

AIM

To develop a DNA barcode for *E. longifolia* from Sumatra, Indonesia using the *trnL-F* region. We expect to discover nucleotide variations that some of which were specific for samples from Sumatra. The results from this study is expected to assist identification of herbal medicine containing *E. longifolia* from Sumatra, Indonesia





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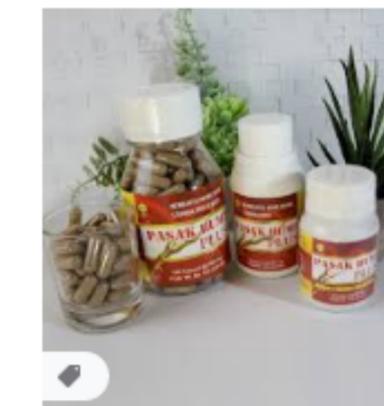
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MATERIALS AND METHOD

Samples:

24 *E. longifolia* from Sumatra

8 reference taxa:

E. longifolia MH751519 (KL. Malaysia)

E. longifolia KP995519 (Unknown origin)

E. apiculata GU593014 (Unknown origin)

Simaba morettii MG599405 (French Guiana)

Odyendyea gabonensis MG599427 (Gabon)

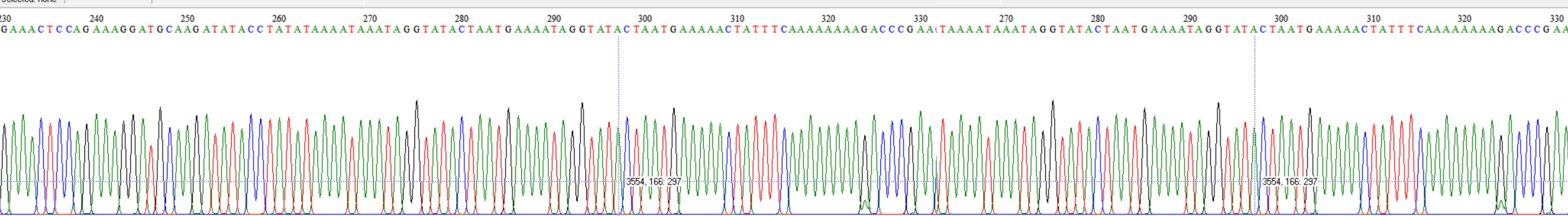
Simaba glabra MG599404 (Mato Grosso, Brazil)

Perriera madagascariensis GU593020 (Unknown origin)

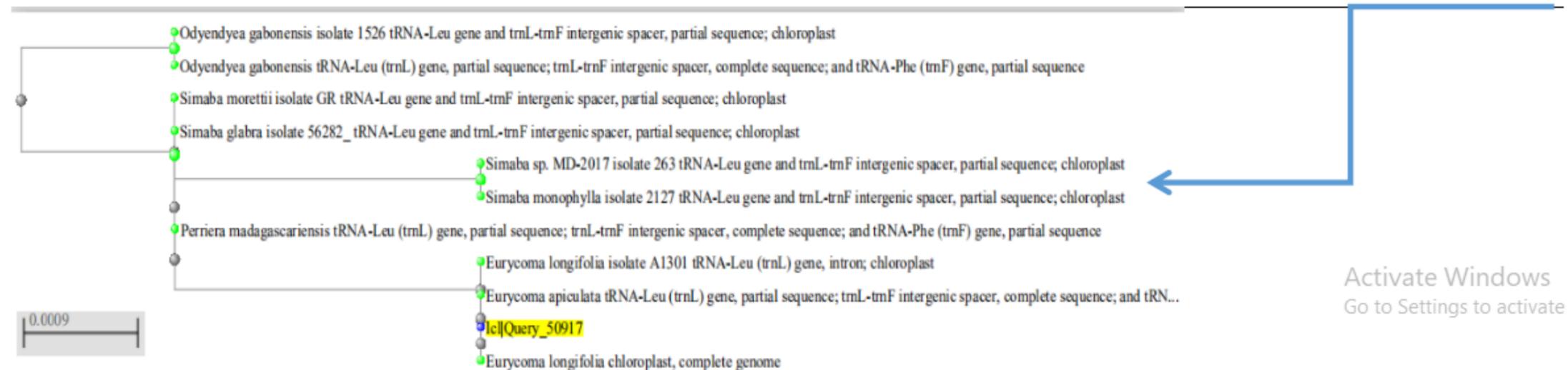
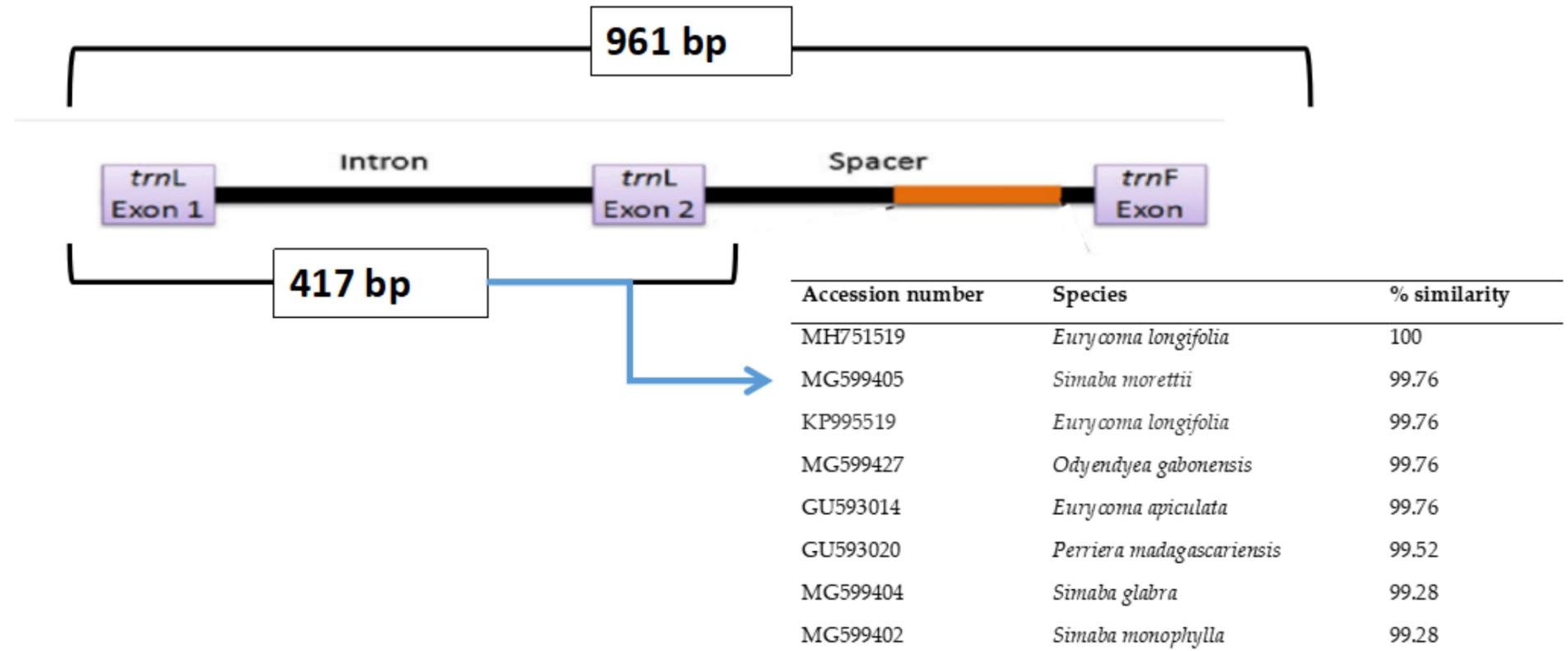
Simaba monophylla MG599402 (Kaieteur Plateau, Guyana)

Marker: *trnL*-F gene





RESULTS



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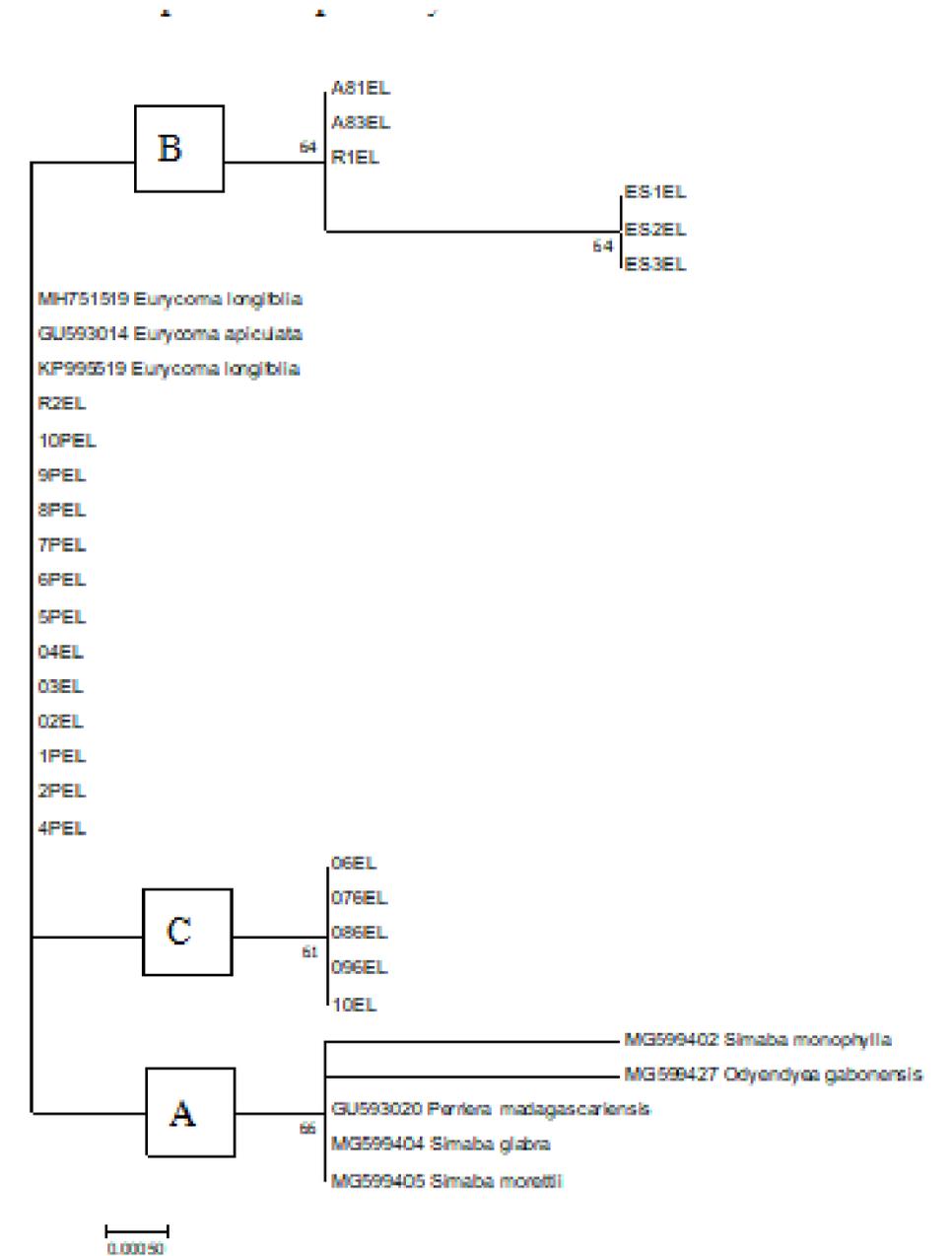
Table 2. Nucleotide composition and variation found in the *trnL-F* sequence of *Eurycoma longifolia* from and the reference accessions

Species	Nucleotide percentage (%)*				Position of point mutations**						
	T	C	A	G	52	55	135	161	371	421	742
<i>Eurycoma longifolia</i> 02EL	27.5	16.6	39.0	16.9	A	C	T	G	C	G	C
<i>Eurycoma longifolia</i> 03EL	27.5	16.6	39.0	16.9
<i>Eurycoma longifolia</i> 04EL	27.5	16.6	39.0	16.9
<i>Eurycoma longifolia</i> 06EL	27.5	16.6	39.0	16.9	G	T	G
<i>Eurycoma longifolia</i> 07EL	27.5	16.6	39.0	16.9	G	T	G
<i>Eurycoma longifolia</i> 08EL	27.2	16.6	39.0	17.1	G	T	G
<i>Eurycoma longifolia</i> 09EL	27.2	16.6	39.0	17.1	G	T	G
<i>Eurycoma longifolia</i> 10EL	27.2	16.6	39.0	17.1	G	T	G
<i>Eurycoma longifolia</i> 1PEL	27.2	16.6	39.0	17.1	G
<i>Eurycoma longifolia</i> 2PEL	27.2	16.6	39.0	17.1	G
<i>Eurycoma longifolia</i> 4PEL	27.2	16.6	39.0	17.1	G
<i>Eurycoma longifolia</i> 5PEL	27.2	16.6	39.0	17.1	G
<i>Eurycoma longifolia</i> 6PEL	27.2	16.6	39.0	17.1	G
<i>Eurycoma longifolia</i> 09EL	27.2	16.6	39.0	17.1	G	T	G
<i>Eurycoma longifolia</i> 10EL	27.2	16.6	39.0	17.1	G	T	G
<i>Eurycoma longifolia</i> 1PEL	27.2	16.6	39.0	17.1	G
<i>Eurycoma longifolia</i> 2PEL	27.2	16.6	39.0	17.1	G
<i>Eurycoma longifolia</i> 4PEL	27.2	16.6	39.0	17.1	G
<i>Eurycoma longifolia</i> 5PEL	27.2	16.6	39.0	17.1	G
<i>Eurycoma longifolia</i> 6PEL	27.2	16.6	39.0	17.1	G
<i>Eurycoma longifolia</i> 7PEL	27.2	16.6	39.0	17.1	G
<i>Eurycoma longifolia</i> 8PEL	27.2	16.6	39.0	17.1	G
<i>Eurycoma longifolia</i> 9PEL	27.2	16.6	39.0	17.1
<i>Eurycoma longifolia</i> 10PEL	27.2	16.6	39.0	17.1
<i>Eurycoma longifolia</i> R1EL	26.9	16.8	39.2	17.1	.	.	C
<i>Eurycoma longifolia</i> R2EL	27.2	16.6	39.0	17.1	G	.	C
<i>Eurycoma longifolia</i> ES1EL	27.2	16.6	39.0	17.1	.	T	C
<i>Eurycoma longifolia</i> ES2EL	27.2	16.6	39.0	17.1	.	T	C
<i>Eurycoma longifolia</i> ES3EL	27.2	16.6	39.0	17.1	.	T	C
<i>Eurycoma longifolia</i> AS1EL	26.9	16.8	39.2	17.1	.	.	C
<i>Eurycoma longifolia</i> AS3EL	26.9	16.8	39.2	17.1	.	.	C
Average	27.2	16.7	39.1	17.1							

Five point mutation for Sumatra: position 52, 55, 135, 421, and 742, Two mutation of reference taxa: position 161 and 371 (Table 3).



Five reference species of non-*Eurycoma* (A) in a separate lineage with 66% BS. Samples of *E. longifolia* from Sumatra and the reference *E. longifolia* have unresolved position on the topology except for samples from Riau (B) and West Sumatra (C)..



<i>Eurycoma longifolia</i> KP995519	27.2	16.6	39.2	17.1
<i>Eurycoma longifolia</i> MH751519	27.2	16.6	39.0	17.1
<i>Eurycoma apiculata</i> GU593014	27.2	16.6	39.2	17.1
<i>Periera madagascariensis</i> GU593020	27.4	16.3	39.2	17.1	T	.	.
<i>Simaba monophylla</i> MG599402	27.6	16.3	39.2	16.8	.	.	.	T	T	.	.
<i>Simaba glabra</i> MG599404	27.3	16.3	39.3	17.0	T	.	.
<i>Simaba moretti</i> MG599405	27.5	16.4	39.0	17.1	T	.	.
<i>Odyendya gabonensis</i> MG599427	27.5	16.6	39.0	16.9	T	.	.

CONCLUSION

Five point mutations were determined from a total of 961 bp *trnL*-F sequence possessed by samples of *E. longifolia* from the West Sumatra dan Riau.

Of the five nucleotides, four were in the *trnL* intron and one in the intergenic spacer between *trnL* and *trnF* gene.

It is suggested that the *trnL* intron can be used as one of potential markers for establishing DNA barcode for *E. longifolia* from Indonesia.

It is recommended to use more DNA barcode markers with a similar mutation rates as *trnL* intron to complement this present results.



THANK YOU.....