl16-rps3 IGS, and *trnG* intron. Each region/gene had several haplotypes that referred to the sampling area due to the variations in certain base sequences.

At the top of the database page, information about user accounts is displayed, starting from the account name and account level. For detailed information and to sign out, click on the account name and a detailed menu will appear, namely, my profile user management (only overall administrator), roles, permissions, and sign out (**Figure 2**).

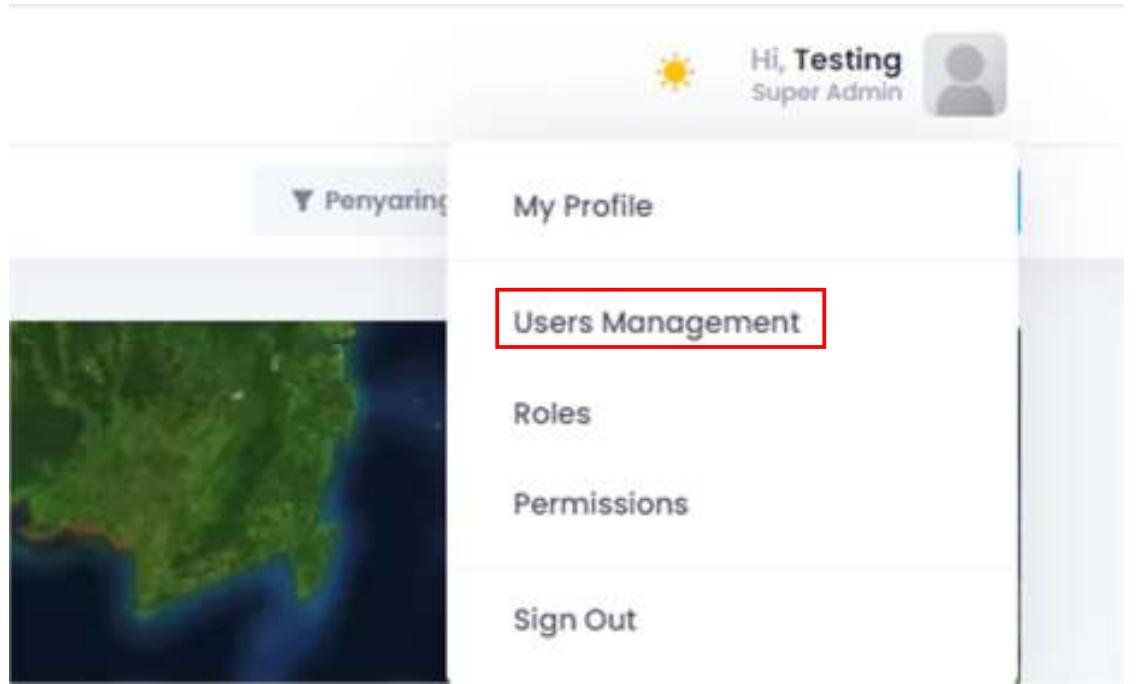


Figure 2. Account tool

To add a new user, one can view registered users by selecting the user management menu. To create a new user, select add user (**Figure 3**) and fill in the form provided (**Figure 4**).

USER	ROLE	USERNAME	LAST LOGIN	STATUS	JONNEED DATE
adminbrin adminbrin@gmail.com	Admin	adminbrin	16 days ago	Enabled	3 months ago
Testing Akun testakun@gmail.com	Super Admin	akuntesting	30 minutes ago	Enabled	8 months ago
Brin brin@gmail.com	Super Admin	Brin023	23 days ago	Enabled	3 months ago
coba okun cobaokun@gmail.com	User	cobaokun	8 months ago	Enabled	8 months ago

Figure 3. User management

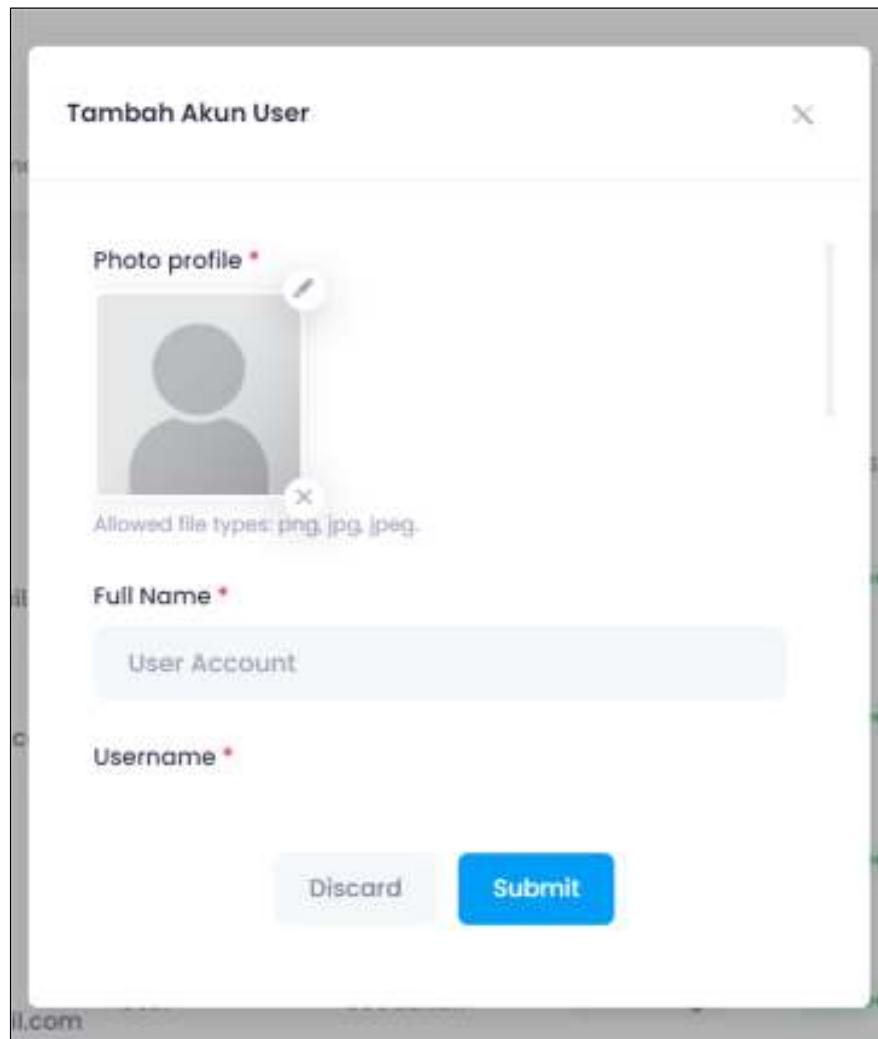


Figure 4. Add user

In the database application, after signing in to the database, it will enter the start page, at the top, there is a map view (**Figure 5**) which can be changed in another layout according to the available templates and also displays the sampling location points. The red dots on the map

represent the sampling location points, and detailed information about the sample can be displayed by clicking on the sampling location.

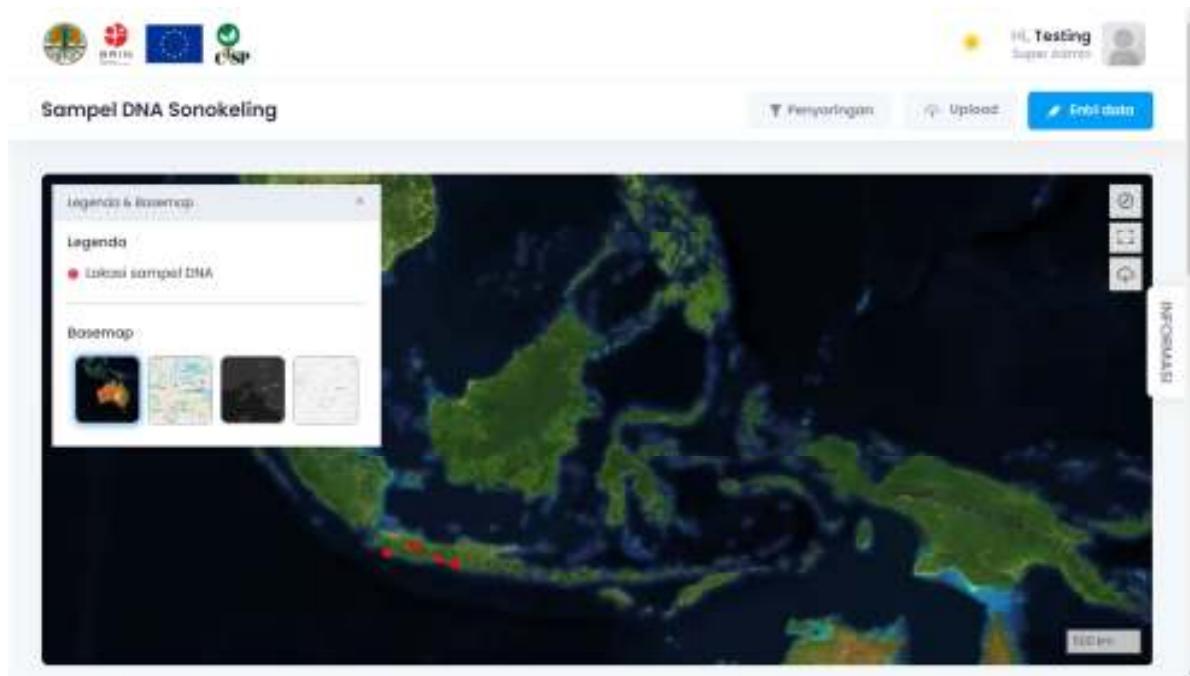


Figure 5. Appearance map

In addition, this page displays account details, username and account level. The lower part of the map displays DNA sample information which consists of summary data and primary data. In the map section, one can see the red dot which is the location of the DNA sampling site. When selected, the red dot will bring up a summary of the data (**Figure 6**) that has been entered and verified by the overall administrator/administrator. One can also select details in the box to see a more complete data summary (**Figure 7**).

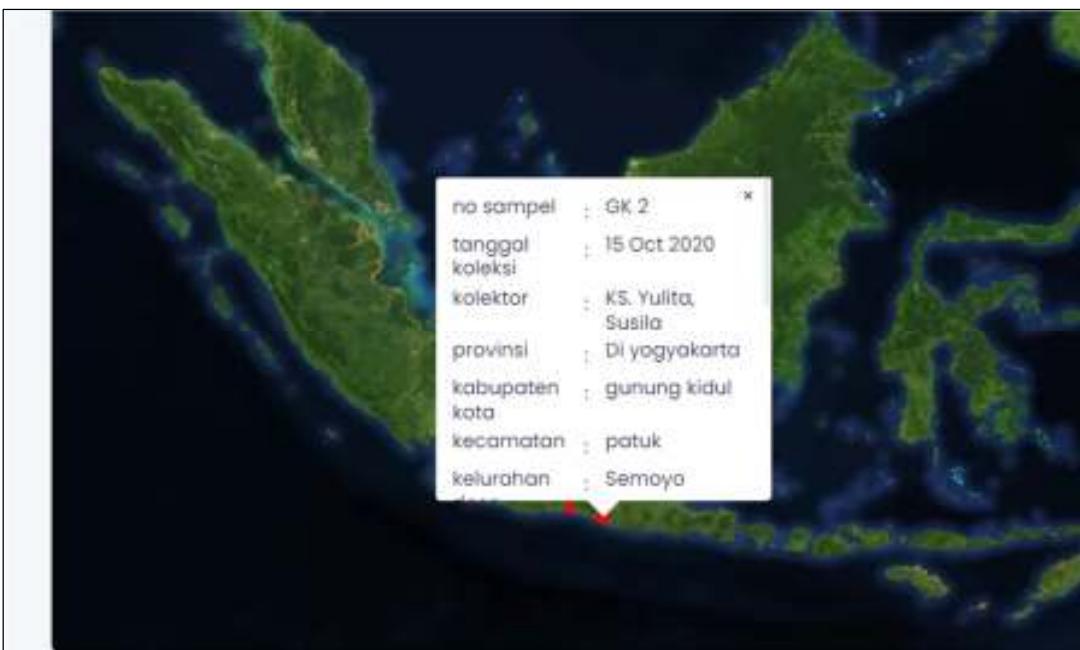


Figure 6. Summary data in red dots

Sampel DNA Sonokeling

Detail

Detail Informasi

Nomor Sampel	GK 2
Tanggal koleksi	15 Oct 2020
Kolektor	K.S. Yulita, Susilo
Provinsi	DI yogyakarta
Kabupaten/Kota	gunung kidul
Kecamatan	patuk
Kelurahan/Desa	Semoyo
Latitude/longitude (X)	80.475074, -7.870275
Altitude	0

Figure 7. Detailed information

The data summary (**Figure 8**) contains information on the number of DNA samples from *D. latifolia*, either from leaves, flowers or from wood. It also displays the type of land system where rosewood grows. There is also data regarding the haplotype of *D. latifolia* DNA from the five regions or genes. Haplotype data refer to the number of haplotypes from each region used in the molecular analysis and the origin of the sampling location or the area where the

D. latifolia information was collected. In addition, graphical data on the number of *D. latifolia* samples that have been uploaded onto the database are also displayed, and grouped by province (Figure 9).

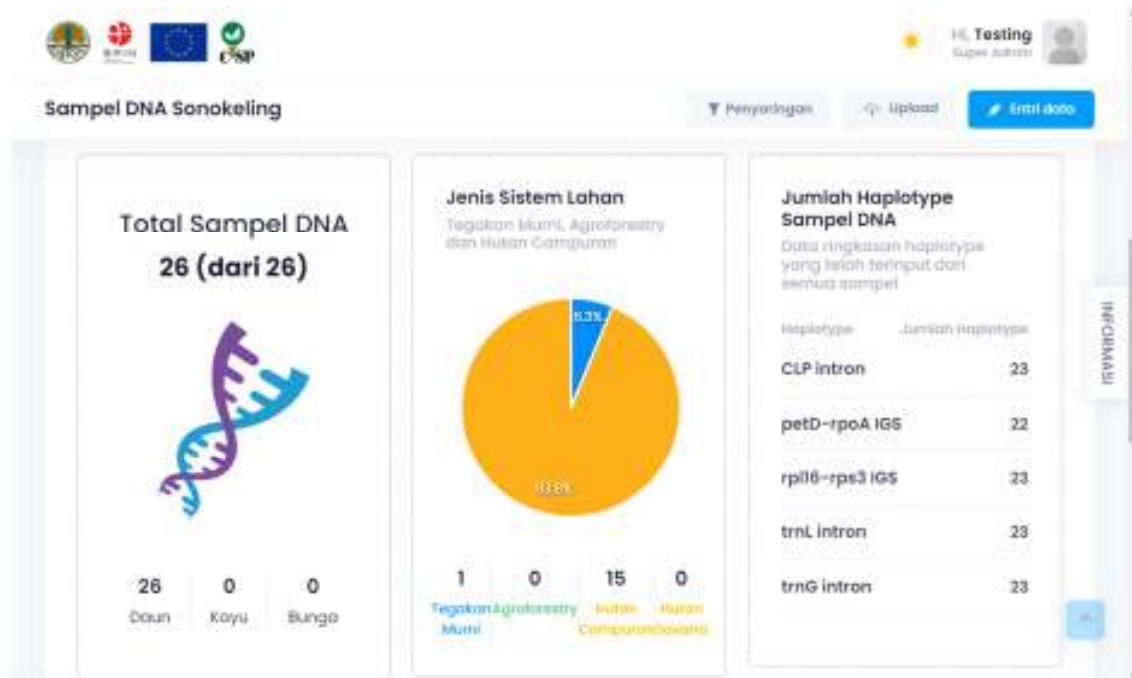


Figure 8. View of data summary 1

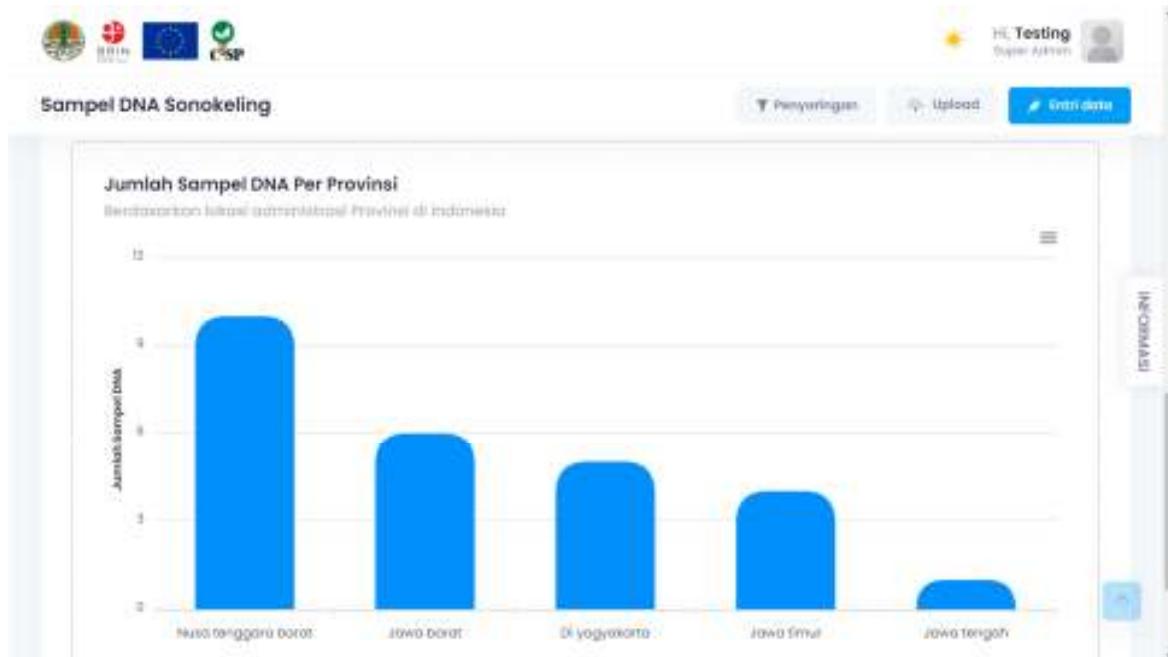


Figure 9. View of data summary 2

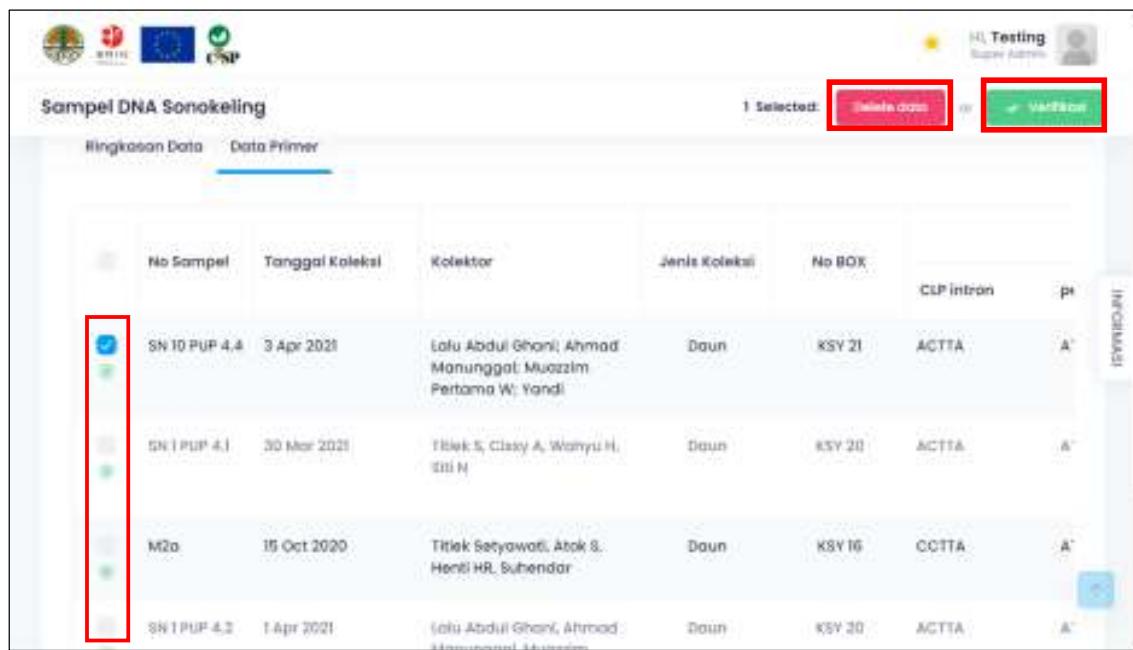
The primary data in the database contain detailed information about samples, both sampling data and DNA sample data. The information displayed includes the sample name, collection

date, collector name, collection category, number box, and haplotype consisting of the five regions, as well as detailed sampling locations from the village level to the district level. In the haplotype section, data on genetic diversity in DNA sequences are displayed in the form of single nucleotide polymorphisms (SNPs) in certain base sequences. The data displayed in the haplotype section is only in the form of the SNPs data of the sample, and to view the sequence details, one has to click the edit section on the selected sample so that the detailed information appears including the sequence data of the selected sample. The DNA data that appear in the haplotype section are only a summary of data from the chloroplast DNA sequence region where the letters (nucleobase) indicate differences or similarities in the sequence of nucleobase as a result of the molecular data analysis conducted. Each nucleobase is in a certain sequence in the gene sequence (**Figure 10**).

No Sampel	Tanggal Koleksi	Kolektor	Jenis Koleksi	No BOX	CLP Intron	peID-rpc
SN 10 PUP 4.4	3 Apr 2021	Lulu Abdul Ghani, Ahmad Manunggal, Muazzim Pertama W, Yandi	Dauh	KSY 21	ACTTA	ATAA
SN 1 PUP 4.1	30 Mar 2021	Titiek S, Cisay A, Wahyu H, STH M	Dauh	KSY 20	ACTTA	ATAA
M30	15 Oct 2020	Titiek Setyowati, Atok S, Henti Ht, Suhendar	Dauh	KSY 16	CCTTA	ATAA
SN 1 PUP 4.2	1 Apr 2021	Lulu Abdul Ghani, Ahmad	Dauh	KSY 20	ACTTA	ATAA

Figure 10. Primary data 1

The overall administrator/administrator needs to check and verify the sample data by clicking the verification button. The data that have been verified can only be seen in the user view. If the data were wrong, they can be removed by pressing the delete data button (**Figure 11**). In addition, the data results that have been entered and verified can be downloaded in excel and pdf formats on the data export menu (**Figure 12**).



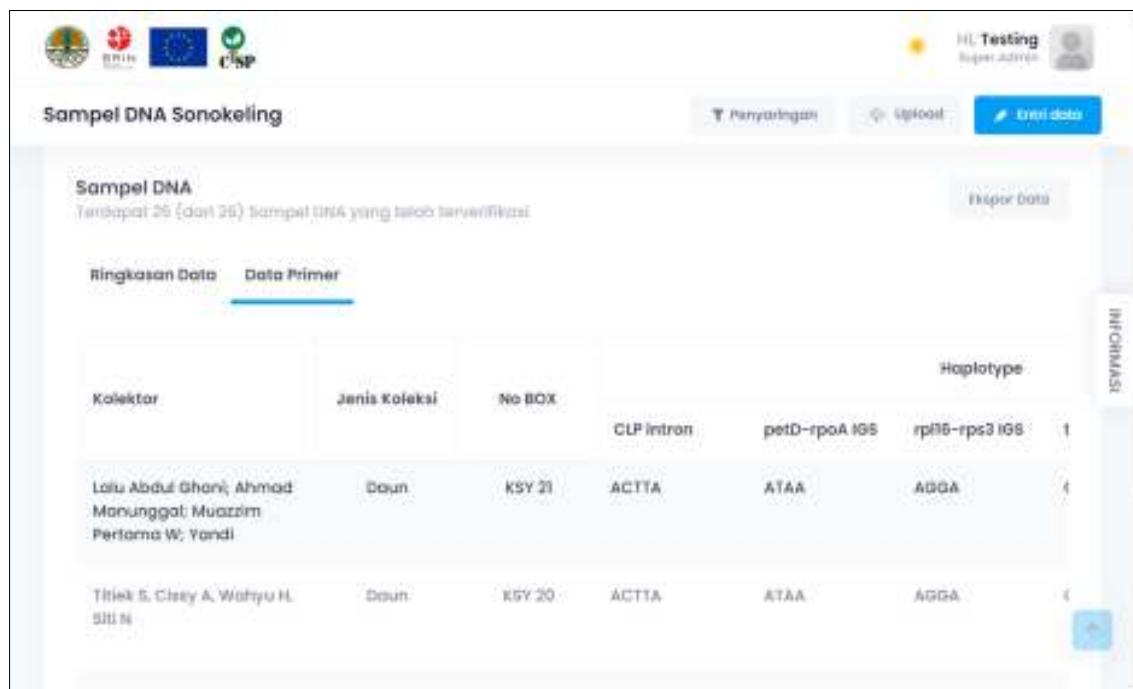
Sampel DNA Sonokeling

1 Selected: [Delete data](#) [Verifikasi](#)

[Ringkasan Data](#) [Data Primer](#)

No Sampel	Tanggal Koleksi	Kolektor	Jenis Koleksi	No BOX	CLP intron	Haplotype	Aksi
SN 10 PUP 4.4	3 Apr 2021	Lulu Abdul Ghoni, Ahmad Manunggat; Muazzim Performa W; Yandi	Daun	KSY 21	ACTTA	A ⁺	Edit
SN 1 PUP 4.1	30 Mar 2021	Titiek S, Clasy A, Wahyu H, Sri N	Daun	KSY 20	ACTTA	A ⁻	Edit
M2o	15 Oct 2020	Titiek Setyawati, Atok S, Hentri HR, Buhendar	Daun	KSY 16	CCTTA	A ⁻	Edit
SN 1 PUP 4.2	1 Apr 2021	Lulu Abdul Ghoni, Ahmad Manunggat; Muazzim	Daun	KSY 20	ACTTA	A ⁻	Edit

Figure 11. Verification data



Sampel DNA Sonokeling

[Pembangkitan](#) [Upload](#) [Delete data](#)

[Ringkasan Data](#) [Data Primer](#)

Sampel DNA
Tempat 26 (dari 26) sampel DNA yang telah terverifikasi

[Rapor Data](#)

Kolektor	Jenis Koleksi	No BOX	Haplotype			
			CLP intron	petD-rpoA iGS	rpl16-rps3 iGS	t
Lulu Abdul Ghoni, Ahmad Manunggat; Muazzim Performa W; Yandi	Daun	KSY 21	ACTTA	ATAA	AGGA	4
Titiek S, Clasy A, Wahyu H, Sri N	Daun	KSY 20	ACTTA	ATAA	AGGA	4

Figure 12. Export data

The detailed sample data, both information on samples and sample DNA data, can be uploaded in two ways through the tools provided in the database, namely, data entry and upload. The data entry tool is used to upload sample data manually by filling out a form containing detailed sample information, but it will take time because one has to fill in the sample information one by one. Alternatively, the data can be uploaded through the upload tool by simply uploading an excel file containing the detailed sample information (**Figure 13**).

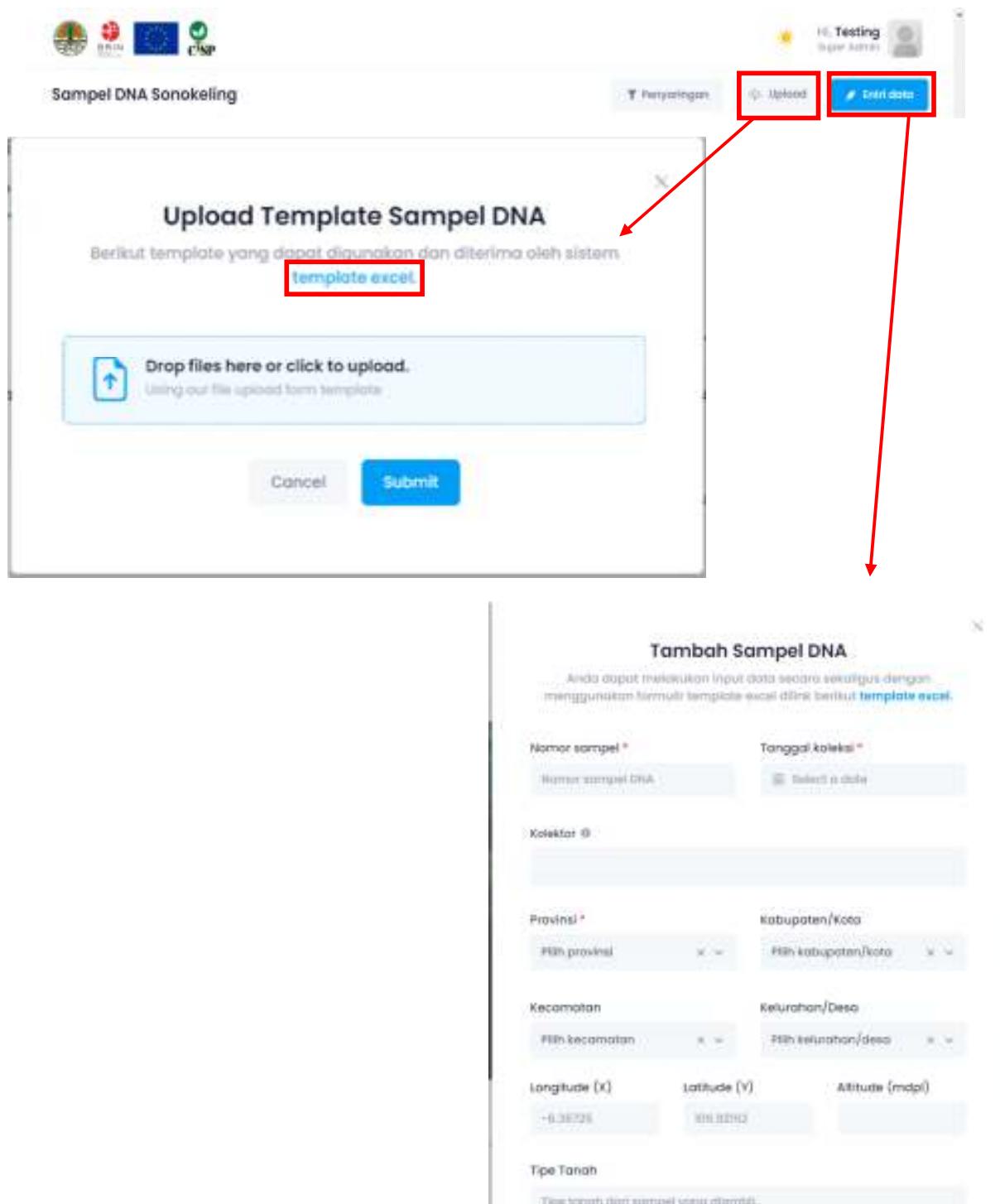


Figure 13. Upload tools

The *D. latifolia* database contains hundreds and thousands of data, so it takes time to sort the desired data, and hence, to make it easier to access certain data needed by users there is a search (filtering) tool (**Figure 14**). The search tool provides tools to search data by sample

name, collector name, collection date, and location. The keywords entered will display the data in the database according to the keywords.

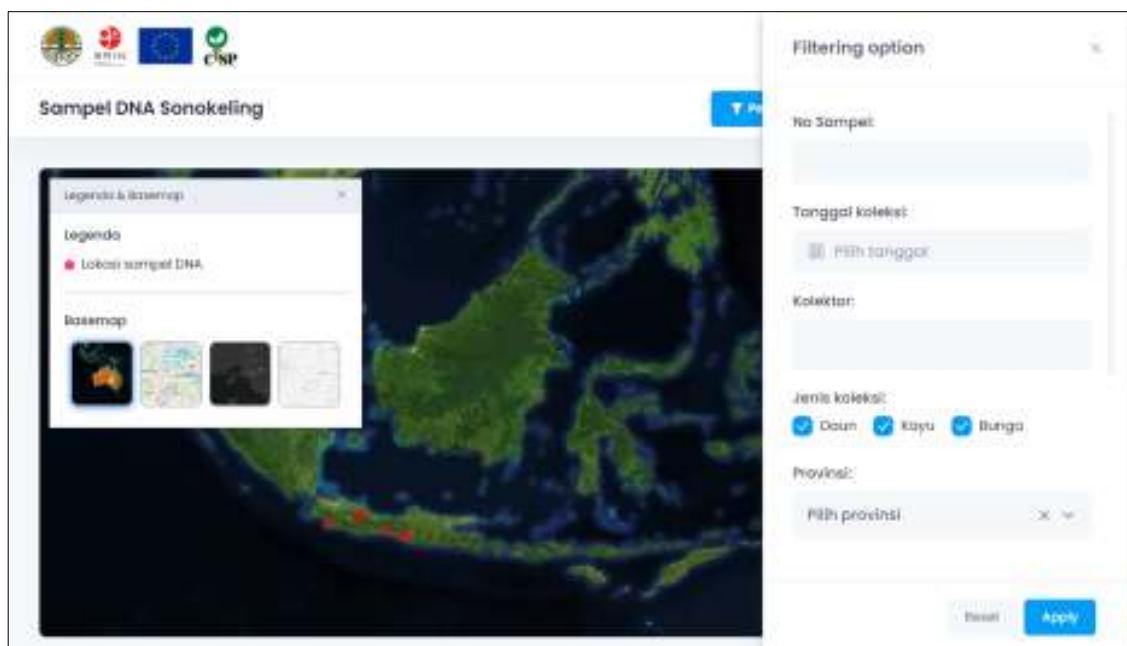


Figure 14. Filtering tool

In general, this database application can still be developed and upgraded according to the needs of the users.

5. Accessibility of the Database

The database was developed by MOEF through KKHSG and BRIN. The *D. latifolia* database could be accessed via the web address <http://103.8.238.15/sonokeling/login>, where the initial view and login for the database are as shown on the sign-in page in **Figure 15**.

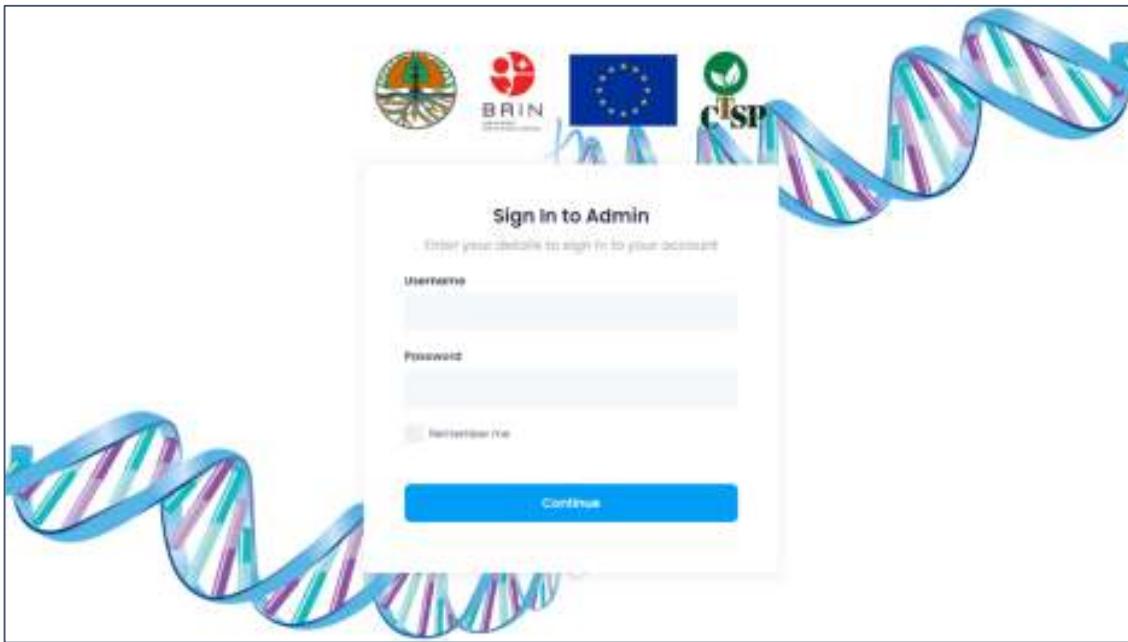


Figure 15. Sign-in page of the database

An account is required to log in to the *D. latifolia* database. There are three criteria for an account that has access to the database, namely, the **overall administrator**, the **administrator** and the **user**. There are also different access levels for the overall administrator, the administrator and the user.

In this regard, the **overall administrator** (only one) has access to read, write or upload, edit, remove and verify the data in the database (has full access to the database), while the **administrator** has access to read, upload or to update, edit, and remove the data from database but does not have the authority to validate any new data, and the **user** has access to the database to just read the data. If the user wishes to get specific data or information on the sample, such as ecological data and locations or DNA data, the user will have to contact the owner of the database (MOEF through KKHS) and (BRIN) or the overall administrator of the *D. latifolia* database. Each account owner will have its own username and password that can only be used by the account owner.

6. Conclusion

The database was designed to store and organize the data of *D. latifolia* derived from the detailed sample and genetic data. The database stores a certain amount of DNA data from *D. latifolia* samples that had been collected.

In addition, the database displays the genetic diversity obtained from the samples that had been collected and uploaded onto the database. The database can be used as a forensic tool to trace the location of the origin of *D. latifolia* wood.

The genetic data can also be used to identify *D. latifolia* at the population and species levels. If needed, this database could be developed further to cover various types of plants and facilitate access for specific purposes, such as a reference database for tracing the origins of plant species in Indonesia. It could also be used to analyze forensic data on timber theft and in undertaking genetic diversity and traceability studies of the species in Indonesia.