Specimen Details Current

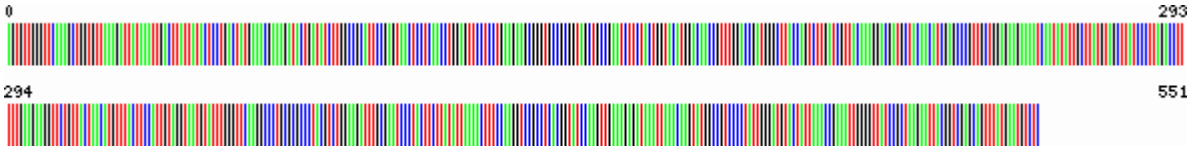
Sample ID:	GCUL-FDGK-142
Process ID:	GCUDG142-12
Project:	GCUDG
Tax Names:	Magnoliophyta, Magnoliopsida, Fabales, Fabaceae, Dalbergia, Dalbergia sissoo
Taxon:	Dalbergia sissoo
Rank Name:	species
Sampling Protocol:	N/A
BIN URI:	N/A
Kingdom:	Plantae

Marker Summary

Marker Code	Sequence Length	GC	Ambiguous	Trace Count
rbcLa	552	43.1%	0%	2
matK	846	28.6%	0%	2

rbcLa

Illustrative Barcode



Nucleotide Sequence

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GCGGTAGCTGCCGAATCTTCTACTGGTACATGGACAACCGTTTGGACCGATGGGCTTACCAGTCTTGAT
CGTTACAAAGGACGATGCTACAACATCGAGCCCGTTGCTGGAGAAGAAAATCAATATATTGCTTATGTA
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TTCCAAGGTCCGCCTCACGGTATCCAAGTTGAAAGAGATAAATTAAACAAGTATGGCCGTCCCCTATTG
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Amino Acid Sequence

```
SVGFKAGVKDYKLTYYTPDYETKDTDILAAFRVTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLD
RYKGRCYNIEPVAGEENQYIAYVAYPLDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDLRIPTSYIKT
FQGPPHGIQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECL
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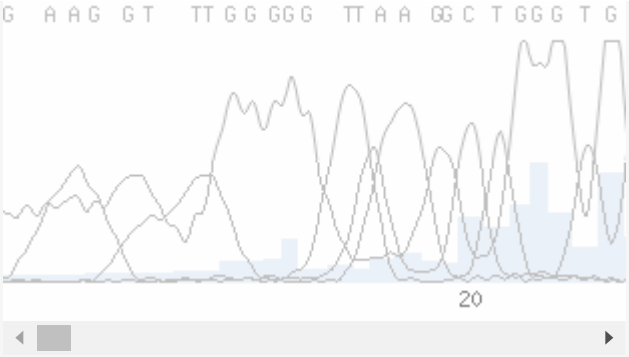
Sequence Metadata

Genbank Accession:	N/A
Translation Matrix:	Standard Code
Last Updated:	2014-03-07 14:30:50.459145
Sequence Runsite:	Biodiversity Institute of Ontario

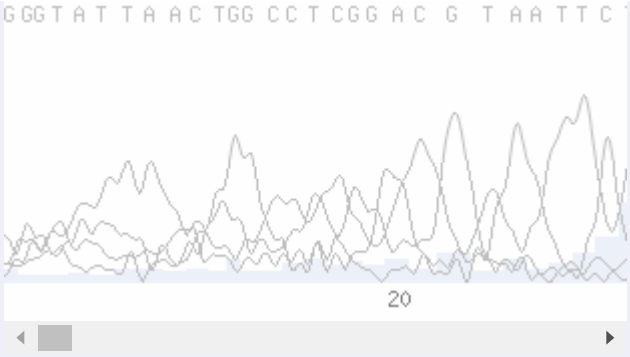
rbcLa Tags & Comments

Sequencing Date	2012-09-06 12:52:13	**Sequencing Date**	2012-09-06 20:01:49
Trace Direction	F	**Trace Direction**	R
Forward Primer	rbcLa-F	**Forward Primer**	rbcLa-F
Reverse Primer	rbcLa-R	**Reverse Primer**	rbcLa-R
Sequence Primer	rbcLa-F	**Sequence Primer**	rbcLa-R
Status	high qual	**Status**	high qual
Trace Runsite	Biodiversity Institute of Ontario	**Trace Runsite**	Biodiversity Institute of Ontario



Trace Tags

Trace Comments

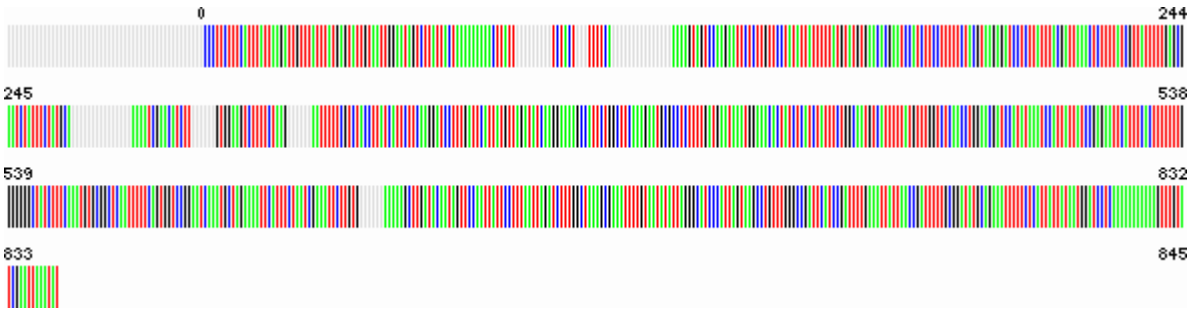


Trace Tags

Trace Comments

matK

Illustrative Barcode



Nucleotide Sequence

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TGTATGTGAACACGAATCCATCTTCCTTTTTCTACGTAAGAGATCCTCTTATTTACGATTAAACTCTTT
TATCGTTATTTTTGAGCGAATCTATTTCTATGCA----------AAAATCGAACATCTT-----
-GTGGAAGTCTTTTCTAAG ----------AATTTTTCGTCTACCTTATCATTCTTCAAGGATCCTTTGATTCA
TTATGTTAGATATCAAGGAAAAGCCATTCTGGCTTCAAAGAATGCGCCTCTTTTGATGAATAAATGGAA
ACACTATCTCATCTATTTCTGGCAATGTCATTTTTATGTTTGGTCTCAACCTGGAACGATCCATATAAA
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GCATCCCATTAGTAAGCCTGTTTGGGCCGATTCATCCGATTTTGAAATTATTAACCGATTTTTGCGGAT
ATGCAGAAATTTTTCTCATTATTATAATGGATCCTCAAAAAAAAAAAGTTTGTATCGAATTAAATAT
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Amino Acid Sequence

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PFFHLLRLFIYEYCNWNSLITKKKLI---ST-FS--------KSSPRILLFLYYFYVCEHESIFLFLRKRSS
YLRLNSFIVIFERIYFYA-----KIEHL--VEVFSK--NFSSTLSFFKDPLIHYVRYQGKAILASKNAP
LLMNKWKHYLIYFWQCHFYVWSQPGTIHINPLLSENSFHFFWGGYLSNVRLNFSVVRNQMLENSFLIEI
LV--KKLDTIVPIIPLIRSLAKAKFCNILGHPISKPVWADSSDFEIINRFLRICRNFSHYYNGSSKKKS
LYRIKY
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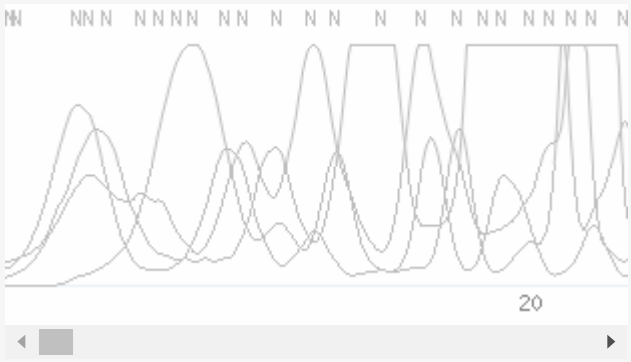
Sequence Metadata

Genbank Accession:	N/A
Translation Matrix:	Standard Code
Last Updated:	2012-10-09 14:40:03.120766
Sequence Runsite:	Biodiversity Institute of Ontario

matK Tags & Comments

Sequencing Date	2012-09-28 12:34:29	**Sequencing Date**	2012-09-28 11:55:43
Trace Direction	R	**Trace Direction**	F
Forward Primer	MatK-1RKIM-f	**Forward Primer**	MatK-1RKIM-f
Reverse Primer	MatK-3FKIM-r	**Reverse Primer**	MatK-3FKIM-r
Sequence Primer	MatK-1FKIM-r	**Sequence Primer**	MatK-1RKIM-f

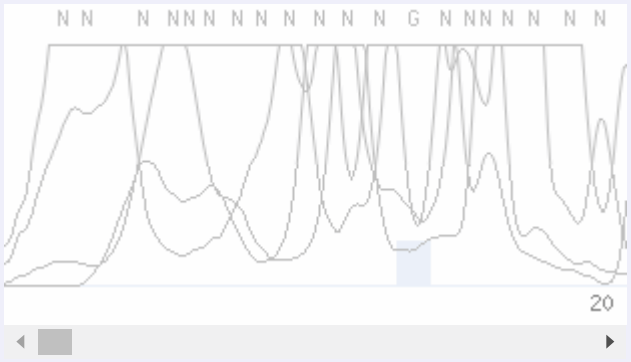
Status	high qual
Trace Runsite	Biodiversity Institute of Ontario



Trace Tags

Trace Comments

Status	high qual
Trace Runsite	Biodiversity Institute of Ontario



Trace Tags

Trace Comments