

1. INTRODUCTION

CPTree is a web-based Phylogenetic Tree Generator using Chloroplast Genomes. It defined two methodologies to generate the phylogenetic trees, one uses single ribosomal RNA in cpDNA to provide a fast preview of the evolutionary relationship; the other uses full cpDNA to calculate a relatively accurate tree. Meanwhile, the key model of CPTree, Chloroplast Database (CPDB), contains a local database of all available cpDNA from Genome Information by Organism in NCBI <https://www.ncbi.nlm.nih.gov> .

DATA SOURCE

The Fast Mode uses ribosomal RNA data as the material for phylogenetic analysis. Meanwhile, an input of the whole cpDNA is supported in the Normal Mode.

CPDB synchronized with NCBI <https://www.ncbi.nlm.nih.gov> maintains over 1000 cpDNAs and their key features extracted from its original NCBI database, including: full Sequence file(.fa), GenBank file(.gb), Nucleotide and Protein in CDS, Feature table, stand-alone 16S and 23S ribosomal RNA Sequence, and also Summary pages for each cpDNA.

DATA FORMAT

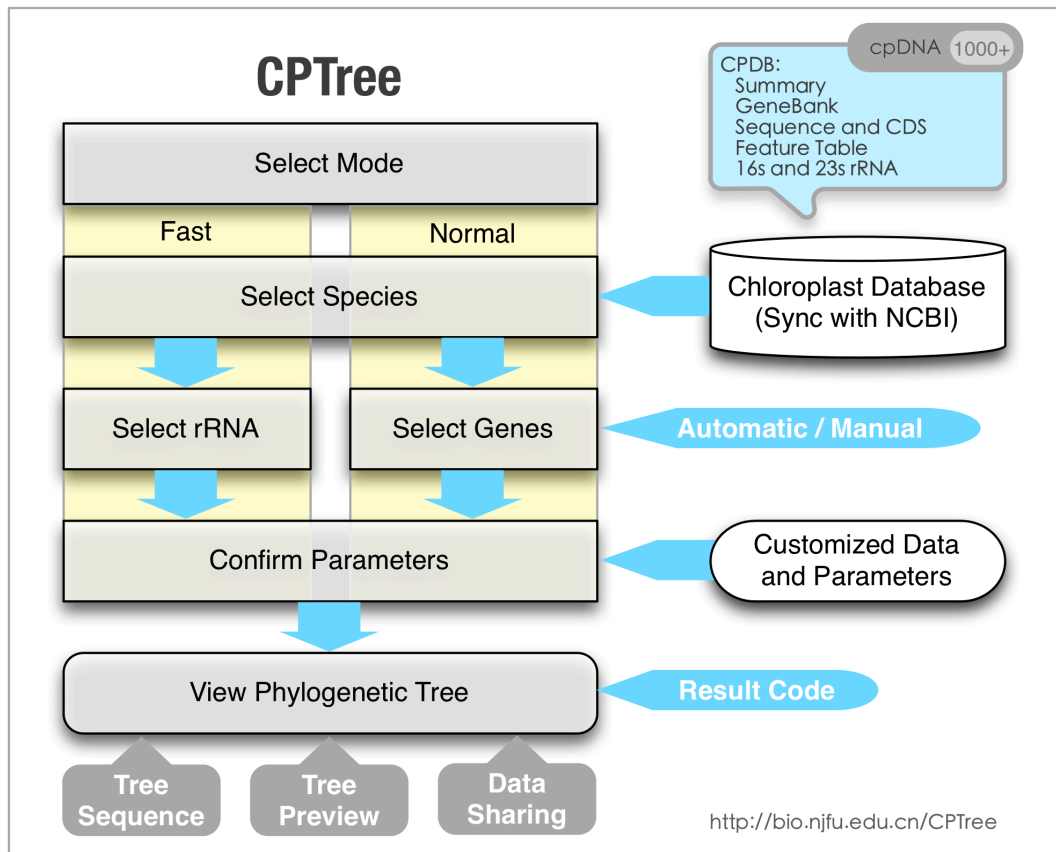
GeneBank (.gb): GenBank format is a flat file format for sequence data related to genomes. The file format we used here is **NMPDR** (<http://www.nmpdr.org/FIG/wiki/view.cgi/FIG/GBK>).

FASTA (.fa): FASTA format is a text-based format for representing either nucleotide sequences or peptide sequences, in which nucleotides or amino acids are represented using single-letter codes. The file format we used here is https://en.wikipedia.org/wiki/FASTA_format.

Txt feature table: The table, which is synchronized with NCBI <https://www.ncbi.nlm.nih.gov> ,organizes information of Chloroplast genomes including Organism/Name, RefSeq, INSDC, number of genes, RNAs, GC percentage and so on.

WORKFLOW

The flow chart is as follows:



When you choose the fast mode to build a tree, the first step is to select the species you need. What follows is a ribosomal RNA selection. After confirming parameter, the calculation starts. About one to five minutes later, the result of data is presented in newick tree. You can also view the result in tree view and circular view. Moreover, you can send the data to iTOL to open an editable tree view.

When the normal mode is selected, the first step is to select species. What follows is genes selection. You can use the automated selected genes. After confirming parameter, the calculation starts. About five to thirty minutes, the result of data is presented in newick tree. You can also view the result in tree view and circular view. Moreover, you can send the data to iTOL to open an editable tree view.

2. CPDB: A CHLOROPLAST DATABASE

Chloroplast Database

[Home](#) / [CPDB](#)

Database reloaded.

<input type="checkbox"/> NC_028027.1 Silyb...	<input type="checkbox"/> NC_029705.1 Dend...	<input type="checkbox"/> NC_031420.1 Aconl...	<input type="checkbox"/> NC_031299.1 Chas...
<input type="checkbox"/> NC_011930.1 Ketel...	<input type="checkbox"/> NC_030178.1 lochr...	<input type="checkbox"/> NC_015543.1 Jacob...	<input type="checkbox"/> NC_030488.1 Ischa...
<input type="checkbox"/> NC_015990.1 Panic...	<input type="checkbox"/> NC_026562.1 Cann...	<input type="checkbox"/> NC_008114.1 Pseu...	<input type="checkbox"/> NC_022390.1 Eucal...
<input type="checkbox"/> NC_030044.1 lochr...	<input type="checkbox"/> NC_023237.1 Magn...	<input type="checkbox"/> NC_015645.1 Schiz...	<input type="checkbox"/> NC_029370.1 Lava...
<input type="checkbox"/> NC_031194.1 Pelar...	<input type="checkbox"/> NC_030220.1 Verdi...	<input type="checkbox"/> NC_027235.1 Wolle...	<input type="checkbox"/> NC_028593.1 Hafni...
<input type="checkbox"/> NC_029712.1 Cymb...	<input type="checkbox"/> NC_023238.1 Magn...	<input type="checkbox"/> NC_004993.1 Calyc...	<input type="checkbox"/> NC_014676.2 Theo...
<input type="checkbox"/> NC_028732.1 Inga...	<input type="checkbox"/> NC_032711.1 Yucca...	<input type="checkbox"/> NC_029485.1 Polyg...	<input type="checkbox"/> NC_029433.1 Pach...
<input type="checkbox"/> NC_029669.1 Pseu...	<input type="checkbox"/> NC_025534.1 Xyloc...	<input type="checkbox"/> NC_024060.1 Hirte...	<input type="checkbox"/> NC_023092.1 Liqui...
<input type="checkbox"/> NC_027151.1 Lathyr...	<input type="checkbox"/> NC_029394.1 Ligus...	<input type="checkbox"/> NC_022400.1 Eucal...	<input type="checkbox"/> NC_026979.1 Nyho...
<input type="checkbox"/> NC_015206.1 Fraga...	<input type="checkbox"/> NC_024829.1 Neph...	<input type="checkbox"/> NC_030061.1 Gymn...	<input type="checkbox"/> NC_029214.1 Meta...
<input type="checkbox"/> NC_031189.1 Perse...	<input type="checkbox"/> NC_016708.2 Millet...	<input type="checkbox"/> NC_032691.1 Cara...	<input type="checkbox"/> NC_028705.1 Cyrt...
<input type="checkbox"/> NC_021091.1 Vigna...	<input type="checkbox"/> NC_024232.1 Ascle...	<input type="checkbox"/> NC_010776.1 Fago...	<input type="checkbox"/> NC_024816.1 Aegil...
<input type="checkbox"/> NC_027824.1 Allote...	<input type="checkbox"/> NC_030756.1 Perill...	<input type="checkbox"/> NC_026041.1 Stang...	<input type="checkbox"/> NC_024061.1 Chrys...
<input type="checkbox"/> NC_032066.1 Medic...	<input type="checkbox"/> NC_016433.2 Sesa...	<input type="checkbox"/> NC_016729.1 Silen...	<input type="checkbox"/> NC_030527.1 Spon...
<input type="checkbox"/> NC_029674.1 Bract...	<input type="checkbox"/> NC_024732.1 Hana...	<input type="checkbox"/> NC_030559.1 Gaula...	<input type="checkbox"/> NC_022399.1 Eucal...
<input type="checkbox"/> NC_022386.1 Eucal...	<input type="checkbox"/> NC_015623.1 Olea...	<input type="checkbox"/> NC_009259.1 Phas...	<input type="checkbox"/> NC_029460.1 Cyna...
<input type="checkbox"/> NC_029483.1 Bletill...	<input type="checkbox"/> NC_022403.1 Eucal...	<input type="checkbox"/> NC_031825.1 Lager...	<input type="checkbox"/> NC_031371.1 Popu...
<input type="checkbox"/> NC_027959.1 Viscu...	<input type="checkbox"/> NC_024064.1 Lican...	<input type="checkbox"/> NC_032054.1 Ment...	<input type="checkbox"/> NC_029429.1 Euple...
<input type="checkbox"/> NC_024845.1 Orob...	<input type="checkbox"/> NC_031187.1 Actini...	<input type="checkbox"/> NC_026462.1 Salik...	<input type="checkbox"/> NC_030065.1 Glorio...

.....



<input type="checkbox"/> NC_030347.1 Arabi...	<input type="checkbox"/> NC_030319.1 Gentl...	<input type="checkbox"/> NC_022379.1 Eucal...	<input type="checkbox"/> NC_018051.1 Vigna...
<input type="checkbox"/> NC_030577.1 Mara...	<input type="checkbox"/> NC_023835.1 Chlor...	<input type="checkbox"/> NC_030486.1 Eleus...	<input type="checkbox"/> NC_032700.1 Cama...
<input type="checkbox"/> NC_030490.1 Onco...	<input type="checkbox"/> NC_026907.1 Querc...	<input type="checkbox"/> NC_014348.1 Pterid...	<input type="checkbox"/> NC_010323.1 Caric...
<input type="checkbox"/> NC_024421.1 Cyprid...	<input type="checkbox"/> NC_025545.1 Botry...	<input type="checkbox"/> NC_030177.1 lochr...	<input type="checkbox"/> NC_028734.1 Gnetu...
<input type="checkbox"/> NC_022378.1 Eucal...	<input type="checkbox"/> NC_029227.1 Iris_s...	<input type="checkbox"/> NC_029049.1 Mese...	<input type="checkbox"/> NC_024659.1 Came...
<input type="checkbox"/> NC_007499.1 Phala...	<input type="checkbox"/> NC_028328.1 Pseu...	<input type="checkbox"/> NC_030493.1 Panic...	<input type="checkbox"/> NC_007977.1 Heli...
<input type="checkbox"/> NC_024067.1 Parin...	<input type="checkbox"/> NC_018552.1 Caps...	<input type="checkbox"/> NC_029333.1 Ionop...	<input type="checkbox"/> NC_029334.1 Arabi...
<input type="checkbox"/> NC_029431.1 Sabia...	<input type="checkbox"/> NC_016736.1 Ricin...	<input type="checkbox"/> NC_024544.1 Galan...	<input type="checkbox"/> NC_003386.1 Psilot...
<input type="checkbox"/> NC_029363.1 Good...	<input type="checkbox"/> NC_016670.1 Goss...	<input type="checkbox"/> NC_023367.1 Arabi...	<input type="checkbox"/> NC_022411.1 Ango...
<input type="checkbox"/> NC_020019.1 Came...	<input type="checkbox"/> NC_028586.1 Bract...	<input type="checkbox"/> NC_026065.1 Sedu...	<input type="checkbox"/> NC_031509.1 Torice...
<input type="checkbox"/> NC_021649.1 Glyci...	<input type="checkbox"/> NC_016468.1 Boea...	<input type="checkbox"/> NC_027146.1 Sarrid...	<input type="checkbox"/> NC_026785.1 Camp...
<input type="checkbox"/> NC_008235.1 Popu...	<input type="checkbox"/> NC_031833.1 Mikan...	<input type="checkbox"/> NC_026212.1 Ortho...	<input type="checkbox"/> NC_008796.1 Ranu...
<input type="checkbox"/> NC_030571.1 Lican...	<input type="checkbox"/> NC_026787.1 Lilium...	<input type="checkbox"/> NC_030576.1 Magn...	<input type="checkbox"/> NC_015605.1 Nelu...
<input type="checkbox"/> NC_030761.1 Aconl...	<input type="checkbox"/> NC_030556.1 Dacty...	<input type="checkbox"/> NC_015308.1 Heve...	<input type="checkbox"/> NC_029746.1 lochr...
<input type="checkbox"/> NC_031422.1 Aconl...	<input type="checkbox"/> NC_024734.1 Popu...	<input type="checkbox"/> NC_009618.1 Cyca...	<input type="checkbox"/> NC_030502.1 Danth...
<input type="checkbox"/> NC_024545.1 Magn...	<input type="checkbox"/> NC_026876.1 Solan...	<input type="checkbox"/> NC_032296.1 Vibur...	<input type="checkbox"/> NC_000932.1 Arabi...
<input type="checkbox"/> NC_028032.1 Humu...	<input type="checkbox"/> NC_024681.1 Salix...	<input type="checkbox"/> NC_021426.1 Troch...	<input type="checkbox"/> NC_015621.1 Agera...
<input type="checkbox"/> NC_008117.1 Zygne...	<input type="checkbox"/> NC_009766.1 Cusc...	<input type="checkbox"/> NC_032284.1 Lamb...	<input type="checkbox"/> NC_027838.1 Lathr...
<input type="checkbox"/> NC_008359.1 Moru...	<input type="checkbox"/> NC_027834.1 Buple...	<input type="checkbox"/> NC_021102.1 Pachy...	<input type="checkbox"/> NC_032712.1 Yucca...
<input type="checkbox"/> NC_024062.1 Lican...	<input type="checkbox"/> NC_029719.2 Utricu...	<input type="checkbox"/> NC_028073.1 Mach...	<input type="checkbox"/> NC_023096.1 Aegil...
<input type="checkbox"/> NC_025652.1 Genil...	<input type="checkbox"/> NC_025668.1 Sanio...	<input type="checkbox"/> NC_024814.1 Triticu...	<input type="checkbox"/> NC_029339.1 Tetras...
<input type="checkbox"/> NC_031427.1 Joinv...	<input type="checkbox"/> NC_004766.1 Adrian...	<input type="checkbox"/> NC_028430.1 Dend...	<input type="checkbox"/> NC_023465.1 Pheili...
<input type="checkbox"/> NC_032696.1 Agav...	<input type="checkbox"/> NC_008269.1 Ostre...	<input type="checkbox"/> NC_029942.1 Epim...	<input type="checkbox"/> NC_024608.1 Oryza...
<input type="checkbox"/> NC_030371.1 Spath...	<input type="checkbox"/> NC_023357.1 Agros...	<input type="checkbox"/> NC_014675.1 Isoete...	<input type="checkbox"/> NC_009599.1 Buxu...
<input type="checkbox"/> NC_030783.1 Carth...	<input type="checkbox"/> NC_030299.1 Ziziph...	<input type="checkbox"/> NC_029825.1 Stach...	<input type="checkbox"/> NC_000188.1 Solan...
<input type="checkbox"/> NC_022135.1 Aegil...	<input type="checkbox"/> NC_028719.1 Echinh...	<input type="checkbox"/> NC_028005.1 Cyna...	<input type="checkbox"/> NC_032040.1 Sinad...
<input type="checkbox"/> NC_014063.1 Lathyr...	<input type="checkbox"/> NC_026040.1 Zami...	<input type="checkbox"/> NC_024262.1 Neyra...	<input type="checkbox"/> NC_030180.1 Bruin...
<input type="checkbox"/> NC_022133.1 Aegil...	<input type="checkbox"/> NC_031207.1 Illex_p...	<input type="checkbox"/> NC_030574.1 Lican...	<input type="checkbox"/> NC_007942.1 Glyci...
<input type="checkbox"/> NC_033411.1 Aletris...			

1209 Species listed in CPDB, updated in 2017-02-03.
Report to [web master](#) now.

[Back to](#)

Cite: CPTree, A web-based Phylogenetic Tree Generator using Chloroplast Genomes by yiqingxu @ 2016

CPDB contains all available cpDNA from genome information by organisms in NCBI. It maintains over 1000 cpDNAs in the current version. To one cpDNA correspond to a link and once click it, the page for the cpDNA will be opened.

Chloroplast Database: NC_028027.1  

Species Name: [Silybum marianum](#)

[Home](#) / [CPDB](#) / CPDB: Silybum_marianum_voucher_SMAR20150709 (NC_028027.1)



Species Name: *Silybum marianum*

Summary

[View in NCBI](#) [Download Summary](#)





Eukaryota > Viridiplantae > Streptophyta > Embryophyta > Tracheophyta > Spermatophyta > Magnoliophyta > eudicotyledons > Gunneridae > Pentapetalae > asterids > campanulids > Asterales > Asteraceae > Carduoideae > Cardueae > Carduinae > *Silybum* > *Silybum marianum*


Q_Gene_Bank	Download
Q_CDS_Nucleotide	Download
Q_CDS_Protein	Download
Q_Feature_Table	Download
Q_Sequence	Download
Q_CP16S	Download
Q_CP23S	Download


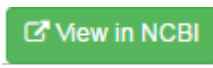
 button to open the original NCBI page in a new tab (<https://www.ncbi.nlm.nih.gov>). The  button is used to download the summary information for the cpDNA.

Eukaryota > Viridiplantae > Streptophyta > Embryophyta > Tracheophyta > Spermatophyta > Magnoliophyta > Liliopsida > Poales > Poaceae > PACMADclade > Panicoideae > Panicoideae > Paniceae > Panicinae > Panicum > Panicum virgatum

Below the “Taxonomy” title, we provide the taxonomy links towards NCBI (<https://www.ncbi.nlm.nih.gov>), so the users can access the taxonomy information of the species.

Below the “Data Files” title, seven accordions all have two buttons:  and . The details in accordions will be shown after clicking the left-most button , while the right-most button  can download file of these details. The file format downloaded by the first five buttons is txt and the others’ file format is FASTA.

If you require downloading all these files, you should use the button  on the right at the top of the page. It will compress all these file into zip.

The button  has the same feature as the “View in NCBI” button  to open a new page from NCBI which introduces the detail of the species.

3. STANDALONE PERL SCRIPT

DATA EXTRACTOR FROM NCBI

Download the species data from NCBI by typing the command: `perl batchDownload.pl -i list.txt -o cpdb`

- -i: The `-i` command allows you to input the name of the text file with information about species' refseqs.
- -o: The `-o` command allows you to input the name of the output directory. For example: `-o cpdb` outputs species' data to the folder named cpdb.

FAST MODE

If you choose the fast mode to build a tree, just type the command: `perl rRNA2tree.pl -i list.txt -g cp_16s -c default_config.txt -o result_16s`

- -i: The `-i` command allows you to input the name of the text file with information about species' refseqs.
- -g: The `-g` command allows you to select gene type between cp_16s and cp_23s.
- -c: The `-c` command allows you to input the name of the file with information about parameter value of **phylogenetic tree drawn by ClustalW**.
- -o: The `-o` command allows you to input the name of the output directory. For example: `-o result_16s` outputs the result data to the folder named result_16s.

NORMAL MODE

When you select the normal mode to generate a **phylogenetic tree**, the first step is to type the command: `perl pickGene.pl -i list.txt > gene.txt`

- -i: The `-i` command allows you to input the name of the text file with information about species' refseqs.

The next step is to install clustalw. Refer to <http://www.clustal.org/clustal2> for more information about installing and using clustalw.

Then type the command: `perl Protein2Tree.pl -i list.txt -g gene.txt -c default_config.txt -o result_protein.`

- -i: The `-i` command allows you to input the name of the text file with information about species' refseqs.
- -g: The `-g` command allows you input the name of the text file with information about genes used to build the tree.
- -c: The `-c` command allows you to input the name of the file with information about parameter value of **phylogenetic tree drawn by ClustalW**.
- -o: The `-o` command allows you to input the name of the output directory. For example: `-o result_protein` outputs the result data to the folder named result_protein.

4. ONLINE SERVICES

FAST MODE

STEP 1: SELECT SPECIES

Step 1: Select the species

Home / Service / Mode: fast


Advance search:

Last updated: 2017-02-03

<input type="checkbox"/>	Organism/Name	RefSeq	INSDC	Size (Kb)	GC%	Gene	Protein	Release Date	Modify Date
<input type="checkbox"/>	Abies koraiensis	NC_026892.1	KP742350	121.373	38.3499	74	4	2015/4/22	2015/4/22
<input type="checkbox"/>	Acacia ligulata	NC_026134.2	LN655649	174.233	35.3745	89	8	2015/1/5	2015/2/11
<input type="checkbox"/>	Solenum lycopersicum	AC_000188.1	-	155.461	37.8603	87	8	2006/2/24	2013/9/17
<input type="checkbox"/>	Arabidopsis thaliana	NC_000932.1	AP000423	154.478	36.2938	85	7	1999/9/15	2010/3/26
<input type="checkbox"/>	Marchantia polymorpha	NC_001319.1	X04465	121.024	28.8083	89	8	1986/11/18	2009/5/5
<input type="checkbox"/>	Epifagus virginiana	NC_001568.1	M81884	70.028	35.9985	25	8	1993/8/3	2009/5/6
<input type="checkbox"/>	Pinus thunbergii	NC_001631.1	D17510	119.707	38.4957	123	4	1994/8/13	2015/4/22
<input type="checkbox"/>	Zea mays	NC_001666.2	X86563	140.384	38.4624	111	8	1995/7/17	2009/4/15
<input type="checkbox"/>	Chlorella vulgaris	NC_001865.1	AB001684	150.613	31.5597	174	3	1997/6/27	2009/4/15
<input type="checkbox"/>	Lotus japonicus Accession MG-20	NC_002694.1	AP002983	150.519	36.0307	82	8	2001/3/1	2009/4/15

Go to page: Show rows: 1-10 of 1088



RefSeq here:



Online service may experience performance problem when the number of species is OVER 20
Due to performance limit, the online service supports only LESS THAN 50 species.

After choosing the fast mode to build a tree, the first step is to select the species you need. The table in the page of “Select the species” organizes information of Chloroplast genomes including Organism/Name, RefSeq, INSDC, number of genes, RNAs, GC percentage and so on, and the top right of the table shows this update time. The table provides paging, sorting and filtering facilities to ease the selection of the species.

How to page

On the bottom right corner, besides the “go to page” label, enter the page number in the text field, the table will update the information. To scroll back and forth through the pages of data, click   arrow symbols.

How to filter

Search the species by inputting terms into the Search box located at the top left of the table and clicking the “Go” button. The left-most column lists the filters, which are selected by checking the boxes at the left of the species name. Once the filters are selected, its RefSeq information appears in the text field below the table. To clear all the filters, click the “clear” button. After selecting the species, proceed to the next step via clicking the “next” button. There is one important caution that needs to be noted: Online service may experience performance problem when the number of species is **OVER 20**

Due to performance limit, the online service supports only **LESS THAN 50** species.

How to sort

me	RefSeq	INSDC	Size (Kb)	GC%
	NC_026892.1	<div> <div>Sort Ascending</div> <div>Sort Descending</div> <div>Remove Sort</div> <div>Show rows where:</div> <div>contains</div> <div>And</div> <div>contains</div> <div>Filter</div> <div>Clear</div> </div>		38.24
	NC_026134.2			35.37
	NC_029371.1			37.81
	NC_015820.1			38.89
	NC_030185.1			37.67
ochromacy...	NC_030056.1			37.67
	NC_029829.1			38.10
	NC_010093.1			38.59
	NC_026690.1			37.19
	NC_026691.1			37.16

Hover your mouse over the any column of the first row and click the arrow symbols, it produces a new dialog allowing you to sort the column cells.

Detailed information

Last updated: 2016-08-27									
<input type="checkbox"/>	Organism/Name	RefSeq	INSDC	Size (Kb)	GC%	Gene	Protein	Release Date	Modify Date
<input type="checkbox"/>	<i>Abies koreana</i>	NC_026892.1	KP742350	121.373	38.2499	74	4	2015/4/22	2015/4/22
<input type="checkbox"/>	<i>Acacia ligulata</i>	NC_026134.2	LN555649	174.233	35.3745	89	8	2015/1/5	2016/2/11
<input type="checkbox"/>	<i>Acer morrisonense</i>	NC_029371.1	KT970611	157.197	37.8188	86	8	2016/3/1	2016/3/1
<input type="checkbox"/>	<i>Acidosasa purpurea</i>	NC_015820.1	HQ337793	139.697	38.897	82	8	2011/7/15	2011/7/15
<input type="checkbox"/>	<i>Acnistus arborescens</i>	NC_030185.1	KU568472	156.898	37.6773	84	8	2016/5/19	2016/5/19
<input type="checkbox"/>	<i>Acnistus arborescens</i> x <i>lochroma cyaneum</i>	NC_030056.1	KU306735	156.841	37.6796	83	8	2016/5/4	2016/5/4
<input type="checkbox"/>	<i>Aconitum chilsanense</i>	NC_029829.1	KT820665	155.934	38.1039	85	8	2016/4/9	2016/4/9
<input type="checkbox"/>	<i>Acorus americanus</i>	NC_010093.1	EU273602	153.819	38.5934	84	8	2007/12/4	2011/4/29
<input type="checkbox"/>	<i>Actinidia chinensis</i>	NC_026690.1	KP297242	156.346	37.1963	83	8	2015/3/27	2015/8/4
<input type="checkbox"/>	<i>Actinidia deliciosa</i>	NC_026691.1	KP297244	156.741	37.1613	83	8	2015/3/20	2015/8/4

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☐ More Detail

Last updated: 2016-08-27

<input type="checkbox"/>	Organism/Name	SubGroup	RefSeq	INSDC	Size (Kb)	GC%	Gene	Protein	rRNA	tRNA	Other
<input type="checkbox"/>	Abies koreana	Land Plants	NC_026892.1	KP742350	121.373	38.2499	74	4	35	-	11
<input type="checkbox"/>	Acacia ligulata	Land Plants	NC_026134.2	LN555649	174.233	35.3745	89	8	37	-	13
<input type="checkbox"/>	Acer morrissonense	Land Plants	NC_029371.1	KT970611	157.197	37.8188	86	8	40	-	13
<input type="checkbox"/>	Acidosasa purpurea	Land Plants	NC_015820.1	HQ337793	139.697	38.897	82	8	38	-	12
<input type="checkbox"/>	Acnistus arborescens	Land Plants	NC_030185.1	KU568472	156.898	37.6773	84	8	36	-	13
<input type="checkbox"/>	Acnistus arborescens x lochroma cyaneum	Land Plants	NC_030056.1	KU306735	156.841	37.6796	83	8	37	-	13
<input type="checkbox"/>	Aconitum chilense	Land Plants	NC_029829.1	KT820665	155.934	38.1039	85	8	37	-	13
<input type="checkbox"/>	Acorus americanus	Land Plants	NC_010093.1	EU273602	153.819	38.5934	84	8	38	-	13
<input type="checkbox"/>	Actinidia chinensis	Land Plants	NC_026690.1	KP297242	156.346	37.1963	83	8	40	-	13
<input type="checkbox"/>	Actinidia deliciosa	Land Plants	NC_026691.1	KP297244	156.741	37.1613	83	8	39	-	13

Go to page: Show rows: 1-10 of 880

To see all of the columns, you need to click on [More Detail](#) at the lower left

table. Clicking on the arrow symbol besides the “show rows” label, you can choose the number of species on this page from the drop down menu. Click on the “[↑Back to Top](#)” at the lower-right side of the page to go back to the top of the page.

STEP 2: SELECT RIBOSOMAL RNA

Step 2: Parameter Confirmation

[Home](#) / [Service](#) / [Confirm](#)

Mode

Species Selected

Gene Selected

Custom Sequence ☒ Use Additional Sequence [?](#)

Sequence in Fasta

Custom Tree-building ☒ Use Default Tree Parameters [?](#)

Clustalw Para

[Confirm](#) [Cancel](#)

Cite: CPTree, A web-based Phylogenetic Tree Generator using Chloroplast Genomes by Ethan @ 2016


There are four text areas and one drop down menu vertically arranged in the “Parameter Confirmation” page. You can select the ribosomal RNA in the drop down menu .The first text area shows user-selected mode. The gene sequences are displayed in the second text

area. The users have to upload custom sequence in FASTA format to the third one, if they need additional sequence. The tree parameters are presented in the last text area.

How to select Ribosomal RNA

Clicking the arrow symbol in the lower-right hand corner of the second box will appears a drop-down menu including 16s RNA and 23s RNA, which the user can choose from.

How to use additional Sequence


Custom Sequence ☒ Use Additional Sequence 

Sequence in Fasta



Click the small icon besides “Use Additional Sequence” , and then upload custom sequence in FASTA format.

Tree Parameter

Custom Tree-building ☒ Use Default Tree Parameters 

Clustalw Para

-ALIGN -TREE -OUTPUT=NEXUS -TYPE=DNA -BOOTSTRAP=1000

If the users don’ t want to use the default parameters to build the tree, click the small icon with checkmark besides “Use Default Tree Parameters” and the checkmark will disappear. Then input the new parameter value in the text area below.

After data determination, click the “confirm” button located below the boxes to submit the data. The user needs reselect data by checking the “cancel” button.

STEP 3: CALCULATION

Data Submitted

[Home](#) / [Service](#) / [Accepted](#)

Data accepted.

Result code: [20161006upgawvid](#)

Name List

NC_029371.1, NC_015820.1, NC_030185.1, NC_030056.1

Gene List

cp_16s

Cite: CPTree, A web-based Phylogenetic Tree Generator using Chloroplast Genomes by Ethan @ 2016

The page of “data Submitted” where you can view the progress of computing and download file, will be displayed after parameter confirmation. If “Data accepted” are seen in green, it shows that the data has been submitted successfully.

View the result

Result of Data: 20170326qukpy7aa

[Home](#) / [Service](#) / [Result](#)

This page will reload in 36 second.

Result Link: [20170326qukpy7aa](#)


Calculation is still in process, please try later.

Running Log

```
[2017-03-26 19:06:14] SYSTEM: perl rRNA2Tree.pl -i result/20170326qukpy7aa/namelist.txt -g cp_16s -o result/20170326qukpy7aa -c result/20170326qukpy7aa/treePara.txt &
[2017-03-26 19:06:14] INFO: Start.
```

You can view the result of data by clicking on the link named ‘Result code’. If the phylogenetic tree hasn’t been constructed, a progress bar will be shown to indicate the progress of construction. The user can share the results by simply sharing the link whenever the final result is still in process or finalized. If the process takes too much calculation time, the users can use the code to retrieve the final result without waiting online. The running log is also represented in the text area below the progress bar.

Download

The gene sequences and ribosomal RNA are available for download in textual format by clicking  button.

NORMAL MODE

STEP 1: SELECT SPECIES

Step 1: Select the species

Home / Service / Mode: normal

Advance search:


Last updated: 2017-02-03

<input type="checkbox"/>	Organism/Name	RefSeq	INSDC	Size (Kb)	GC%	Gene	Protein	Release Date	Modify Date
<input type="checkbox"/>	Abies koraiensis	NC_026892.1	KP742350	121.373	38.2499	74	4	2015/4/22	2015/4/22
<input type="checkbox"/>	Acacia ligulata	NC_026134.2	LN555649	174.233	95.5745	89	8	2015/1/5	2016/2/11
<input checked="" type="checkbox"/>	Acer morrissonense	NC_029371.1	KT970611	157.197	57.8188	86	8	2016/3/1	2016/3/1
<input checked="" type="checkbox"/>	Acidosa purpurea	NC_015820.1	HQ337793	139.697	38.897	82	8	2011/7/15	2011/7/15
<input checked="" type="checkbox"/>	Acridus arboreus	NC_030185.1	KU568472	156.898	37.6773	84	8	2016/5/19	2016/5/19
<input checked="" type="checkbox"/>	Acridus arboreus x Ichroma cyaneum	NC_030056.1	KU506735	156.841	37.6796	83	8	2016/5/4	2016/5/4
<input checked="" type="checkbox"/>	Aconitum chinsenense	NC_029829.1	KT820665	155.934	38.1039	85	8	2016/4/9	2016/4/9
<input checked="" type="checkbox"/>	Acorus americanus	NC_010093.1	EU273602	153.819	38.5934	84	8	2007/12/4	2011/4/29
<input checked="" type="checkbox"/>	Actinidia chinensis	NC_026690.1	KP297242	156.346	37.1963	83	8	2015/3/27	2015/8/4
<input type="checkbox"/>	Actinidia deliciosa	NC_026691.1	KP297244	156.741	37.1613	83	8	2015/3/20	2015/8/4

Go to page: Show rows: 1-10 of 1193

☒ More Detail



NC_029371.1, NC_015820.1, NC_030185.1, NC_030056.1, NC_029829.1, NC_010093.1, NC_026690.1



Online service may experience performance problem when the number of species is OVER 20
Due to performance limit, the online service supports only LESS THAN 50 species.

After choosing the normal mode, the first step is to select the species you need. The table in the page of “Select the species” organizes information of Chloroplast genomes including Organism/Name, RefSeq, INSDC, number of genes, RNAs, GC percentage and so on, and the top right of the table shows this update time. The table provides paging, sorting and filtering facilities to ease the selection of the species.

How to page

On the bottom right corner, besides the “go to page” label, enter the page number in the text field, the table will update the information. To scroll back and forth through the pages of data, click   arrow symbols.

How to filter

Search the species by inputting terms into the Search box located at the top left of the table and clicking the “Go” button. The left-most column lists the filters, which are selected by checking the boxes at the left of the species name. Once the filters are selected, its RefSeq information appears in the text field below the table. To clear all the filters, click the “clear” button. After selecting the species, proceed to the next step to choose an appropriate mode via clicking the “next” button.

How to sort

me	RefSeq	INSDC	Size (Kb)	GC%
	NC_026892.1	Sort Ascending		38.24
	NC_026134.2	Sort Descending		35.37
	NC_029371.1	Remove Sort		37.81
	NC_015820.1	Show rows where:		38.89
	NC_030185.1	contains		37.67
ochromacy...	NC_030056.1			37.67
	NC_029829.1	And		38.10
	NC_010093.1	contains		38.59
	NC_026690.1			37.19
	NC_026691.1			37.16

Filter Clear Go to page

Hover your mouse over the any column of the first row and click the arrow symbols, it will produce a new dialog allowing you to sort the column cells.

Detailed information

Last updated: 2016-08-27									
<input type="checkbox"/>	Organism/Name	RefSeq	INSDC	Size (Kb)	GC%	Gene	Protein	Release Date	Modify Date
<input type="checkbox"/>	<i>Abies koreana</i>	NC_026892.1	KP742350	121.373	38.2499	74	4	2015/4/22	2015/4/22
<input type="checkbox"/>	<i>Acacia ligulata</i>	NC_026134.2	LN555649	174.233	35.3745	89	8	2015/1/5	2016/2/11
<input type="checkbox"/>	<i>Acer morrisonense</i>	NC_029371.1	KT970611	157.197	37.8188	86	8	2016/3/1	2016/3/1
<input type="checkbox"/>	<i>Acidosasa purpurea</i>	NC_015820.1	HQ337793	139.697	38.897	82	8	2011/7/15	2011/7/15
<input type="checkbox"/>	<i>Acnistus arborescens</i>	NC_030185.1	KU568472	156.898	37.6773	84	8	2016/5/19	2016/5/19
<input type="checkbox"/>	<i>Acnistus arborescens x lochroma cyaneum</i>	NC_030056.1	KU306735	156.841	37.6796	83	8	2016/5/4	2016/5/4
<input type="checkbox"/>	<i>Aconitum chiisanense</i>	NC_029829.1	KT820665	155.934	38.1039	85	8	2016/4/9	2016/4/9
<input type="checkbox"/>	<i>Acorus americanus</i>	NC_010093.1	EU273602	153.819	38.5934	84	8	2007/12/4	2011/4/29
<input type="checkbox"/>	<i>Actinidia chinensis</i>	NC_026690.1	KP297242	156.346	37.1963	83	8	2015/3/27	2015/8/4
<input type="checkbox"/>	<i>Actinidia deliciosa</i>	NC_026691.1	KP297244	156.741	37.1613	83	8	2015/3/20	2015/8/4

Go to page: 1 Show rows: 10 1-10 of 880

☐ More Detail

Last updated: 2016-08-27

<input type="checkbox"/>	Organism/Name	SubGroup	RefSeq	INSDC	Size (Kb)	GC%	Gene	Protein	rRNA	tRNA	Other
<input type="checkbox"/>	Abies koreana	Land Plants	NC_026892.1	KP742350	121.373	38.2499	74	4	35	-	11
<input type="checkbox"/>	Acacia ligulata	Land Plants	NC_026134.2	LN555649	174.233	35.3745	89	8	37	-	13
<input type="checkbox"/>	Acer morrisonense	Land Plants	NC_029371.1	KT970611	157.197	37.8188	86	8	40	-	13
<input type="checkbox"/>	Acidosasa purpurea	Land Plants	NC_015820.1	HQ337793	139.697	38.897	82	8	38	-	12
<input type="checkbox"/>	Acnistus arborescens	Land Plants	NC_030185.1	KU568472	156.898	37.6773	84	8	36	-	13
<input type="checkbox"/>	Acnistus arborescens x lochroma cyaneum	Land Plants	NC_030056.1	KU306735	156.841	37.6796	83	8	37	-	13
<input type="checkbox"/>	Aconitum chilense	Land Plants	NC_029829.1	KT820665	155.934	38.1039	85	8	37	-	13
<input type="checkbox"/>	Acorus americanus	Land Plants	NC_010093.1	EU273602	153.819	38.5934	84	8	38	-	13
<input type="checkbox"/>	Actinidia chinensis	Land Plants	NC_026690.1	KP297242	156.346	37.1963	83	8	40	-	13
<input type="checkbox"/>	Actinidia deliciosa	Land Plants	NC_026691.1	KP297244	156.741	37.1613	83	8	39	-	13

Go to page: Show rows: 1-10 of 880

To see all of the columns, you need to click on [More Detail](#) at the lower left table. Clicking on the arrow symbol besides the “show rows” label, you can choose the number of species on this page from the drop down menu. Click on the “[↑Back to Top](#)” at the lower-right side of the page to go back to the top of the page.

STEP 2: SELECT GENE

Step 2: Select the Genes

Home / Service / Mode: normal

Gene	Sum	Acidosasa purpurea	Acer morrisonense voucher Amor2015	Acnistus arborescens	Acnistus arborescens x lochroma cyaneum
<input checked="" type="checkbox"/> ccslA	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> cemA	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> clpP	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="checkbox"/> hnfA	1	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="checkbox"/> hnfB	2	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> matK	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> ndhA	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> ndhB	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> ndhC	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> ndhD	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> ndhE	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> ndhF	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> ndhG	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> ndhH	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> ndhI	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> ndhJ	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> ndhK	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> petA	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input checked="" type="checkbox"/> petB	4	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

77 genes selected.

accD, atpA, atpB, atpE, atpF, atpH, atpI, ccslA, cemA, clpP, matK, ndhA, ndhB, ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, ndhK, petA, petB, petD, petG, petL, petN, psalA, psalB, psalC, psalD, psalE, psalF, psalH, psalI, psalJ, psalK, psalL, psalM, psalN, psalO, psalP, psalQ, psalR, psalS, psalT, psalU, psalV, psalW, psalX, psalY, psalZ, rpl1, rpl2, rpl3, rpl4, rpl5, rpl6, rpl7, rpl8, rpl9, rpl10, rpl11, rpl12, rpl13, rpl14, rpl15, rpl16, rpl17, rpl18, rpl19, rpl20, rpl21, rpl22, rpl23, rpl24, rpl25, rpl26, rpl27, rpl28, rpl29, rpl30, rpl31, rpl32, rpl33, rpl34, rpl35, rpl36, rpl37, rpl38, rpl39, rpl40, rpl41, rpl42, rpl43, rpl44, rpl45, rpl46, rpl47, rpl48, rpl49, rpl50, rpl51, rpl52, rpl53, rpl54, rpl55, rpl56, rpl57, rpl58, rpl59, rpl60, rpl61, rpl62, rpl63, rpl64, rpl65, rpl66, rpl67, rpl68, rpl69, rpl70, rpl71, rpl72, rpl73, rpl74, rpl75, rpl76, rpl77, rpl78, rpl79, rpl80, rpl81, rpl82, rpl83, rpl84, rpl85, rpl86, rpl87, rpl88, rpl89, rpl90, rpl91, rpl92, rpl93, rpl94, rpl95, rpl96, rpl97, rpl98, rpl99, rpl100, rps1, rps2, rps3, rps4, rps5, rps6, rps7, rps8, rps9, rps10, rps11, rps12, rps13, rps14, rps15, rps16, rps17, rps18, rps19, rps20, rps21, rps22, rps23, rps24, rps25, rps26, rps27, rps28, rps29, rps30, rps31, rps32, rps33, rps34, rps35, rps36, rps37, rps38, rps39, rps40, rps41, rps42, rps43, rps44, rps45, rps46, rps47, rps48, rps49, rps50, rps51, rps52, rps53, rps54, rps55, rps56, rps57, rps58, rps59, rps60, rps61, rps62, rps63, rps64, rps65, rps66, rps67, rps68, rps69, rps70, rps71, rps72, rps73, rps74, rps75, rps76, rps77, rps78, rps79, rps80, rps81, rps82, rps83, rps84, rps85, rps86, rps87, rps88, rps89, rps90, rps91, rps92, rps93, rps94, rps95, rps96, rps97, rps98, rps99, rps100, ycf1, ycf2, ycf3

[Auto Selection](#) [Next](#)

[↑ Back to Top](#)


Cite: CPTree, A web-based Phylogenetic Tree Generator using Chloroplast Genomes by Ethan @ 2016

The selected species are listed in the first row of the table. The first column of lists all the cpDNA genes contained in the selected species. All genes are filtered and matched for

each species. The text field under the table shows all the genes used to **build phylogenetic trees**.

How to select genes

To search the cpDNA genes, move the mouse to the left-most column and select the check box on the left of the name of the gene molecules needed. Once the filters are selected, these gene molecules will be listed in the text area at the bottom of the page and the number of the gene molecules selected will appear below the table. If you want to select all the genes, you can choose the check box at the top of the left-most column.

Moreover, if you click  at the bottom of the page, **all genes will be filtered and matched for each species in order to build phylogenetic trees.**

Parameter confirmation

Step 3: Parameter Confirmation

[Home](#) / [Service](#) / [Confirm](#)

Mode

Normal

Species Selected

NC_029371.1,NC_015820.1,NC_030056.1,NC_029829.1,NC_010093.1

Gene Selected

atpA,atpB,atpE,atpF,atpH,atpI,ccsA,cmrA,clpP,matK,ndhA,ndhB,ndhC,ndhD,ndhE,ndhF,ndhG,ndhH,ndhI,ndhJ,ndhK,petA,petB,petD,petG,petL,petN,psaA,psaB,psaC,psal,psaJ,psbA,psbB,psbC,psbD,psbE,psbF,psbH,psbI,psbJ,psbK,psbL,psbM,psbN,psbT,psbZ,psb1,psb2,psb3,psb4,psb5,psb6,psb7,psb8,psb9,psb10,psb11,psb12,psb13,psb14,psb15,psb16,psb17,psb18,psb19,psb20,psb21,psb22,psb23,psb24,psb25,psb26,psb27,psb28,psb29,psb30,psb31,psb32,psb33,psb34,psb35,psb36,psb37,psb38,psb39,psb40,psb41,psb42,psb43,psb44,psb45,psb46,psb47,psb48,psb49,psb50,psb51,psb52,psb53,psb54,psb55,psb56,psb57,psb58,psb59,psb60,psb61,psb62,psb63,psb64,psb65,psb66,psb67,psb68,psb69,psb70,psb71,psb72,psb73,psb74,psb75,psb76,psb77,psb78,psb79,psb80,psb81,psb82,psb83,psb84,psb85,psb86,psb87,psb88,psb89,psb90,psb91,psb92,psb93,psb94,psb95,psb96,psb97,psb98,psb99,psb100,psb101,psb102,psb103,psb104,psb105,psb106,psb107,psb108,psb109,psb110,psb111,psb112,psb113,psb114,psb115,psb116,psb117,psb118,psb119,psb120,psb121,psb122,psb123,psb124,psb125,psb126,psb127,psb128,psb129,psb130,psb131,psb132,psb133,psb134,psb135,psb136,psb137,psb138,psb139,psb140,psb141,psb142,psb143,psb144,psb145,psb146,psb147,psb148,psb149,psb150,psb151,psb152,psb153,psb154,psb155,psb156,psb157,psb158,psb159,psb160,psb161,psb162,psb163,psb164,psb165,psb166,psb167,psb168,psb169,psb170,psb171,psb172,psb173,psb174,psb175,psb176,psb177,psb178,psb179,psb180,psb181,psb182,psb183,psb184,psb185,psb186,psb187,psb188,psb189,psb190,psb191,psb192,psb193,psb194,psb195,psb196,psb197,psb198,psb199,psb200,psb201,psb202,psb203,psb204,psb205,psb206,psb207,psb208,psb209,psb210,psb211,psb212,psb213,psb214,psb215,psb216,psb217,psb218,psb219,psb220,psb221,psb222,psb223,psb224,psb225,psb226,psb227,psb228,psb229,psb230,psb231,psb232,psb233,psb234,psb235,psb236,psb237,psb238,psb239,psb240,psb241,psb242,psb243,psb244,psb245,psb246,psb247,psb248,psb249,psb250,psb251,psb252,psb253,psb254,psb255,psb256,psb257,psb258,psb259,psb260,psb261,psb262,psb263,psb264,psb265,psb266,psb267,psb268,psb269,psb270,psb271,psb272,psb273,psb274,psb275,psb276,psb277,psb278,psb279,psb280,psb281,psb282,psb283,psb284,psb285,psb286,psb287,psb288,psb289,psb290,psb291,psb292,psb293,psb294,psb295,psb296,psb297,psb298,psb299,psb300,psb301,psb302,psb303,psb304,psb305,psb306,psb307,psb308,psb309,psb310,psb311,psb312,psb313,psb314,psb315,psb316,psb317,psb318,psb319,psb320,psb321,psb322,psb323,psb324,psb325,psb326,psb327,psb328,psb329,psb330,psb331,psb332,psb333,psb334,psb335,psb336,psb337,psb338,psb339,psb340,psb341,psb342,psb343,psb344,psb345,psb346,psb347,psb348,psb349,psb350,psb351,psb352,psb353,psb354,psb355,psb356,psb357,psb358,psb359,psb360,psb361,psb362,psb363,psb364,psb365,psb366,psb367,psb368,psb369,psb370,psb371,psb372,psb373,psb374,psb375,psb376,psb377,psb378,psb379,psb380,psb381,psb382,psb383,psb384,psb385,psb386,psb387,psb388,psb389,psb390,psb391,psb392,psb393,psb394,psb395,psb396,psb397,psb398,psb399,psb400,psb401,psb402,psb403,psb404,psb405,psb406,psb407,psb408,psb409,psb410,psb411,psb412,psb413,psb414,psb415,psb416,psb417,psb418,psb419,psb420,psb421,psb422,psb423,psb424,psb425,psb426,psb427,psb428,psb429,psb430,psb431,psb432,psb433,psb434,psb435,psb436,psb437,psb438,psb439,psb440,psb441,psb442,psb443,psb444,psb445,psb446,psb447,psb448,psb449,psb450,psb451,psb452,psb453,psb454,psb455,psb456,psb457,psb458,psb459,psb460,psb461,psb462,psb463,psb464,psb465,psb466,psb467,psb468,psb469,psb470,psb471,psb472,psb473,psb474,psb475,psb476,psb477,psb478,psb479,psb480,psb481,psb482,psb483,psb484,psb485,psb486,psb487,psb488,psb489,psb490,psb491,psb492,psb493,psb494,psb495,psb496,psb497,psb498,psb499,psb500,psb501,psb502,psb503,psb504,psb505,psb506,psb507,psb508,psb509,psb510,psb511,psb512,psb513,psb514,psb515,psb516,psb517,psb518,psb519,psb520,psb521,psb522,psb523,psb524,psb525,psb526,psb527,psb528,psb529,psb530,psb531,psb532,psb533,psb534,psb535,psb536,psb537,psb538,psb539,psb540,psb541,psb542,psb543,psb544,psb545,psb546,psb547,psb548,psb549,psb550,psb551,psb552,psb553,psb554,psb555,psb556,psb557,psb558,psb559,psb560,psb561,psb562,psb563,psb564,psb565,psb566,psb567,psb568,psb569,psb570,psb571,psb572,psb573,psb574,psb575,psb576,psb577,psb578,psb579,psb580,psb581,psb582,psb583,psb584,psb585,psb586,psb587,psb588,psb589,psb590,psb591,psb592,psb593,psb594,psb595,psb596,psb597,psb598,psb599,psb600,psb601,psb602,psb603,psb604,psb605,psb606,psb607,psb608,psb609,psb610,psb611,psb612,psb613,psb614,psb615,psb616,psb617,psb618,psb619,psb620,psb621,psb622,psb623,psb624,psb625,psb626,psb627,psb628,psb629,psb630,psb631,psb632,psb633,psb634,psb635,psb636,psb637,psb638,psb639,psb640,psb641,psb

There are five text areas vertically arranged in the middle of the page. The first area shows user-selected mode. The RefSeq and genes you have chosen are displayed in the second and third text areas respectively. To see all genes, you need click on the arrow symbol in the right of the third area. The users have to upload custom sequence in FASTA format to the fourth one, if they need additional sequence. The tree parameters are presented in the last area.

How to use additional Sequence

Custom Sequence ☒ Use Additional Sequence ?

Sequence in Fasta

Click the small icon besides “Use Additional Sequence” , and then upload custom sequence in FASTA format to the text area below.

Tree Parameter

Custom Tree-building ☒ Use Default Tree Parameters ?

Clustalw Para

-ALIGN -TREE -OUTPUT=NEXUS -TYPE=DNA -BOOTSTRAP=1000

If the users don’ t want to use the default parameters to build the tree, click the small icon with checkmark besides “Use Default Tree Parameters” and the checkmark will disappear. Then input the new parameter value in the text area below.

After data determination, click the “confirm” button to submit the data. The user needs reselect data by checking the “cancel” button.

STEP 3: CALCULATION

Data Submitted

[Home](#) / [Service](#) / Accepted

Data accepted.

Result code: 20170326630em0l6

Name List

NC_026134.2,NC_029371.1,NC_015820.1,NC_030185.1,NC_030056.1,NC_029829.1,NC_010093.1,NC_026690.1,NC_026691.1

Gene List

atpA,atpB,atpE,atpF,atpH,atpI,ccsA,cemA,matK,ndhA,ndhB,ndhC,ndhD,ndhE,ndhF,ndhG,ndhH,ndhI,ndhJ,ndhK,petA,petB,petD,petG,petL,petN,psaA,psaB,psaC,psaI,psaJ,psbA,psbB,psbC,psbD,psbE,psbF,psbH,psbI,psbJ,psbK,psbL,psbM,psbN,psbT,rbcl,rp114,rp116,rp12,rp120,rp122,rp123,rp132,rp133,rp136,rpoA,rpoB,rpoC1,rpoC2,rps11,rps12,rps14,rps15,rps18,rps19,rps2,rps3,rps4,rps7,rps8,ycf1,ycf2,ycf3

Cite: CPTree, A web-based Phylogenetic Tree Generator using Chloroplast Genomes by yiqingxu @ 2016

The page of “data Submitted” where you can view the progress of computing and download files, will be displayed after parameter confirmation. If “Data accepted” are seen in green, it shows that the data has been submitted successfully.

[View the result](#)

Result of Data: 20170326630em0l6

[Home](#) / [Service](#) / [Result](#)

This page will reload in 44 second.

Result Link: 20170326630em0l6

Calculation is still in process, please try later.

Running Log


```
Sequence 9: NC_030056.1 64401 bp
Sequence 8: NC_026134.2 63996 bp
Sequence 7: NC_029829.1 63666 bp
Sequence 6: NC_030185.1 63543 bp
Sequence 5: NC_010093.1 64281 bp
Sequence 4: NC_029371.1 64044 bp
Sequence 3: NC_015820.1 53214 bp
Sequence 2: NC_026690.1 65712 bp
Sequence 1: NC_026691.1 65712 bp
Sequence format is Pearson
Sequence type explicitly set to DNA

CLUSTAL 2.1 Multiple Sequence Alignments

[2017-03-26 21:49:35] INFO : Building tree with clustalw...
[2017-03-26 21:49:35] INFO : Protein list is ready: result/20170326630em0l6/tree.fa
[2017-03-26 21:49:35] WARN : Miss rpl22, please check.
[2017-03-26 21:49:34] WARN : Miss rpl32, please check.
[2017-03-26 21:49:34] WARN : Miss psb8, please check.
[2017-03-26 21:49:34] WARN : Miss rps2, please check.
[2017-03-26 21:49:34] WARN : Miss ycf2, please check.
[2017-03-26 21:49:34] WARN : Miss ycf1, please check.
[2017-03-26 21:49:34] INFO : Reading input gene list.
[2017-03-26 21:49:34] INFO : Reading data file.
[2017-03-26 21:49:34] INFO : Reading input name list.
[2017-03-26 21:49:34] SYSTEM: perl Protein2Tree.pl -i result/20170326630em0l6/namelist.txt -g re
sult/20170326630em0l6/genelist.txt -o result/20170326630em0l6 -c result/20170326630em0l6/treePar
a.txt &
[2017-03-26 21:49:34] INFO: Start.
```

There is a link named 'Result code' that you can view the result of data by clicking on. If the phylogenetic tree hasn't been constructed, a progress bar will be shown to indicate the progress of construction. The running log is represented in the text area below the progress bar.

Download

The name list of selected species and gene list are available for download in textual format by clicking  button.

RESULT

How

/ S

Result

x

Result Link: [Capsicum_chinense_Jacq_normal](#)

Phylogenetic Tree

Download

 **Tree Preview**

© Circular Preview

[Opne in iTOL](#)

```
((NC_007943.1:0.00126,NC_008096.2:0.00167):0.00134,(((NC_007500.1:0.00297,NC_007602.1:0.00547):0.00631,NC_026703.1:0.09141):0.00284,(NC_018552.1:0.00694,NC_026551.1:0.00954):0.00920):0.00827,NC_007898.3:0.00576);
```

Tree Sequence [Download](#) [Use Latin Name](#)

>NC_007943.1
 MTTHLLVFYAHRIQGENSHERWGFNSHLFKKFEERRCGLNKSMSGLSPGIENTSEDPNLKVKNIHSCSMVDYLVGVKDIWFIISDQTLVSDRNGISVSYIFDINEQIFEVONDHSFLESESSFSYINSS
 YLNGFGRGEPYPPSYHYNDYQTSWNHINISCDINYLQSGICITDTSII56GESGDSYIVRAICSGESLGENESESRRTRTKGSLTRESSNDLVQTKYKHLVQCEHCYGLNYIKFLKSKNII
 CEQGYKSHNSSDORELFDVDTGNPDHDEPDEHDTFTHSEEPPEYKIDVSEYQKGLTKAQTQVQGLQIGLPAVIGDQFQMGSGSVEGKITRLTEHAFHAKNQLLITVCASGAGRGESGLS
 MOKMTSSALVMDYIKLIPWSTISDPTGGVYTSFGMIGDITFAPNATYAGKGVKTFOTLVEAGTQVQGLQIGLPAVIGDQFQMGSGSVEGKITRLTEHAFHAKNQLLITVCASGAGRGESGLS
 ...

• • • • •

TGTGTCGAT(GACCCGCTGCAGTCTGTGATCAACGCTGTAAAGTATCCCGCTGGGAGATGTTT(GCAAGAATGAACCTCAAGAAGTATGACGGGGGCCGACAAAGCGTGGAGCATGTGGTTTAATTC
 GTGCAAAAGGAGAGCAACTTACGAGGCTGTGATCGCGCGAATCGCTCTTGAAGAGAGAGAGGTCGCTTGGGAAACGGGACAGAGTGGTATCGTGTGTGCTGTCCGCTATGCTGTGGTATGTGGGTA
 AGTCCGCTACGACGACGACCTTACGATGTGATTTGGCTCTGTAATTTGTGGAACCTGGAACAGATCGCGGACAGAGCAGAGAGAGTGGAGTGAATGCTACAGTCTACATGCCCTTAATGCTCCGCTGG
 GCGACACAGTGTCTAACGCGCGGACAAAGGTCGCGATCCGCGAGGTCGAGCTACCCAAAAACCGTCTCGATTCGGAATTCGACGTCGACATGCTGTCTGCATGAAGCGGAAATCGCTAGTAAT
 TCCGCGCTCAGCCTACGCGGGTGAATTAATTCGCGGGCTGTACACACCGCCGCTACATGTGAAGATGCGCATGCCGAAAGTCGATTTATTAACCAAAAGAGGGGGGTGCGAAAGCGAGGCTAG
 TCGCTGGAGTGAAGTGATGCAAGTAGGAGCTGCTGGAAGGTCGACGTCGATCACTCTT

Name List [Download](#) [Use Latin Name](#)

NC_026892.1,NC_026134.2,AC_000188.1,NC_000932.1,NC_001319.1,NC_001568.1,NC_001631.1

Gene List [Download](#)

cp_16s

Running Log [Download](#)

[2017-03-26 22:12:45] INFO : Done.

• • • • •

```
Start of Pairwise alignments
Sequence 7: NC_001568.1 1492 bp
Sequence 6: NC_026134.2 1496 bp
Sequence 5: AC_000188.1 1512 bp
Sequence 4: NC_000932.1 1491 bp
Sequence 3: NC_026892.1 1491 bp
Sequence 2: NC_001631.1 1491 bp
Sequence 1: NC_001319.1 1496 bp
Sequence format is Pearson
Sequence type explicitly set to DNA

CLUSTAL 2.1 Multiple Sequence Alignments

[2017-03-26 22:12:42] INFO : Building tree with clustalw...
[2017-03-26 22:12:42] INFO : rRNA List is ready.
[2017-03-26 22:12:42] INFO : Reading data file.
[2017-03-26 22:12:42] INFO : Reading input list.
[2017-03-26 22:12:42] SYSTEM: perl rRNA2Tree.pl -i result/20170326paaaj:21t/namelist.txt -g cp_16s -o result/20170326paaaj:21t -c re
sult/20170326paaaj:21t/treePara.txt &
[2017-03-26 22:12:42] INFO: Start.
```

After calculation, click on the result link and the “result of data” page will appear.

Phylogenetic Tree

[Download](#) [Tree Preview](#) [Circular Preview](#) [Use Latin Name](#) [Opne in iTOL](#)

```
(NC_016730.1:0.00000,(((NC_016728.1:0.00717,(NC_023358.1:0.00000,NC_016729.1:0.00044):0.00279):0.00098,NC_023359.1:0.00345):0.00035,((((NC_007578.1:0.00137,NC_007977.1:0.00077):0.00261,NC_008096.2:0.00629):0.00300,NC_010776.1:0.00795):0.00826,NC_023357.1:0.00107):0.00071):0.00000,NC_016727.1:0.00000);
```

Below “Phylogenetic Tree” title, there are five buttons and a text area. The phylogenetic tree in red area is in **Newick format**, which is available for download by clicking

[Download](#) button. The [Tree Preview](#) button and the [Circular Preview](#) button

are used to watching the result in the tree view and in the circular view. The users can also download the generated plots as either PNG raster image or SVG vector graphics. To send

the tree view to iTOL <http://itol.embl.de/help.cgi#manage>, click the [Opne in iTOL](#)

button. Click [Use Latin Name](#) button, the RefSeq in the red area will be replaced by Latin name of species and vice versa.

Tree Sequence [Download](#) [Use Latin Name](#)


```
>NC_016730.1
TTCAAACGAGGAAAGGCTTATGGTGGATACCTAGGCACCCAGAGACGAAGAAGGGCGTATTAATCGACGAAATGCTTCGGGGAGTTGAAAAAAGCATAGATCCGGAG
ATCCCCGAATAGGTCAACCTTTCGAACCTGCTGCTGAATCCATGGGCAGGCAAGAGACAACCTGGCGAACTGAAACATCTTACTAGCCAGAGGAAAAGAAAAGCAAAAGC
GATTCCCGTAGTAGCGGCGAGCGAAATGGGAACAGCCTAAACCGTGAAAAACGGGGTTGTGGGAGAGCAATACAAGCGTCGTGCTGCTAGGCGAAGCGGTGGAGTACCG
CACCCTAGATGGCTAGAGTCCAGTAGCCGAAAGCATCACTAGCTTATGCTCTGACCCGAGTAGCATGGGGCACGTGGAATCCCGTGTGAATCAGCAAGGACCACCTTG
CAAGGCTAAATACTCTTGGGTGACCGATAGCGAAGTAGTACCGTGAGGGAAGGGTGAAAAGAACCCCATCGGGGAGTGAAATAGAACATGAAACCGTAAGCTCTCAA
GCAGTGGGAGGAGGCGCGCTGGAAGCTCTGACCGCGTGCCTGTTGAAGAATGAGCCGGCGACTCATAGGCAGTGGCTTGGTTAAGGGAACCCACCGGAGCCGTAGCGA
AAGCGAGTCTTCATAGGGCAATTGTCACTGCTTATGGACCCGAACCTGGGTGATCTATCCATGACCAGGATGAAGCTTGGGTGAAACTAAGTGAGGTCGGAACCGAC
TGATGTTGAAGAATCAGCGGATGAGTTGTGGTTAGGGGTGAAATGCCACTCGAACCCAGAGCTAGCTGGTTCTCCCCGAAATGCGTTGAGGCGCAGCAGTTGACTGGA
CATCTAGGGGTAAAGCACTGTTTCGGTGGGGCCGCGAGAGCGGTACCAATCGAGGCAAACTCTGAATACTAGATATGACCTCCAAATAACAGGGGTCAAGGTCGGC
CAGTGAGACGATGGGGGATAAGCTTCATCGTCGAGAGGGAAACAGCCCGGATCACCAGCTAAGGCCCTAAATGACCGCTCAGTGATAAAGGAGGTAGGGGTGCAGAG
ACAGCCAGGAGGTTTGCTAGAAAGCAGCCACCTTGAAAGAGTGCGTAATAGTCTACTGATCAGCGCTCTTGCGCCGAAGATGAACGGGGCTAAGCGATCTGCCGAA
GCTGTGGGATGTAAAAAACATCGGTAGGGGAGCGTTCCGCTAGAGGGAAGTACCGGCGCAGCCGCTGATGGACGAAGCGGAAGCGAGAATGTCTGGCTTGAGTAAC
GCAAAATTGGTGAGAATCCAATGCCCGAAAACCTAAGGGTTCTTCGCAAGGTTCTCCACGGAAGGAGTGAAGTCAAGGCTAAGTCAAGGCGGAAAGGCGTATGTCG
TGGACAACAGGTAATAATCTCTGTACTACCCCTTGTGGTCCCGAGGAGCGAGGAGGCTAGGTTAGCCGAAAGATGGTTATCGGTTCAAGGACACAAGGTGACCCCTG
```

The tree sequence shown in the green area below the title of “Tree Sequence” is the re-organized sequence (in fasta format) for phylogenetic calculation, which is

downloadable by clicking [Download](#) button. Click [Use Latin Name](#) button, the RefSeq will be replaced by Latin name of species and vice versa.

Name List [Download](#) [Use Latin Name](#)


```
NC_016729.1,NC_023358.1,NC_016728.1,NC_023359.1,NC_016727.1,NC_016730.1,NC_023357.1,NC_010776.1,NC_007977.1,
NC_007578.1,NC_008096.2
```

The RefSeqs in the green area below the title of " Gene list" lists the selection of species, which can be downloaded in the textual format by clicking  button. Click

 button, the RefSeq will be replaced by Latin name of species.

Gene List

cp_23s

The genes you have selected are listed in the green area below the title of "Gene List" , which is available for download by clicking  button.


Running Log


```
[2016-09-21 12:18:59] INFO : Done.
NEXUS-Alignment file created [result/2016092103yw@hum/tree.nxs]

Alignment Score 4080884
Group 8: Sequences: 9 Score:412138
Group 7: Sequences: 8 Score:405194
Group 6: Sequences: 5 Score:427362
Group 5: Sequences: 3 Score:448085
Group 4: Sequences: 2 Score:465288
Group 3: Sequences: 2 Score:421779
Group 2: Sequences: 3 Score:425920
Group 1: Sequences: 2 Score:433010
Aligning...

Start of Multiple Alignment
There are 8 groups

Guide tree file created: [result/2016092103yw@hum/tree.dnd]
Sequences (8:9) Aligned. Score: 81
Sequences (7:9) Aligned. Score: 83
Sequences (7:8) Aligned. Score: 83
Sequences (6:9) Aligned. Score: 83
Sequences (6:8) Aligned. Score: 91
Sequences (6:7) Aligned. Score: 86
Sequences (5:9) Aligned. Score: 82
Sequences (5:8) Aligned. Score: 92
Sequences (5:7) Aligned. Score: 86
Sequences (5:6) Aligned. Score: 95
Sequences (4:9) Aligned. Score: 81
```

The content in the red area below the title of " Running Log" records the running log , which can be downloaded in the log format by clicking  button besides the "Running Log" title.

If all the files are needed to be downloaded, the download button  at the top of the page can compress all files into zip format. Click on the "↑Back to Top" at the lower-right side of the page to go back to the top of the page.

5. DATA VISUALIZATION AND SHARING

The Phylogenetic Tree in the result page installed a data sharing interface, so it can transmit the tree data to iTOL (<http://itol.embl.de/help.cgi#manage>) and will generate an online tree for further manipulation.

Phylogenetic Tree

[Download](#) [Tree Preview](#) [Circular Preview](#) [Opne in iTOL](#)

(NC_016433.2:0.00000,NC_007898.3:0.00336,NC_029719.1:0.00135);

Each result page is numbered by an experiment code, and user can share the result by simple share the link, whenever the final result is still in process or finalized.

Result of Data: 20161012618n6kbc

[Home](#) / [Service](#) / [Result](#)

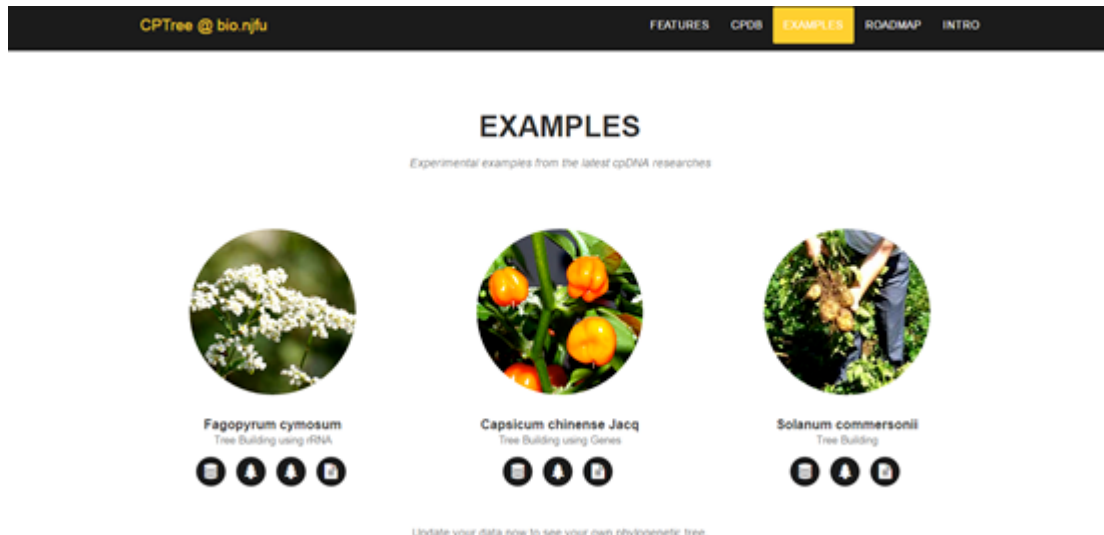
Calculation is still in process, please try later.

Result Link: [20161012618n6kbc](#)

93%


In this way, if the process cost too much time calculating, user can use the code to retrieve the final result without waiting online.

6. SAMPLES






The service homepage of CPTree <http://bio.njfu.edu.cn/CPTree/service> lists three experimental examples including the cpDNA research of *Fagopyrum cymosum*, *Capsicum chinense* Jacq and *Solanum commersonii* in 2015–2016.

There are four buttons below the research of *Fagopyrum cymosum*, using ribosomal RNA


to build trees. The left-most button  allows you to open the “Step 1: Select the species” page of fast mode. Click on the green

button  to select ribosomal RNA in the “Step 2:


Parameter Confirmation” page. Next, click the button  and skip to the page of “Data Submitted” . You can click the link beside “Result code” to view result of the research. You can also download the name lists and gene lists by checking the

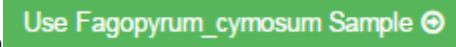
button . The second button on the left  opens the “Result of Data: *Fagopyrum_cymosum_cp_16s*” page, which displays the result of tree building using 16s

ribosomal RNA. Meanwhile, the third button on the left  allows you to view the tree,

which is built from 23s ribosomal RNA. After clicking the right-most  button, you can read the article which provides the original tree in the cpDNA research of *Fagopyrum cymosum*.


There are three buttons respectively below the research of *Capsicum chinense* Jacq and

Solanum commersonii using genes to build trees. The left-most button  allows you to open the “Step 1: Select the species” page of fast mode. Click on the green


button  to go to the “Step 2: Select the Genes” page, where you need to check the button

 to open the page of “Step 3:

Parameter Confirmation” . Next, click the button  and skip to the page of

“Data Submitted” . You can click the link beside “Result code” to view result of the research. You can also download the name list and gene list by checking  button. The

middle button  opens the “Result of Data” page, which displays the result of tree

building using genes. After clicking the right-most button  , you can read the article which provides the original tree in the cpDNA research of *Capsicum chinense* Jacq and *Solanum commersonii*.