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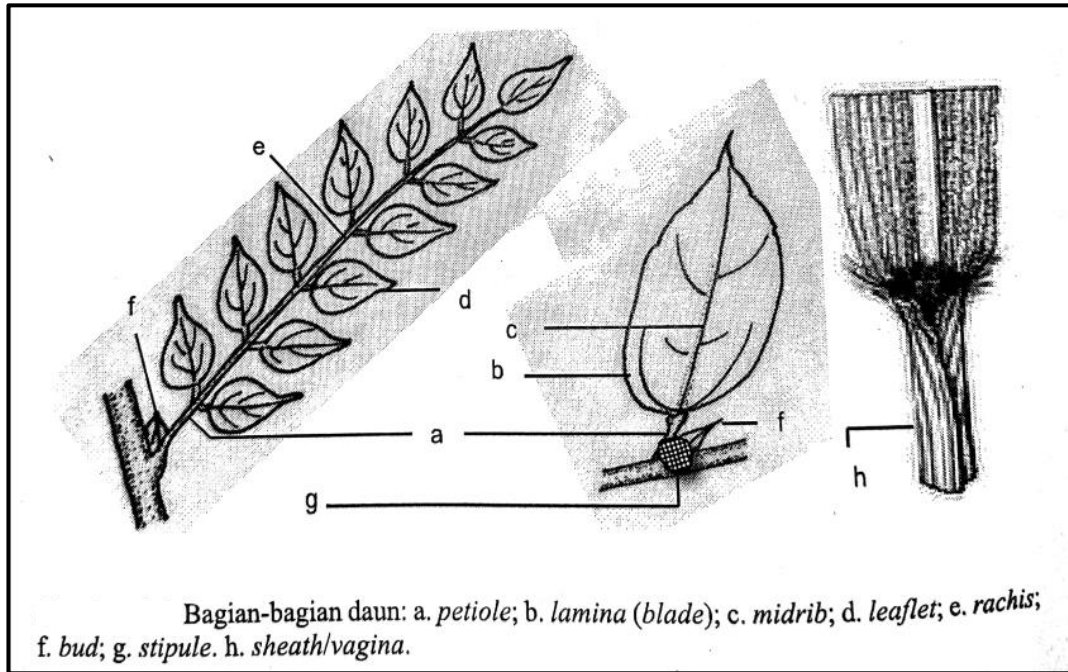
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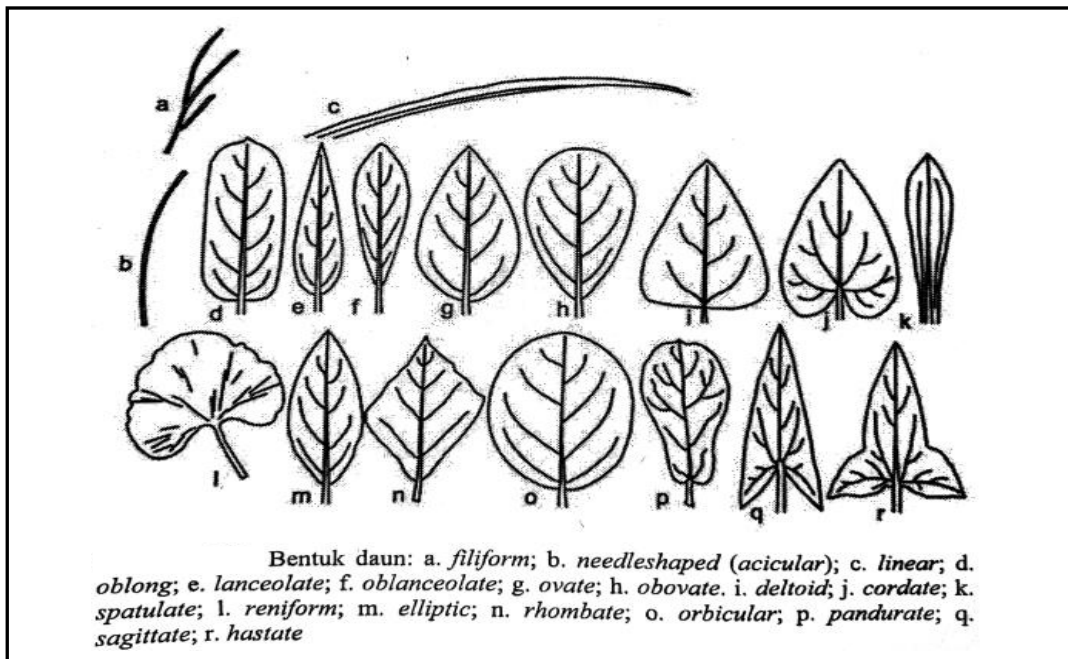
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LAMPIRAN

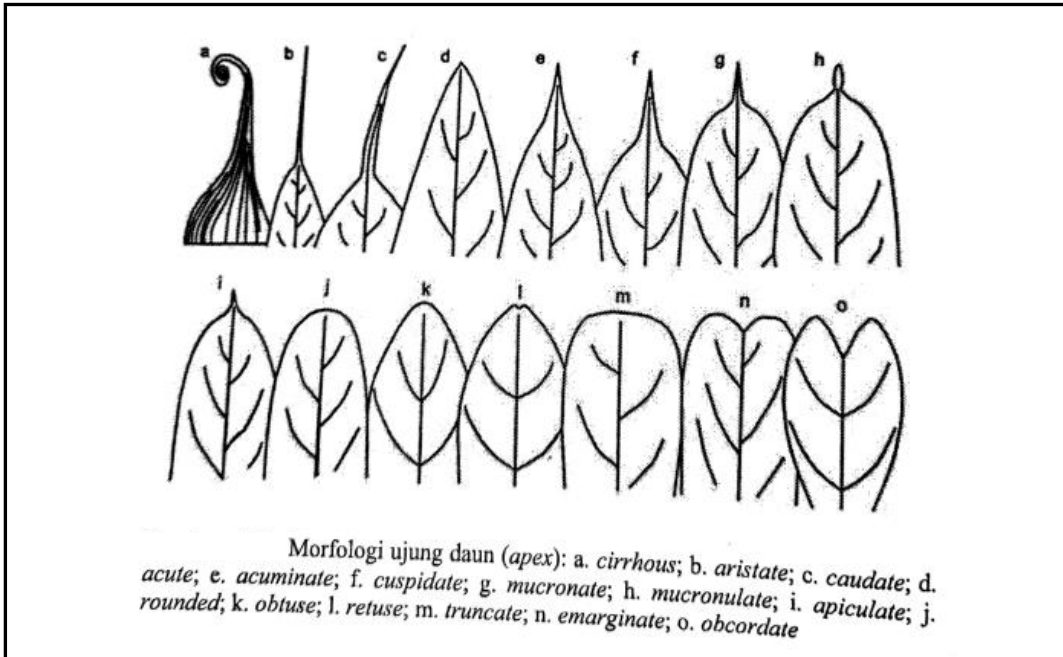
Lampiran 1. Bagian-bagian daun



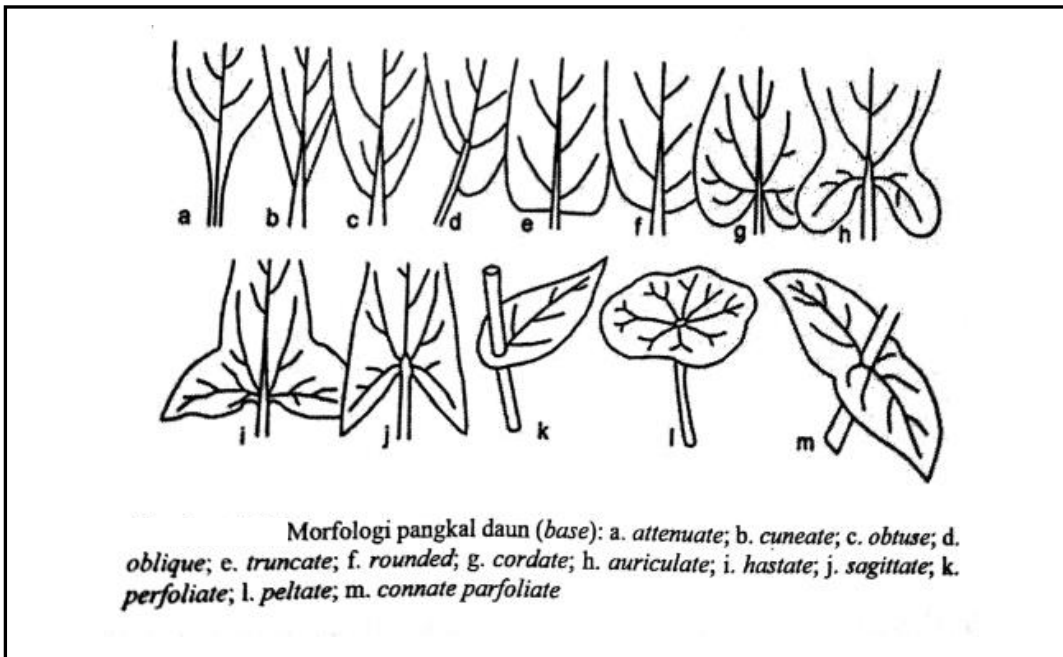
Lampiran 2. Bentuk daun



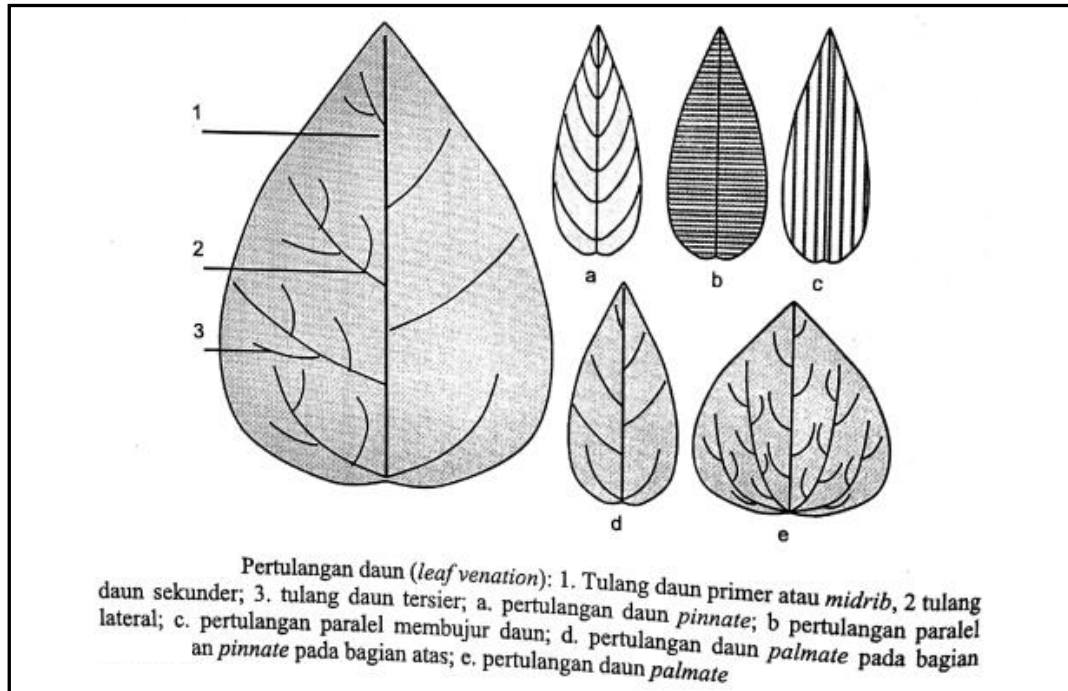
Lampiran 3. Bentuk ujung daun



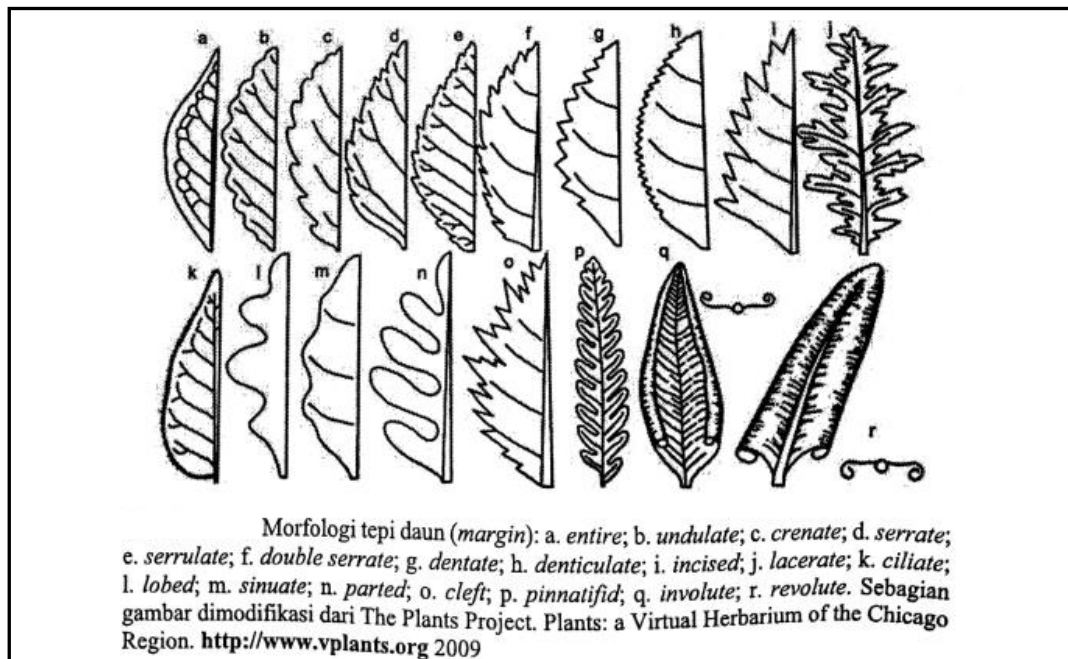
Lampiran 4. Bentuk pangkal daun



Lampiran 5. Pertulangan daun



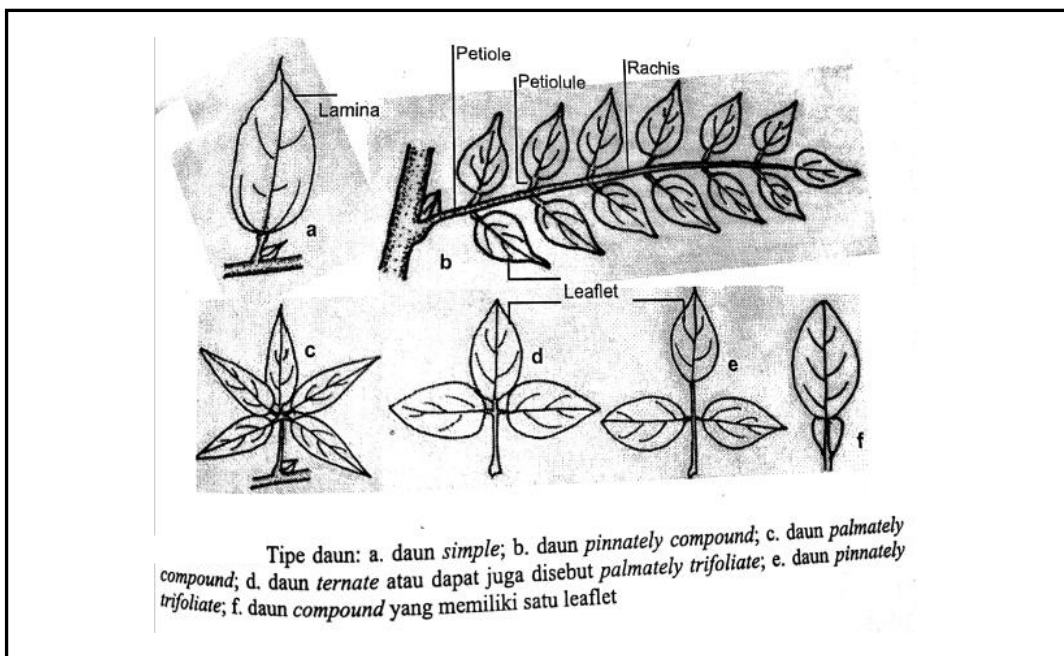
Lampiran 6. Tepi daun



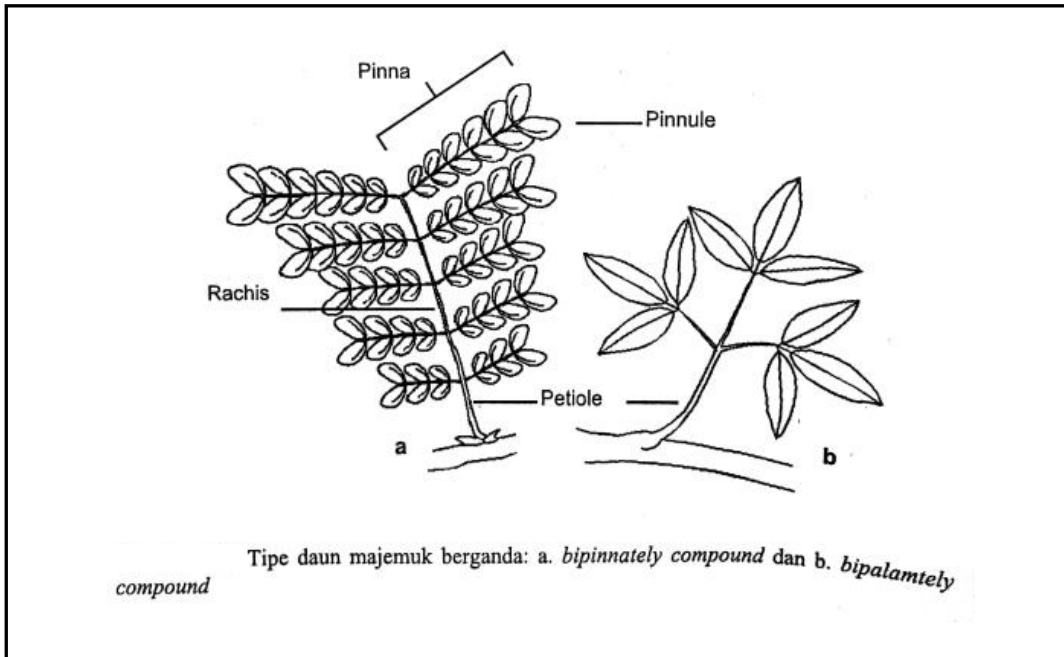
Lampiran 7. 30 Karakter morfologi daun hasil seleksi untuk identifikasi jenis famili dikotiledon

No	Kelompok ciri morfologi daun makro/ level	No. ID	Karakter	Jumlah state (inapplicable bukan state)
1	IX/Primer	46	Ada tidaknya rambut, tonjolan dan bintik-bintik pd permukaan daun atas	2
2	XVI/Primer	92	Dapat tidaknya sudut asal urat daun tersier ditentukan	2
3	X/Primer	51	Ada tidaknya rambut, sisik, tonjolan, bintik-bintik, dan domatia pd permukaan daun bawah	2
4	VIII/Primer	43	Ada tidaknya kelenjar daun	2
5	II/Primer	15	Susunan daun pada cabang	5
6	I/Primer	1	Jenis daun berdasarkan ada tidaknya anak daun	2
7	I/Sekunder	4	Bebas tidaknya ujung ibu tangkai daun menyirip	2
8	I/Sekunder	2	Genap tidaknya jumlah anak daun majemuk menyirip	2
9	I/Sekunder	3	Susunan anak daun majemuk menyirip pada ibu tangkai daun	3
10	XIV/Primer	75	Arah urat daun primer	3
11	XV/Primer	90	Ada tidaknya urat daun intramarginal	2
12	XV/Sekunder	91	Banyaknya tingkatan urat daun intramarginal	2
13	VII/Primer	33	Rata tidaknya tepi daun	2
14	VII/Sekunder	153	Jenis tepi daun tidak rata	3
15	XI/Primer	58	Ada tidaknya tangkai daun	2
16	XI/Sekunder	59	Bentuk tangkai daun	8
17	XIII/Primer	65	Tipe pertulangan daun	3
18	XIII/Sekunder	152	Jenis pertulangan daun menyirip	2
19	XIII/Tersier	67	Jenis pertulangan daun menyirip camptodromous	2
20	XIV/Primer	76	Bentuk urat daun primer	7
21	XV/Primer	81	Ketebalan relatif urat daun sekunder	3
22	XV/Primer	85	Ada tidaknya loop-forming urat daun sekunder	2
23	VI/Primer	32	Pangkal daun	13
24	XVI/Primer	94	Pola urat daun tersier	3
25	XVI/Sekunder	101	Susunan urat daun tersier berpola pecurrent	3
26	IV/Primer	30	Ujung daun	14
27	XV/Primer	77	Sudut divergensi urat daun sekunder	4
28	III/Primer	22	Ada tidaknya stipula	2
29	XVIII/Primer	108	Ada tidaknya veinlets *	2
30	XVIII/Sekunde	111	Banyaknya areola yang memiliki veinlets	3
Jumlah Tipe Morfologi Daun				1.268.047.872.000

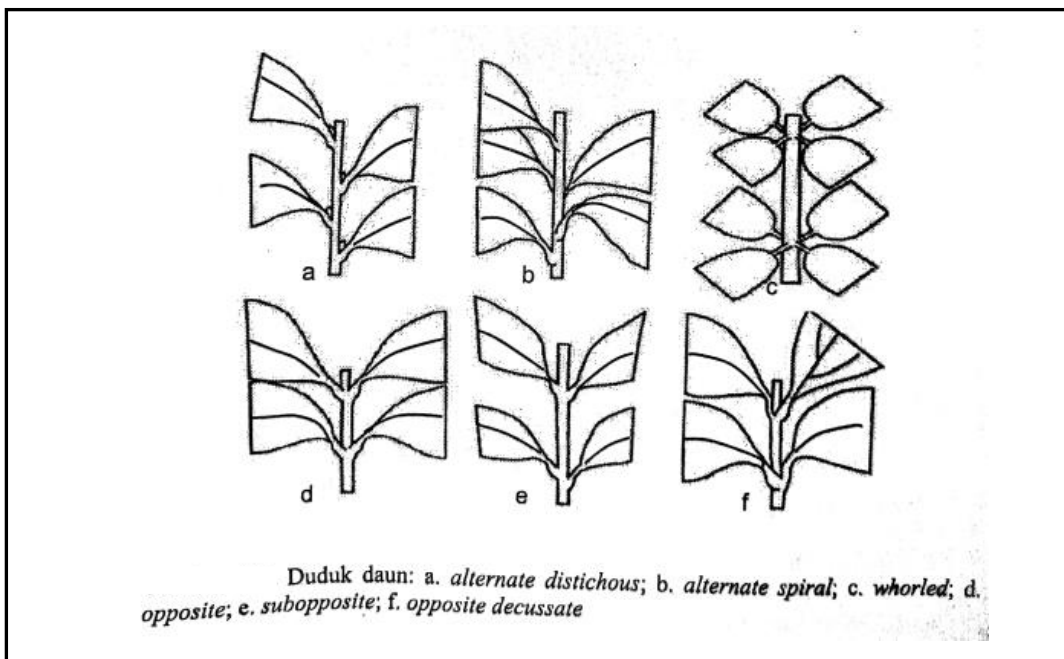
Lampiran 8. Tipe daun



Lampiran 9. Tipe daun majemuk berganda



Lampiran 10. Duduk daun



Lampiran 11. Data lengkap daun majemuk utuh *Toona* sp.

No	Kode Sampel	Tipe Daun	Susunan Anak Daun	Duduk Daun	Posisi Anak Daun	Panjang (cm)	Lebar (cm)	Jumlah Anak Daun
1	SA.1	Pinnately Compound	Abrupte Pinnatus	Opposite	Ujung	82.6	37.5	32
					Tengah	73.5	33.7	29
					Pangkal	76.5	39.3	33
2	SA.2	Pinnately Compound	Abrupte Pinnatus	Opposite	Ujung	61.2	33.1	30
					Tengah	59	31.5	29
					Pangkal	46.6	30.3	24
3	SA.3	Pinnately Compound	Abrupte Pinnatus	Opposite	Ujung	57.7	33.6	26
					Tengah	93.8	43.7	38
					Pangkal	81.9	38.2	33
4	SA.4	Pinnately Compound	Abrupte Pinnatus	Opposite	Ujung	99	40.4	41
					Tengah	106.5	43.7	39
					Pangkal	110	44	42
5	SA.5	Pinnately Compound	Abrupte Pinnatus	Opposite	Ujung	94.5	43	39
					Tengah	99.7	36.4	39
					Pangkal	80.8	37.3	33
1	SB.1	Pinnately Compound	Abrupte Pinnatus	Opposite	Ujung	21.3	23.5	16
					Tengah	23.5	22	16
					Pangkal	24.7	22.5	16

2	SB.2	Pinnately Compound	Abrupte Pinnatus	Opposite	Ujung	51	28	27
					Tengah	45.8	36	24
					Pangkal	52.3	36.1	23
3	SB.3	Pinnately Compound	Abrupte Pinnatus	Opposite	Ujung	31.4	26.3	16
					Tengah	37	26.7	19
					Pangkal	45	31.6	18
4	SB.4	Pinnately Compound	Abrupte Pinnatus	Opposite	Ujung	19.2	10.5	17
					Tengah	40.4	29	20
					Pangkal	40.3	30.1	17
5	SB.5	Pinnately Compound	Abrupte Pinnatus	Opposite	Ujung	28.6	19.4	17
					Tengah	34.4	22.3	13
					Pangkal	32.6	24.9	18

Lampiran 12. Data lengkap anak daun majemuk utuh *Toona* sp.

No	Kode Sampel	Posisi Anak Daun	Bentuk Daun (<i>Circumscriptio</i>)	Tepi Daun (<i>Margo Folii</i>)	Ujung Daun (<i>Apex Folii</i>)	Pangkal Daun (<i>Basis Folii</i>)	Pola Tulang Daun (<i>Nervatio</i>)	Warna Atas Daun	Warna Bawah Daun
1	S1.1	Ujung	Lanceolate	Serrate	accuminate	rounded	pinnate	5GY 3/4	7.5 GY 6/6
		Tengah	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY 3/4	7.5 GY 6/4
		Pangkal	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY3/4	7.5 GY 6/4

No	Kode Sampel	Posisi Anak Daun	Bentuk Daun (<i>Circumscriptio</i>)	Tepi Daun (<i>Margo Folii</i>)	Ujung Daun (<i>Apex Folii</i>)	Pangkal Daun (<i>Basis Folii</i>)	Pola Tulang Daun (<i>Nervatio</i>)	Warna Atas Daun	Warna Bawah Daun
2	S1.2	Ujung	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY 4/4	7.5GY 6/6
		Tengah	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY 4/4	7.5GY 6/6
		Pangkal	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY 4/4	7.5GY 6/6
3	S1.3	Ujung	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY 3/2	5GY 3/4
		Tengah	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY 3/2	5GY 3/4
		Pangkal	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY 3/2	5GY 3/4
4	S1.4	Ujung	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY 3/2	7.5GY 4/2
		Tengah	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY 3/4	5GY 3/4
		Pangkal	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY 3/2	7.5GY 4/2
5	S1.5	Ujung	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY 3/2	5GY 3/4
		Tengah	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY 3/2	5GY 3/4
		Pangkal	Lanceolate	Serrate	accuminate	rounded	pinnate	7.5GY 3/2	5GY 3/4
1	S2.1	Ujung	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 3/4	5GY 4/4
		Tengah	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 3/4	5GY 4/4
		Pangkal	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 3/4	5GY 4/4
2	S2.2	Ujung	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 3/4	5GY 4/4
		Tengah	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 3/4	5GY 4/4
		Pangkal	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 3/4	5GY 4/4
3	S2.3	Ujung	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 4/4	7.5GY 5/4
		Tengah	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 4/4	7.5GY 5/4
		Pangkal	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 4/4	7.5GY 5/4
4	S2.4	Ujung	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 4/4	7.5GY 5/4
		Tengah	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 3/4	7.5GY 5/4

No	Kode Sampel	Posisi Anak Daun	Bentuk Daun (<i>Circumscriptio</i>)	Tepi Daun (<i>Margo Folii</i>)	Ujung Daun (<i>Apex Folii</i>)	Pangkal Daun (<i>Basis Folii</i>)	Pola Tulang Daun (<i>Nervatio</i>)	Warna Atas Daun	Warna Bawah Daun
		Pangkal	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 4/4	7.5GY 5/4
5	S2.5	Ujung	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 3/4	7.5GY 5/4
		Tengah	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 3/4	7.5GY 5/4
		Pangkal	Lanceolate	Sinuate	Cuspidate	obtuse	pinnate	5GY 3/4	7.5GY 5/4

Lampiran 13. Data lingkungan Sampel *Toona* sp.

No.	Kode Sampel	Ketinggian (mdpl)	Tinggi Total (m)	Keliling (cm)	Suhu Udara (C)	Intensitas Cahaya	Koordinat
1	S1.1	558	6,35	22	30.5	8986	806480, 9447514
2	S1.2	542	7,85	19	31.8	6195	806040, 9447533
3	S1.3	557	5,65	11	32.9	5949	806051, 9447523
4	S1.4	550	9,90	13	32.8	7269	806054, 9447536
5	S1.5	548	8,65	12	32.2	5552	806067, 9447542
6	S2.1	418	5,81	63.5	28.5	820	807374, 9448053

No.	Kode Sampel	Ketinggian (mdpl)	Tinggi Total (m)	Keliling (cm)	Suhu Udara (C)	Intensitas Cahaya	Koordinat
7	S2.2	418	6,35	49	28.7	760	807384, 9448065
8	S2.3	525	4,86	26	32.6	6534	807689, 9450176
9	S2.4	517	5,65	61	31.6	7124	807693, 8450156
10	S2.5	498	5,38	45	31.6	7045	807703, 9449939

Lampiran 14. Hasil uji T pada panjang daun majemuk *Toona* sp. menggunakan software Rstudio

```
RGui (64-bit) - [R Console]
File Edit View Misc Packages Windows Help

alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.3357296 2.9785875
sample estimates:
ratio of variances
1

> print(hasil_jumlah_anak_daun)

      F test to compare two variances

data:  jumlah_anak_daun_suren_A and jumlah_anak_daun_suren_A
F = 1, num df = 14, denom df = 14, p-value = 1
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.3357296 2.9785875
sample estimates:
ratio of variances
1

> # Uji t pada variabel panjang daun antara Suren A dan Suren B
> t_test_panjang_daun <- t.test(panjang_daun_suren_A, panjang_daun_suren_B)
>
> # Menampilkan hasil uji t
> print(t_test_panjang_daun)

      Welch Two Sample t-test

data:  panjang_daun_suren_A and panjang_daun_suren_B
t = 8.1775, df = 21.755, p-value = 4.445e-08
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 34.61505 50.15829
sample estimates:
mean of X mean of y
 81.55333 35.16667

> |
```

Lampiran 15. Hasil uji T pada lebar daun majemuk *Toona* sp. menggunakan software Rstudio

```
RGui (64-bit) - [R Console]
File Edit View Misc Packages Windows Help

> ggplot(data, aes(x = jenis_suren, y = panjang_daun, fill = jenis_suren)) +
+   geom_boxplot() +
+   xlab("Jenis Suren") +
+   ylab("Panjang Daun") +
+   ggtitle("Perbandingan Panjang Daun Suren A dan Suren B") +
+   scale_fill_manual(values = c("blue", "green")) # Menentukan warna untuk setiap kategori
+   library(ggplot2)
>
> # Membuat data frame untuk Suren A dan Suren B
> data <- data.frame(
+   jenis = c(rep("Suren A", length(lebar_daun_suren_A)), rep("Suren B", length(lebar_daun_suren_B))),
+   lebar_daun = c(lebar_daun_suren_A, lebar_daun_suren_B)
+ )
>
> # Membuat grafik menggunakan ggplot2
> ggplot(data, aes(x = jenis, y = lebar_daun, fill = jenis)) +
+   geom_boxplot() +
+   labs(x = "Jenis Suren", y = "Lebar Daun") +
+   ggtitle("Perbandingan Lebar Daun antara Suren A dan Suren B") +
+   theme_minimal()
>
> # Uji t pada variabel lebar daun
> t_test_lebar_daun <- t.test(lebar_daun_suren_A, lebar_daun_suren_B)
>
> # Menampilkan hasil uji t
> print(t_test_lebar_daun)

      Welch Two Sample t-test

data:  lebar_daun_suren_A and lebar_daun_suren_B
t = 5.7067, df = 25.211, p-value = 5.882e-06
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 7.534719 16.03615
sample estimates:
mean of X mean of y
 37.71333 25.92667

> |
```

Lampiran 16. Hasil uji T pada jumlah anak daun majemuk *Toona sp.* menggunakan software Rstudio

```

RGui (64-bit) - [R Console]
File Edit View Misc Packages Windows Help

+ labs(x = "Jenis Suren", y = "Lebar Daun") +
+ ggtitle("Perbandingan Lebar Daun antara Suren A dan Suren B") +
+ theme_minimal()
> # Uji t pada variabel lebar daun
> t_test_lebar_daun <- t.test(lebar_daun_suren_A, lebar_daun_suren_B)
>
> # Menampilkan hasil uji t
> print(t_test_lebar_daun)

Welch Two Sample t-test

data: lebar_daun_suren_A and lebar_daun_suren_B
t = 5.7067, df = 25.211, p-value = 5.882e-06
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 7.534719 16.039615
sample estimates:
mean of x mean of y
37.71333 25.92667

> # Uji t pada variabel jumlah anak daun
> t_test_jumlah_anak_daun <- t.test(jumlah_anak_daun_suren_A, jumlah_anak_daun_suren_B)
>
> # Menampilkan hasil uji t
> print(t_test_jumlah_anak_daun)

Welch Two Sample t-test

data: jumlah_anak_daun_suren_A and jumlah_anak_daun_suren_B
t = 8.8658, df = 24.1, p-value = 4.712e-09
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 11.76464 18.90202
sample estimates:
mean of x mean of y
33.80000 18.46667

> |

```

Lampiran 17. Hasil uji normalitas Shapiro-wilk pada data panjang, lebar, dan jumlah anak daun majemuk sampel A *Toona sp.*

```

RGui (64-bit) - [R Console]
File Edit View Misc Packages Windows Help

Shapiro-Wilk normality test

data: jumlah_anak_daun_suren_B
W = 0.88494, p-value = 0.05626

> # Persiapan Data
> panjang_daun_suren_A <- c(82.6, 73.5, 76.5, 61.2, 59, 46.6, 57.7, 93.8, 81.9, 99, 106.5, 110, 94.5, 99.7, 80.8)
> lebar_daun_suren_A <- c(37.5, 33.7, 39.3, 33.1, 31.5, 30.5, 33.6, 43.7, 35.2, 40.4, 43.7, 44, 43, 36.4, 37.3)
> jumlah_anak_daun_suren_A <- c(32, 28, 33, 30, 29, 24, 26, 38, 33, 41, 38, 42, 38, 35, 33)
>
> # Uji Shapiro-Wilk
> hasil_shapiro_panjang_daun_A <- shapiro.test(panjang_daun_suren_A)
> hasil_shapiro_lebar_daun_A <- shapiro.test(lebar_daun_suren_A)
> hasil_shapiro_jumlah_anak_daun_A <- shapiro.test(jumlah_anak_daun_suren_A)
>
> # Menampilkan hasil uji normalitas
> print(hasil_shapiro_panjang_daun_A)

Shapiro-Wilk normality test

data: panjang_daun_suren_A
W = 0.85739, p-value = 0.6472

> print(hasil_shapiro_lebar_daun_A)

Shapiro-Wilk normality test

data: lebar_daun_suren_A
W = 0.93293, p-value = 0.3017

> print(hasil_shapiro_jumlah_anak_daun_A)

Shapiro-Wilk normality test

data: jumlah_anak_daun_suren_A
W = 0.94035, p-value = 0.3868

> |

```

Lampiran 18. Hasil uji normalitas Shapiro-wilk pada data panjang, lebar, dan jumlah anak daun majemuk sampel B *Toona* sp.

```

RGui (64-bit) - [R Console]
File Edit View Misc Packages Windows Help

'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[Previously saved workspace restored]

> # Persiapan Data
> panjang_daun_suren_B <- c(21.3, 23.5, 24.7, 51, 45.8, 52.3, 31.4, 37, 45, 19.2, 40.4, 40.3, 29.6, 34.4, 32.6)
> lebar_daun_suren_B <- c(23.5, 22, 22.5, 28, 36, 36.1, 26.3, 26.7, 31.6, 10.5, 29, 30.1, 19.4, 22.3, 24.5)
> jumlah_anak_daun_suren_B <- c(16, 16, 16, 27, 24, 23, 16, 19, 18, 17, 20, 17, 13, 18)
>
> # Uji Shapiro-Wilk
> hasil_shapiro_panjang_daun_B <- shapiro.test(panjang_daun_suren_B)
> hasil_shapiro_lebar_daun_B <- shapiro.test(lebar_daun_suren_B)
> hasil_shapiro_jumlah_anak_daun_B <- shapiro.test(jumlah_anak_daun_suren_B)
>
> # Menampilkan hasil uji normalitas
> print(hasil_shapiro_panjang_daun_B)

      Shapiro-Wilk normality test

data:  panjang_daun_suren_B
W = 0.96051, p-value = 0.7013

> print(hasil_shapiro_lebar_daun_B)

      Shapiro-Wilk normality test


data:  lebar_daun_suren_B
W = 0.55599, p-value = 0.6231

> print(hasil_shapiro_jumlah_anak_daun_B)

      Shapiro-Wilk normality test

data:  jumlah_anak_daun_suren_B
W = 0.88494, p-value = 0.05626
> |
    
```

Lampiran 19. Hasil sekuensing pada sampel A dan sampel B *Toona* sp. di Laboratorium Genetika Science Indonesia



CUSTOMER DETAILS	
Siti Halimah Larengkeng Fahutan UNHAS Kampus Unhas Tamalanrea, Jl. Perintis Kemerdekaan Km. 10, Fakultas Kehutanan, LAB BIOTEK, 90245, Makassar, Sulawesi Selatan Telp : - HP : 0852-4229-1851 Email : SitiH5h.82@gmail.com	Service Order ID : GMS – 2978 Type of Service : Species Barcoding Date of Submission : 27/09/2023 Date Completed (with deliverables) : 10/10/2023

SAMPLE INFORMATION	
Sample Name	: See List Table 1.
PCR Primer	: RBCL
PCR Products	: Species Barcoding RBCL (~600bp)

METHODS

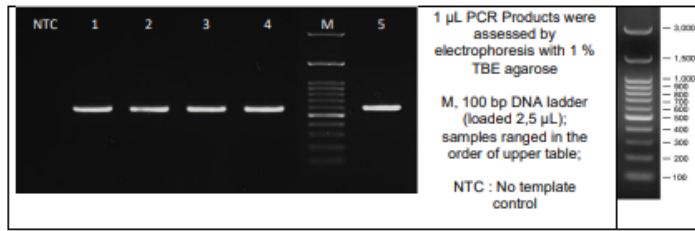
1. Genomic DNA extraction with Quick-DNA Magbead Plus Kit (Zymo Research, D4082)
2. PCR amplification with MyTaq HS Red Mix, 2X (Bioline, BIO-25048)
3. Bi-directional Sequencing

RESULTS

1. Nucleic Acid (Genomic DNA) Quantification (Nanodrop)

No.	Sample Name	Code Sample	Conc. (ng/µl)	A _{260/280}	A _{260/230}	Volume (µl)
1.	SA	2978-1	105.4	1.85	2.04	50
2.	SB	2978-2	42.0	1.81	1.61	50
3.	ZA	2978-3	122.0	1.95	1.65	50
4.	ZF	2978-4	45.7	1.78	1.09	50
5.	ZG	2978-5	60.2	1.74	1.55	50

2. Gel Photo – PCR Products – RBCL Primer



3. – Sequence Assembly Result – PCR Products RBCL Primer

No	Sample Name	Sequences
1	SA	Sequence Assembly 590bp
		1 CACCACAAC AGAGACTAAA GCAAGTGTG GATTCAAAG CGGTGTTAA GATTATAAT
		61 TGACTTATTA TACTCCTGAC TATGTAACCA AAGATACTGA TATCTTGCA GCATTCGGAG
		121 TAACCTCTCA ACCCGGAGTC CGGCCGAGG AAGCAGGGG TGGGTAGCT CGGGAATCTT
		181 CTACTGGTAC ATGGACAAC GTGTGGACG ATGGGCTTAC TAGCCTTGT GGTTACAAG
		241 GACGATGCTA CAACATTGAG CCAAGTTCGT GAGAAGAAA TCAATATATA TGTTATGTAG
		301 CTTACCCCTT AGACCTTTT GAAGAAGTT CTGTACTAA CATGTTTACG TCCATTCTGG
		361 GTAATGTATT TGGGTTCAA GGCCTGGGG CTCTACGTC AGAGGATCTA CGAATCCCTC
		421 CCGGCTATTC TAAAACCTTC CAAGGCCCCG CTCATGGCAT CCAAGTTGAG AGAGATAAAT
		481 TGAACAAGTA TGGTCTGTC CCTATTGGAT GTACTATTAA ACCTAAATTT GGGTTATCCG
541 CTAGAATTA CGGTAGACT GTTATGAAZ GTCTACGTG TGGACTGAT		
2	SB	Sequence Assembly 591bp
		1 CCCCCAAA CAGAGACTAA AGCAAGTGTG GGATTCAAAG CCGGTGTTAA AGATTATAAA
		61 TTGACTTATT ATACTCTGTA CTATGTAACC AAGATACTG ATATCTTGGC AGCATTCCGA
		121 GTAACCTCTC AACCGGAGT TCCGCCGAG GAGCAGGGG CTGACGTAGC TGGGAATCTT
		181 TCTACTGGTA CATGGACAAC TGTGTGGAC GATGGCTTA CTAGCCTTGA TCGTTACAAA
		241 GAGAGATGCT ACAACATTGA GCAAGTTCGT GAGAAGAAA ATCAATATAT ATGTTATGTA
		301 GCTTACCCCT TAGACCTTTT TGAAGAAGT TCTGTACTA ACATGTTTAC TCCCATCTGG
		361 GGTAAATGAT TTGGGTTCAA AGCCTGGGG GCTCTACGTC TAGAGGATCT ACGAATCCCT
		421 CCGGCTATTC TAAAACCTTC CCAAGGCCCC CCTCATGGCA TCCAAGTTGA GAGAGATAAA
		481 TTGAACAAGT ATGGTCTGTC CCTATTGGGA TGTACTATTA AACCTAAATTT GGGGTTATCC
541 GCTAAGAATT ACGGAAGAGC TGTATTGAA TGTCTACGTG GTGGACTTGA T		

4. Top 10 Hit BLAST Results Against NCBI Database, Excluding Uncultured Sample Sequences (RBCL Primer)

No	Sample Name	Result Links																																																																													
1	SA	<table border="1"> <thead> <tr> <th>Description</th> <th>Max Score</th> <th>Total Score</th> <th>Query Cover</th> <th>E-value</th> <th>Per Ident</th> <th>Accession</th> </tr> </thead> <tbody> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>Drosophila obscura</i> <i>obscura</i> <i>obscura</i></td> <td>1077</td> <td>1077</td> <td>99%</td> <td>0.0</td> <td>99.97%</td> <td>OK572863.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>Drosophila obscura</i> <i>obscura</i> <i>obscura</i></td> <td>1077</td> <td>1077</td> <td>99%</td> <td>0.0</td> <td>99.97%</td> <td>U818893.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>Drosophila obscura</i> <i>obscura</i> <i>obscura</i></td> <td>1077</td> <td>1077</td> <td>99%</td> <td>0.0</td> <td>99.99%</td> <td>NC_238933.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. obscura</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>1077</td> <td>1077</td> <td>99%</td> <td>0.0</td> <td>99.96%</td> <td>U832496.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. varicostata</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>1077</td> <td>1077</td> <td>99%</td> <td>0.0</td> <td>99.96%</td> <td>U832495.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. melanogaster</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>1077</td> <td>1077</td> <td>99%</td> <td>0.0</td> <td>99.99%</td> <td>U832494.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. melanogaster</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>1077</td> <td>1077</td> <td>99%</td> <td>0.0</td> <td>99.99%</td> <td>U832494.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. ferox</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>1077</td> <td>1077</td> <td>99%</td> <td>0.0</td> <td>99.96%</td> <td>U832493.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. ferox</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>1077</td> <td>1077</td> <td>99%</td> <td>0.0</td> <td>99.96%</td> <td>U832493.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. obscura</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>1077</td> <td>1077</td> <td>99%</td> <td>0.0</td> <td>99.96%</td> <td>U832493.1</td> </tr> </tbody> </table> <p>https://www.ncbi.nlm.nih.gov/nucore/OK572863.1.OL693863.1.NC_039592.1.OP373446.1.OP373445.1.OP373444.1.OP373443.1.OP373442.1.OP373441.1.OP373440.1</p>	Description	Max Score	Total Score	Query Cover	E-value	Per Ident	Accession	<input checked="" type="checkbox"/> Dros. obscura <i>Drosophila obscura</i> <i>obscura</i> <i>obscura</i>	1077	1077	99%	0.0	99.97%	OK572863.1	<input checked="" type="checkbox"/> Dros. obscura <i>Drosophila obscura</i> <i>obscura</i> <i>obscura</i>	1077	1077	99%	0.0	99.97%	U818893.1	<input checked="" type="checkbox"/> Dros. obscura <i>Drosophila obscura</i> <i>obscura</i> <i>obscura</i>	1077	1077	99%	0.0	99.99%	NC_238933.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. obscura</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	1077	1077	99%	0.0	99.96%	U832496.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. varicostata</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	1077	1077	99%	0.0	99.96%	U832495.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. melanogaster</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	1077	1077	99%	0.0	99.99%	U832494.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. melanogaster</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	1077	1077	99%	0.0	99.99%	U832494.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. ferox</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	1077	1077	99%	0.0	99.96%	U832493.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. ferox</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	1077	1077	99%	0.0	99.96%	U832493.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. obscura</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	1077	1077	99%	0.0	99.96%	U832493.1
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<input checked="" type="checkbox"/> Dros. obscura <i>var. ferox</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	1077	1077	99%	0.0	99.96%	U832493.1																																																																									
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2	SB	<table border="1"> <thead> <tr> <th>Description</th> <th>Max Score</th> <th>Total Score</th> <th>Query Cover</th> <th>E-value</th> <th>Per Ident</th> <th>Accession</th> </tr> </thead> <tbody> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>Drosophila obscura</i> <i>obscura</i> <i>obscura</i></td> <td>969</td> <td>969</td> <td>99%</td> <td>0.0</td> <td>99.97%</td> <td>NC_238933.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. obscura</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>969</td> <td>969</td> <td>99%</td> <td>0.0</td> <td>99.99%</td> <td>U832493.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. varicostata</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>969</td> <td>969</td> <td>99%</td> <td>0.0</td> <td>99.99%</td> <td>U832493.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. melanogaster</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>969</td> <td>969</td> <td>99%</td> <td>0.0</td> <td>99.99%</td> <td>U832493.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. melanogaster</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>969</td> <td>969</td> <td>99%</td> <td>0.0</td> <td>99.99%</td> <td>U832493.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. ferox</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>969</td> <td>969</td> <td>99%</td> <td>0.0</td> <td>99.99%</td> <td>U832493.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. ferox</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>969</td> <td>969</td> <td>99%</td> <td>0.0</td> <td>99.99%</td> <td>U832493.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. obscura</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>969</td> <td>969</td> <td>99%</td> <td>0.0</td> <td>99.99%</td> <td>U832493.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. obscura</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>969</td> <td>969</td> <td>99%</td> <td>0.0</td> <td>99.99%</td> <td>U832493.1</td> </tr> <tr> <td><input checked="" type="checkbox"/> Dros. obscura <i>var. obscura</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i></td> <td>969</td> <td>969</td> <td>99%</td> <td>0.0</td> <td>99.99%</td> <td>U832493.1</td> </tr> </tbody> </table>	Description	Max Score	Total Score	Query Cover	E-value	Per Ident	Accession	<input checked="" type="checkbox"/> Dros. obscura <i>Drosophila obscura</i> <i>obscura</i> <i>obscura</i>	969	969	99%	0.0	99.97%	NC_238933.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. obscura</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	969	969	99%	0.0	99.99%	U832493.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. varicostata</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	969	969	99%	0.0	99.99%	U832493.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. melanogaster</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	969	969	99%	0.0	99.99%	U832493.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. melanogaster</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	969	969	99%	0.0	99.99%	U832493.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. ferox</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	969	969	99%	0.0	99.99%	U832493.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. ferox</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	969	969	99%	0.0	99.99%	U832493.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. obscura</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	969	969	99%	0.0	99.99%	U832493.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. obscura</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	969	969	99%	0.0	99.99%	U832493.1	<input checked="" type="checkbox"/> Dros. obscura <i>var. obscura</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	969	969	99%	0.0	99.99%	U832493.1
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		<input checked="" type="checkbox"/> Dros. obscura <i>var. ferox</i> <i>obscura</i> <i>Dros. obscura</i> <i>obscura</i> <i>obscura</i>	969	969	99%	0.0	99.99%	U832493.1																																																																							
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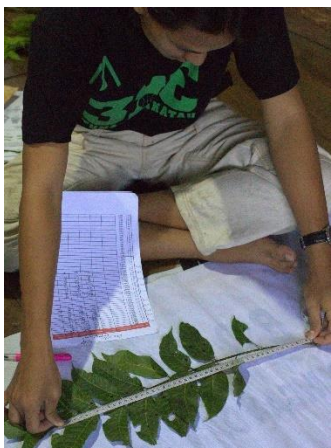
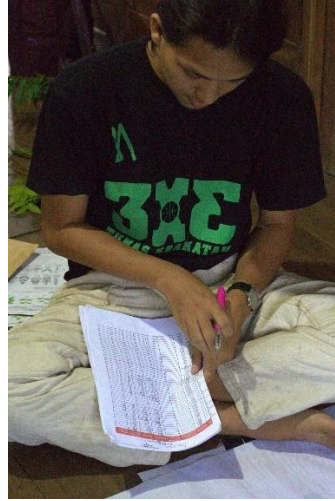
Lampiran 20. Hasil Top 10 hit BLAST terhadap database NCBI pada sampel A
Toona sp.

Sequences producing significant alignments									
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per Ident	Acc. Len	Accession	
<input checked="" type="checkbox"/> Toona sinensis chloroplast_complete genome	Toona sinensis	1077	1077	99%	0.0	99.83%	159139	OK572965.1	
<input checked="" type="checkbox"/> Toona sinensis chloroplast_complete genome	Toona sinensis	1077	1077	99%	0.0	99.83%	158970	QL693863.1	
<input checked="" type="checkbox"/> Toona ciliata chloroplast_complete genome	Toona ciliata	1072	1072	99%	0.0	99.66%	159502	NC_039592.1	
<input checked="" type="checkbox"/> Toona ciliata var. yunnanensis isolate DHC2 chloroplast_complete genome	Toona ciliata var. yunnanensis	1072	1072	99%	0.0	99.66%	159616	OP373446.1	
<input checked="" type="checkbox"/> Toona ciliata var. yunnanensis isolate DHC1 chloroplast_complete genome	Toona ciliata var. yunnanensis	1072	1072	99%	0.0	99.66%	159546	OP373445.1	
<input checked="" type="checkbox"/> Toona ciliata var. pubescens isolate MHC2 chloroplast_complete genome	Toona ciliata var. pubescens	1072	1072	99%	0.0	99.66%	159616	OP373444.1	
<input checked="" type="checkbox"/> Toona ciliata var. pubescens isolate MHC1 chloroplast_complete genome	Toona ciliata var. pubescens	1072	1072	99%	0.0	99.66%	159615	OP373443.1	
<input checked="" type="checkbox"/> Toona ciliata var. henryi isolate SM2 chloroplast_complete genome	Toona ciliata var. henryi	1072	1072	99%	0.0	99.66%	159561	OP373442.1	
<input checked="" type="checkbox"/> Toona ciliata var. henryi isolate SM1 chloroplast_complete genome	Toona ciliata var. henryi	1072	1072	99%	0.0	99.66%	159616	OP373441.1	
<input checked="" type="checkbox"/> Toona ciliata var. ciliata isolate HC2 chloroplast_complete genome	Toona ciliata var. ciliata	1072	1072	99%	0.0	99.66%	159616	OP373440.1	

Lampiran 21. Hasil Top 10 hit BLAST terhadap database NCBI pada sampel B
Toona sp.

Sequences producing significant alignments									
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	
<input checked="" type="checkbox"/> Toona ciliata chloroplast_complete genome	Toona ciliata	1068	1068	99%	0.0	99.49%	159502	NC_039592.1	
<input checked="" type="checkbox"/> Toona ciliata var. yunnanensis isolate DHC2 chloroplast_complete genome	Toona ciliata var. yunnanensis	1068	1068	99%	0.0	99.49%	159616	OP373446.1	
<input checked="" type="checkbox"/> Toona ciliata var. yunnanensis isolate DHC1 chloroplast_complete genome	Toona ciliata var. yunnanensis	1068	1068	99%	0.0	99.49%	159546	OP373445.1	
<input checked="" type="checkbox"/> Toona ciliata var. pubescens isolate MHC2 chloroplast_complete genome	Toona ciliata var. pubescens	1068	1068	99%	0.0	99.49%	159616	OP373444.1	
<input checked="" type="checkbox"/> Toona ciliata var. pubescens isolate MHC1 chloroplast_complete genome	Toona ciliata var. pubescens	1068	1068	99%	0.0	99.49%	159615	OP373443.1	
<input checked="" type="checkbox"/> Toona ciliata var. henryi isolate SM2 chloroplast_complete genome	Toona ciliata var. henryi	1068	1068	99%	0.0	99.49%	159561	OP373442.1	
<input checked="" type="checkbox"/> Toona ciliata var. henryi isolate SM1 chloroplast_complete genome	Toona ciliata var. henryi	1068	1068	99%	0.0	99.49%	159616	OP373441.1	
<input checked="" type="checkbox"/> Toona ciliata var. ciliata isolate HC2 chloroplast_complete genome	Toona ciliata var. ciliata	1068	1068	99%	0.0	99.49%	159616	OP373440.1	
<input checked="" type="checkbox"/> Toona ciliata var. ciliata isolate HC1 chloroplast_complete genome	Toona ciliata var. ciliata	1068	1068	99%	0.0	99.49%	159617	OP373439.1	
<input checked="" type="checkbox"/> Toona fargesii chloroplast_complete genome	Toona fargesii	1068	1068	99%	0.0	99.49%	159583	NC_069639.1	

Lampiran 22. Pengambilan dan Pegukuran Sampel *Toona* sp. di Hutan Pendidikan, Universitas Hasanuddin



Lampiran 23. Dokumentasi daun majemuk utuh *Toona* sp. di Hutan Pendidikan,
Universitas Hasanuddin

