


# Tour Guide

(Teabase Version 2023-2)

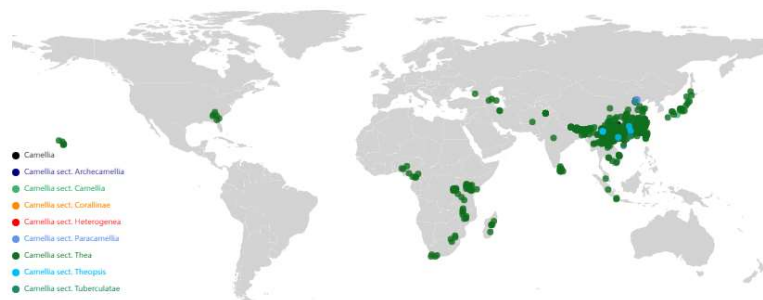
## 1. Browse the 'home' page for the latest statistics and news

(1)  Species Germplasm Panorama Gene Projects Tools Download About

### Statistics

SUMMARY	
Genomes	705
Species	39
Sample location	166
AVG.Gbase	54.04
Cultivated	378
Wild	42

Distribution of populations



If you use Teabase, please cite:  
The Tea Tree Genome Provides Insights into Tea Flavor and Independent Evolution of Caffeine Biosynthesis

(2) [News & Events >>](#)

- 07-15 2019 | The tea plant reference genome and improved gene annotation using long-read and paired-end sequencing data
- 01-25 2022 | The reference genome of *Camellia chekiangoleos* provides insights into *Camellia* evolution and tea oil biosynthesis
- 03-19 2021 | Chromosome-level genome reference and genome editing of the tea geometrid

(3) [External Links >>](#)

(1) Quickly return to the “home” page. (2) Find the latest *Camellia* data news. (3) Exploring omics databases for other non-alcoholic beverage crops.

## 2.Species

Go to “Species” and input “*Camellia sinensis* var. *assamica*” search for this species.

You will find the brief information for the “*Camellia sinensis* var. *assamica*” population.

The screenshot shows the Teabase website navigation bar with options: Species, Germplasm, Panorama, Gene, Projects, Tools, Download, About. Below the navigation bar, there are tabs for 'Jump to section', 'Species Profile', 'Genome Assembly', 'Germplasm', and 'Reference'. A search bar contains the text 'assami' and a 'Search' button. A dropdown menu shows search results: 'Camellia subg. Thea;', 'Camellia sect. Thea;', and 'Camellia sinensis var. assamica'. Below the search bar, the 'Subgenus' is set to 'Camellia subg. Thea' and the 'Group' is set to 'Camellia sect. Thea'. The 'Species' dropdown is also visible, showing 'Camellia sinensis var. sinensis'.

Or you can use filter tools to find your interesting species

The screenshot shows the filter tools section of the Teabase website. A search bar contains 'Camellia chrysanthoides' and a 'Search' button. Below the search bar, there are dropdown menus for 'Subgenus' (Camellia subg. Thea), 'Group' (Camellia sect. Thea), and 'Species'. A dropdown menu for 'Species' is open, showing a list of species: 'Camellia gymnogyna', 'Camellia costata', 'Camellia leptophylla', 'Camellia fangchengensis', 'Camellia ptilophylla', 'Camellia sinensis', 'Camellia sinensis var. assamica' (which is highlighted with a blue selection bar), and 'Camellia sinensis var. sinensis'.

Now you will see the *Camellia sinensis* var. *assamica* subpage.

The screenshot shows the 'Species Profile' page for *Camellia sinensis* var. *assamica*. It includes a photograph of the plant, a world map showing the distribution of populations, and taxonomic information: Genus: *Camellia*, Subgenus: *Camellia* subg. *Thea*, Group: *Camellia* sect. *Thea*, Species: *Camellia sinensis* var. *sinensis*, Chromosome:  $2n = 30, 45, 60$ . A red circle with the number '1' is placed over the species name.

(1) The information for species

**Description**  
*Camellia sinensis* var. *sinensis* 茶 (茶葉) *Thea sinensis* Linnaeus, Sp. Pl. 1: 515, 1753; *Camellia arborescens* Hung T. Chang & F. L. Yu, C. *Anglingensis* F. C. Zhang et al., C. *oleosa* (Lour.) Rehder, C. *sinensis* f. *formosensis* Kitamura, C. *sinensis* f. *macrophylla* (Siebold) Kitamura, C. *sinensis* f. *parvifolia* (Miq.) Scaly, C. *sinensis* var. *waldenae* (S. Y. Hu) Hung T. Chang, C. *thea* Lindl., C. *waldenae* S. Y. Hu, T. *holboelliana* T. Cantoniensis Loureiro, T. *chinesis* Sims, T. *cockburniana* Loureiro, T. *grandifolia* Salisbury, T. *oleata* Loureiro ex Gussone, T. *oleosa* Loureiro, T. *parvifolia* Salisbury (1796), non Hayata (1913); T. *sinensis* var. *macrophylla* Siebold, T. *sinensis* var. *parvifolia* Miq., T. *viridis* Linnaeus, *Theaphylla cantoniensis* (Lour.) Rafinesque. Leaf blade abaxially glabrous or sparsely pubescent only when young, apex bluntly acute. Sepals outside glabrous. Ovary densely white pubescent. Fl. Oct-Dec.  $2n = 30, 45, 60$ . Evergreen broad-leaved forest, thickets, 100-2200 m. Anhui, Fujian, Guangdong, Guangxi, Guizhou, Henan, Hebei, Hubei, Hunan, Jiangsu, Jiangxi, Shaanxi, Sichuan, Taiwan, Xinjiang, Yunnan, Zhejiang [NE India, S Japan, S Korea]. This taxon is widely cultivated in tropical and subtropical parts of the world. Because of its extensive long-term cultivation, the original wild distribution in E Asia is obscure although certainly much more restricted than the current distribution.

(2) Currently available reference genomes for this species, Click on the ‘Download’ button to jump to download these reference genome.

Genome Assembly							
Genome assembly	Assembly level	Assembly size	Contig no.	Contig size	Gene no.	BUSCO%	Author
L343	chromosome scale	3.26Gb	37600	271.57kb	33556	88.36	Wang et al., 2020
ShaochunGX200306	-	3.14Gb	-	47.61kb	13652	45.54	Wu et al., 2018
DASZ	Chromosome	3.15Gb	5403	2.985Mb	33021	93	Weiye Zhang et al.
TCY	Highly resolved	3.09Gb	-	1.945Mb	42821	94	Xingxin Zhang et al. 2021
Huangfan	Chromosome	2.94Gb	-	2.615Mb	43779	95	Pengjie Wang et al. 2021
DipuoMaqian	Chromosome	2.97Gb	15771	723kb	34896	87.78	Wang, F. et al. 2022
Byun	Chromosome	3.25Gb	-	625.18kb	40812	89.85	Zhang, Q.-J. et al. 2020

(3) The corresponding germplasm of the species that have been collected. Click on the database ID to jump to the corresponding ‘Germplasm’ subpage.

Germplasm				
Database ID	Common name	Crop variety number	Utilization	Producing area
TEA0374	Cha	-	-	-
TEA0373	Yuanjinyancha	-	green tea	Yunnan
TEA0372	Dabaihan tea	-	-	-
TEA0371	Xinyang tea	-	green tea	-
TEA0370	Red tea	-	red tea	-
TEA0369	Qianhe tea	-	green tea	-
TEA0368	Xinzecha	-	-	-
TEA0367	Ordang tea	-	oolong tea	-
TEA0320	Banman tea	-	-	-
TEA0319	Pipicha	-	-	-

(4) Reference citation details corresponding to the reference genome.

Reference					
Author	Title	Journal	Year	PubId	
Wang et al., 2020	Population sequencing enhances understanding of the evolution of the tea genome	Nature Communications	2020	doi:10.1038/s41467-020-18228-6	(4)
Wu et al., 2018	Draft genome sequence of <i>Camellia sinensis</i> var. <i>sinensis</i> provides insights into the evolution of the tea genome and tea quality	PNAS	2018	doi:10.1073/pnas.1719622115	
Weiye Zhang et al.	Genome assembly of wild tea tree DASZ reveals pedigree and selection history of tea varieties	Nat Commun	2020	doi.org/10.1038/s41467-020-17408-6	
Xingxin Zhang et al. 2021	Highly-resolved genome assembly provides insights into evolutionary history of the tea plant <i>Camellia sinensis</i>	Nat Genet	2021	doi.org/10.1038/s41588-021-08805-y	
Wang, F. et al. 2022	Chromosome-scale genome assembly of <i>Camellia sinensis</i> combined with multi-omics provides insights into its response to salinization with green tea cultivars	Frontiers in Plant Science	2022	doi.org/10.3389/fpls.2022.1094387	
Zhang, Q.-J. et al. 2020	The Chromosome-Level Reference Genome of Tea That Uncovers Recombination of Non-autonomous LTR Retrotransposons in Driving Genome Size Evolution	Mol Plant	2020	doi.org/10.1016/j.molp.2020.04.009	

### 3. Germplasm

Users have three ways to view the germplasm they are interested in:

1. Go to “Germplasm” and input “Cambod tea” of *Camellia sinensis* var. *assamica* or any of the letters to search for this cultivar.
2. Use filter tools to find your interesting cultivar.
3. Jump through the ‘Species’ page that the user is browsing and click on the germplasm of interest

Now you will see the *Cambod tea* subpage.

(1)

(1) The information for Cambod tea.

**Description**

*Camellia sinensis* var. *assamica* (J. W. Masters) Kitamura, Acta Phytotax. Geobot. 14: 59. 1950. 普洱茶 pu er cha *Thea assamica* J. W. Masters, J. Agric. Soc. India 3: 63. 1844; *Camellia assamica* (J. W. Masters) Hung T. Chang, C. *assamica* var. *kucha* (Hung T. Chang & H. S. Wang) Hung T. Chang & H. S. Wang, C. *assamica* var. *polynura* (Hung T. Chang & Y. J. Tang) Hung T. Chang, C. *multiseptala* Hung T. Chang & Y. J. Tang, C. *polynura* Hung T. Chang & Y. J. Tang, C. *sinensis* var. *kucha* Hung T. Chang & H. S. Wang, C. *theifera* Griffith, T. *chinensis* var. *assamica* (J. W. Masters) Pierre, T. *viridis* var. *assamica* (J. W. Masters) Choisy; Leaf blade elliptic, 8-14 × 3.5-7.5 cm, abaxially densely spreading villous along midvein, apex acuminate. Ovary apically glabrous. Fl. Dec-Feb, fr. Aug-Oct. 2n = 30. Evergreen broad-leaved forests; (100-1500-1900) m. S Guangdong, S Guangxi, Hainan, S Yunnan [Laos, Myanmar, Thailand, Vietnam]; *Camellia sinensis* var. *assamica* is the source of Puer (普洱) tea which is a black (fermented) tea from Yunnan.

(2) Currently available whole-genome sequence data for this cultivar, Click on the ‘Download’ button to jump to download these data.

Sequenced Accessions								Download
Sample ID	Classification	Cultivation	Morphotype	Genetic classification	Sampling location	SRA ID	MBase (G)	
re112	Hybrid	Cultivated	China/Assam type	-	Thailand (Chiang Rai)	-	80.15	
re113	Hybrid	Cultivated	China/Assam type	-	Thailand (Chiang Rai)	-	61.84	
re114	Assamica	Cultivated	Chinese Assam type	-	Laos (Phongsaly)	-	64.05	
re115	Assamica	Cultivated	Chinese Assam type	-	Laos (Phongsaly)	-	65.34	
re116	Assamica	Cultivated	Chinese Assam type	-	Laos (Phongsaly)	-	56.62	
re117	Assamica	Cultivated	Chinese Assam type	-	Laos (Phongsaly)	-	57.15	
re118	Assamica	Cultivated	Chinese Assam type	-	Laos (Phongsaly)	-	62.8	
re119	Sinensis	Cultivated	India Assam type	-	Cambodia (NA)	-	67.63	
re120	Sinensis	Cultivated	India Assam type	-	Cambodia (NA)	-	62.77	
re121	Sinensis	Cultivated	India Assam type	-	Cambodia (NA)	-	63.98	
re126	Hybrid	Cultivated	China/Assam type	-	Thailand (Chiang Rai)	-	90.43	
re127	Hybrid	Cultivated	China/Assam type	-	Indonesia (Java Bogor)	-	68.92	
re376	Hybrid	Cultivated	China/Assam type	-	Indonesia	-	53.79	
re380	Hybrid	Cultivated	China/Assam type	-	Indonesia	-	54.14	

(2)

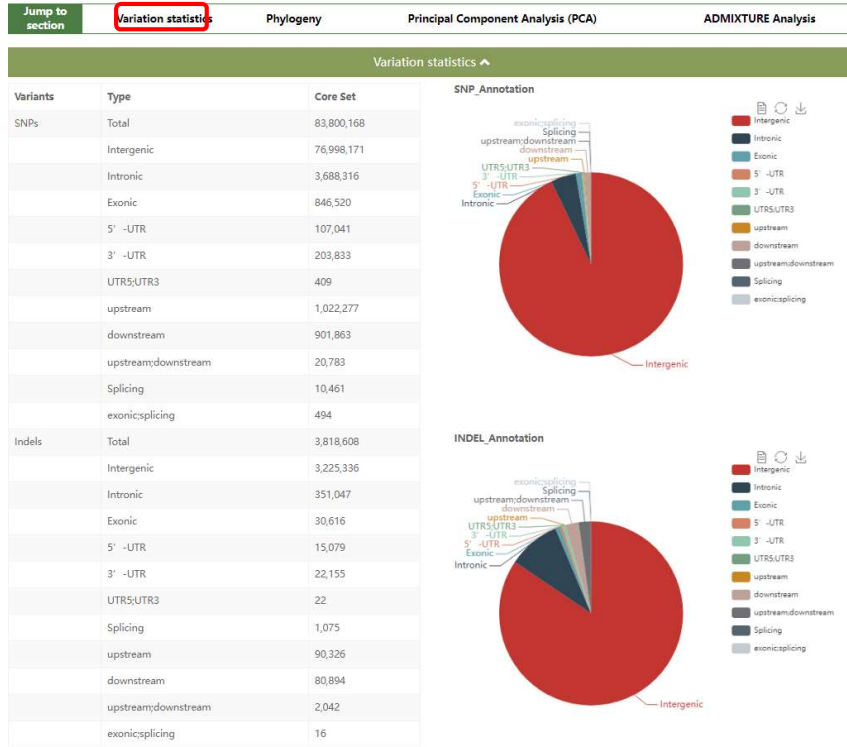
(3) Reference citation details corresponding to the whole genome sequenced.

Reference					
Author	Title	Journal	Year	Pmid	
Xia et al., 2017	The tea tree genome provides insights into tea flavor and independent evolution of caffeine biosynthesis	Molecular Plant	2017	doi:10.1016/j.molp.2017.04.002	
Unpublished	Teabase Unpublished	Teabase Unpublished	Teabase Unpublished	Teabase Unpublished	

(3)

## 4. Panorama

### Variation statistics



Browse variants information in 'Gene' model and 'JBrowse' directly by clicking a button.

## Phylogenetic tree.

Go to “Phylogeny”.



The Phylogeny is an interactive dynamic evolutionary tree based on Phylogeny.IO and can be scalable and collapsible. Users can freely view the whole as well as details for each branch with interests. Here are some tips:

1. User can zoom and pan around the tree using trackpad or mouse.
2. Clicking on a branch: show the sample information.
3. Double-clicking on a node: collapsing or extending a clade.
4. Sliders control the geometry of the tree. User can adjust the relative length of the branches and the space between them.
5. The items for tree displaying.



Note

Sinensis	Landrace	Wild	Assamica	Hybrid
Other	Youcha	Shancha		

# Principal Component Analysis (PCA)

Jump to section

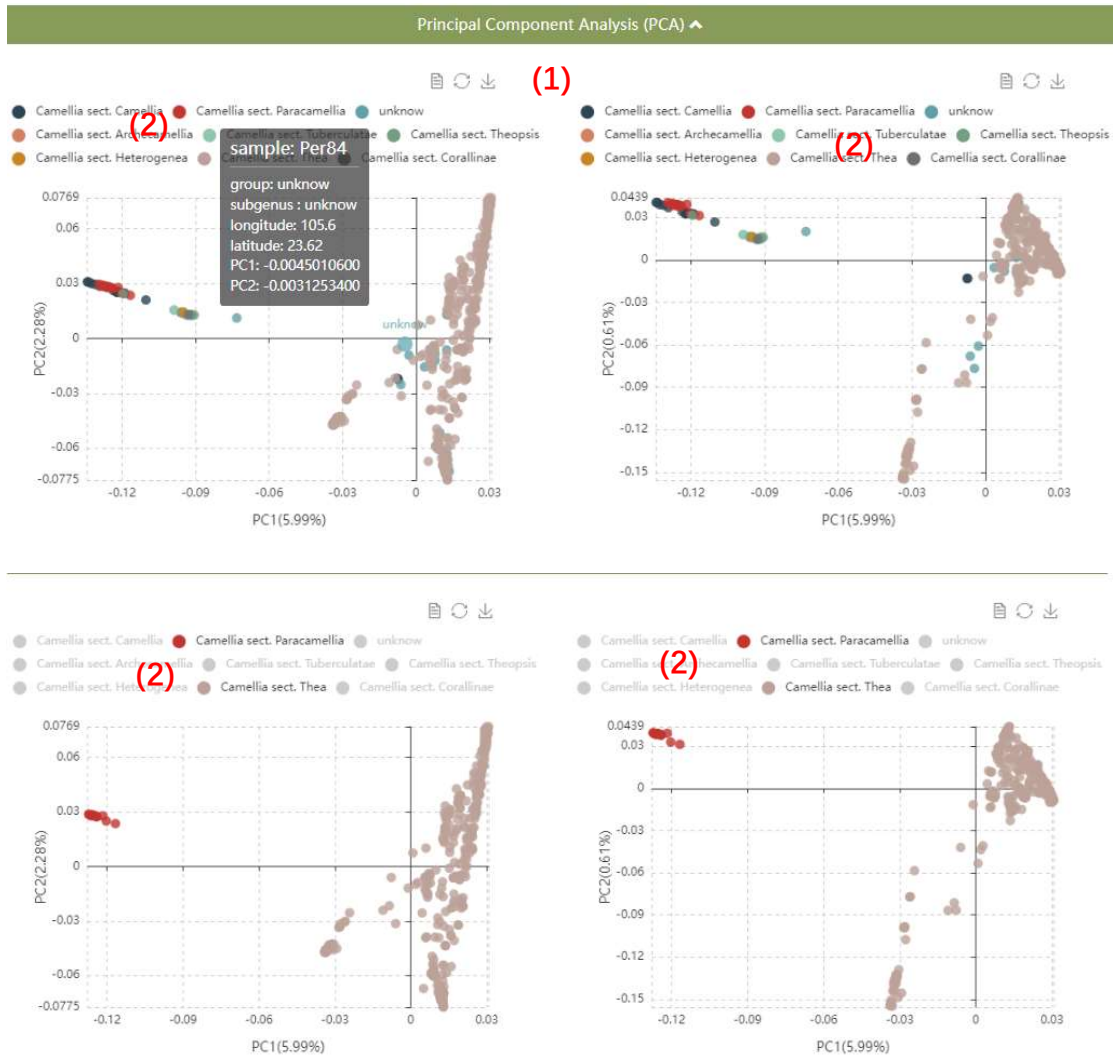
Variation statistics

Phylogeny

Principal Component Analysis (PCA)

ADMIXTURE Analysis

Population genetic affinity was shown by principal component analysis (PCA) under the context of *all species*(1). Users can choose certain *Camellia* populations (e.g. Camellia) to showing genetic affinities under the PCA context (2). One Pu'er tea sample (ID Per84) was indicated (3).



## ADMIXTURE analysis.

Jump to section

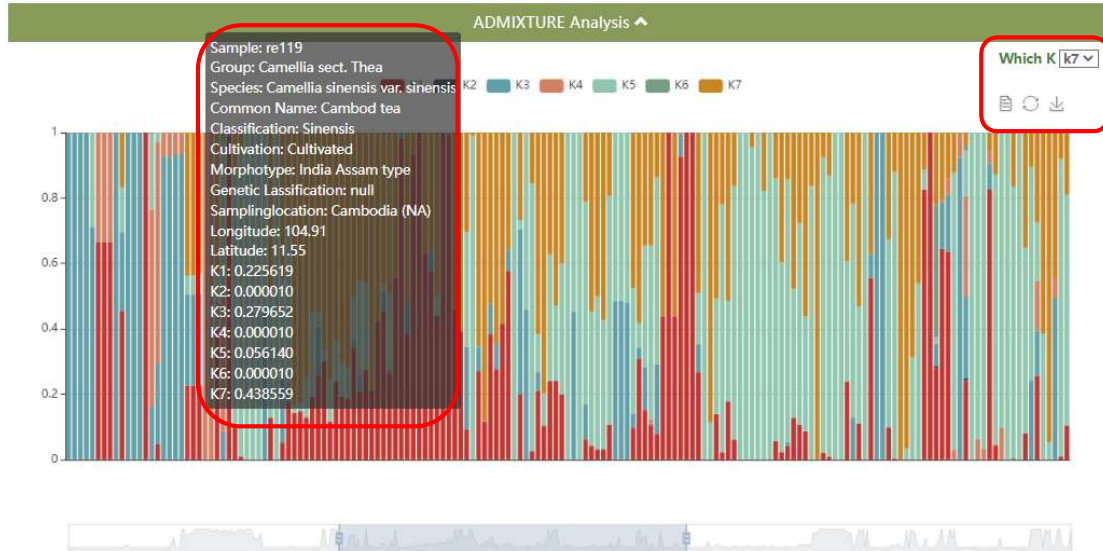
Variation statistics

Phylogeny

Principal Component Analysis (PCA)

ADMIXTURE Analysis

Population structure and genetic admixture were shown by length of each colored bar represents the proposed proportion of representative ancestry in the individual. One Cambod tea sample (ID re119) was indicated under k7 condition.



## 5. Gene

Go to “Gene”.

Reference/ Chr (1) Pos Description Submit Reset

Please select  
 Camellia sinensis  
 Camellia sinensis var. assamica(CSA)  
 Camellia sinensis var. sinensis(CS)(GS2002008)  
 Camellia sinensis var. sinensis(fongjing43)  
 Camellia sinensis var. sinensis(YK10) (2)

Reference	Gene locus	Chr	Start	End	Strand	Length	Description
<input checked="" type="checkbox"/> Camellia sinensis var. sinensis(YK10)	CaS01G000010	1	12157	15937	+	3781	
<input type="checkbox"/> Camellia sinensis var. sinensis(YK10)	CaS01G000020	1	15983	17806	+	1824	
<input type="checkbox"/> Camellia sinensis var. sinensis(YK10)	CaS01G000030	1	17878	19443	+	1566	
<input type="checkbox"/> Camellia sinensis var. sinensis(YK10)	CaS01G000040	1	22778	24294	+	1517	
<input type="checkbox"/> Camellia sinensis var. sinensis(YK10)	CaS01G000050	1	40370	40946	-	577	DNA binding
<input type="checkbox"/> Camellia sinensis var. sinensis(YK10)	CaS01G000060	1	42207	53426	+	11220	
<input type="checkbox"/> Camellia sinensis var. sinensis(YK10)	CaS01G000070	1	176094	176717	-	624	Belongs to the cation transport ATPase (P-type) (TC 3.A.3.) family: Type IV subfamily
<input type="checkbox"/> Camellia sinensis var. sinensis(YK10)	CaS01G000080	1	965467	973993	+	8527	serine threonine-protein kinase
<input type="checkbox"/> Camellia sinensis var. sinensis(YK10)	CaS01G000090	1	1045389	1049511	+	4123	Plant protein of unknown function (3)
<input type="checkbox"/> Camellia sinensis var. sinensis(YK10)	CaS01G000100	1	1060460	1067296	+	6837	E3 ubiquitin-protein ligase

Showing 1 to 10 filtered from 163558 total entries. Display per page 10 records. Previous 1 2 3 4 5 ... 16357 Next Go

(1) Select a reference genome of interest. There are currently four available reference genomes in the gene module.

(2) Choose the information you are interested in to display

(3) Click operate to display the detailed information of the modified gene, including downloading CDS and PEP sequences

Verified Alleles

Gene locus	Chr	Position	Allele	Region	Info
CaS01G000040	1	22777	A/G	upstream	CaS01G000040
CaS01G000040	1	30482	T/G	intergenic	CaS01G000040(dist=6188),CaS01G000050(dist=9888)
CaS01G000040	1	30537	A/G	intergenic	CaS01G000040(dist=6243),CaS01G000050(dist=9833)
CaS01G000040	1	30564	T/C (4)	intergenic	CaS01G000040(dist=6270),CaS01G000050(dist=9806)
CaS01G000040	1	30636	A/T	intergenic	CaS01G000040(dist=6342),CaS01G000050(dist=9734)
CaS01G000040	1	38724	A/G	intergenic	CaS01G000040(dist=14430),CaS01G000050(dist=1646)
CaS01G000040	1	39092	G/C	intergenic	CaS01G000040(dist=14798),CaS01G000050(dist=1278)
CaS01G000040	1	39159	C/A	intergenic	CaS01G000040(dist=14865),CaS01G000050(dist=1211)

Showing 1 to 8 filtered from 8 total entries

(4) Click on any gene to display the gene and its upstream and downstream mutation sites in the verified alleles section.

(5) Click on any gene to display the expression level(FPKM) in different group.

Chen, J.D., Zhang, C., Ma, J.Q., et al. The chromosome-scale genome reveals the evolution and diversification after the recent tetraploidization event in tea plant. *Hortic Res* 7, 63 (2020).

(5)

Jiang, X., Zhao, H., Guo, F., et al. Transcriptomic analysis reveals mechanism of light sensitive albinism in tea plant *Camellia sinensis* Huangjinju. *BMC Plant Biol* 20, 216 (2020).

Li, C.F., Zhu, Y., Yu, Y., et al. Global transcriptome and gene regulation network for secondary metabolite biosynthesis of tea plant (*Camellia sinensis*). *BMC Genomics* 16, 560 (2015).

Wang, X., Feng, H., Chang, Y., et al. Population sequencing enhances understanding of tea plant evolution. *Nat Commun* 11, 4447 (2020).

Wang, X.C., Zhao, Q.Y., Ma, C.L., et al. Global transcriptome profiles of *Camellia sinensis* during cold acclimation. *BMC Genomics* 14, 415 (2013).

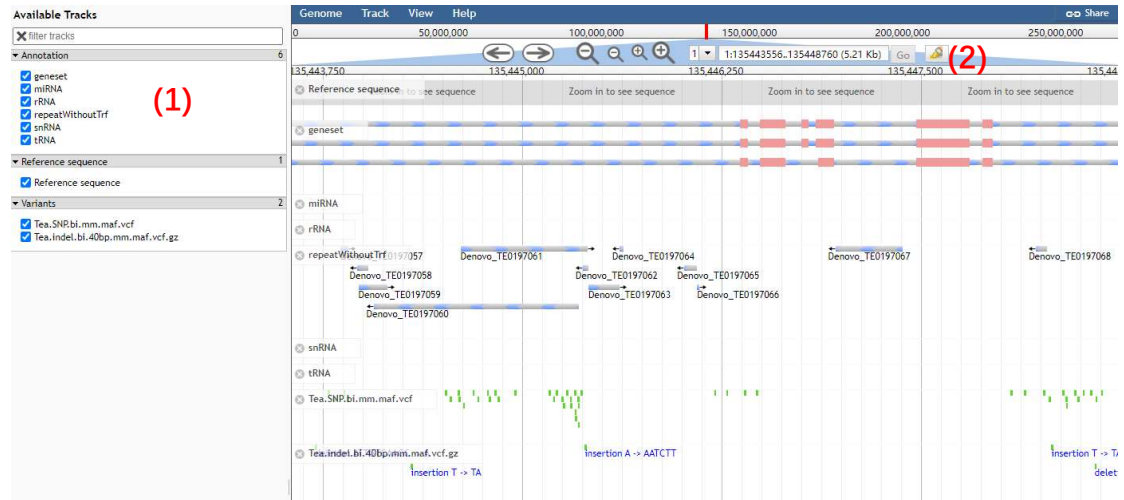
Xia, E.-H., Zhang, H.-B., Sheng, J., Li, K., Zhang, Q.-J., Kim, C., Zhang, Y., Liu, Y., Zhu, T., and Li, W. (2017). The tea tree genome provides insights into tea flavor and independent evolution of caffeine biosynthesis. *Mol. Plant* 10:866-877.

Sample: old\_leaf  
 Lab name: old\_leaf  
 Value: 0.0813718000



## 6. JBrowse

Go to “JBrowse” under the ‘tools’ page

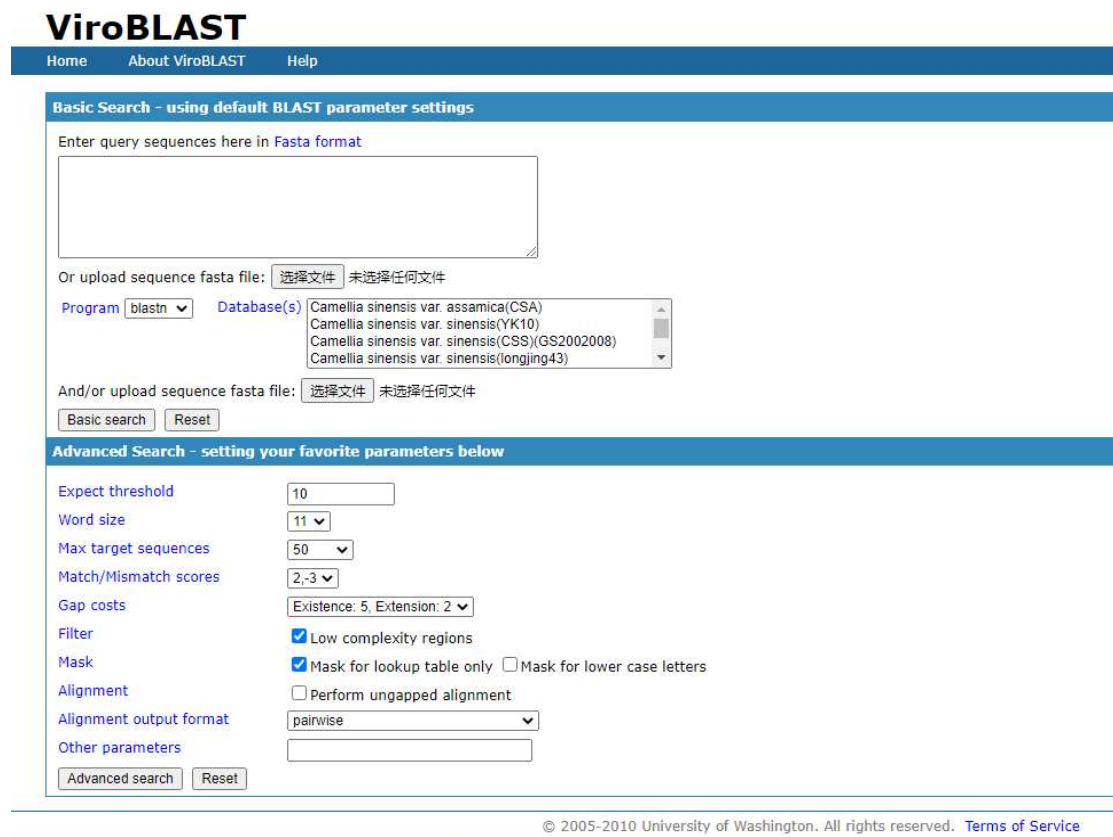


(1) Select the track in which you are interested. (base on reference genome YK10(2022))

(2) Use the tool bar zoom your interested area

## 7. Blast

Go to “Blast” under the ‘tools’ page



There are four reference genome available now.

## 8.Genetic map

Go to “Genetic map” under the ‘tools’ page

species



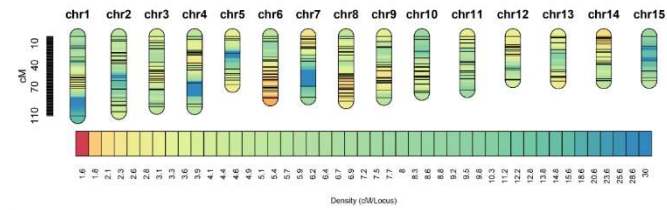
Reset Search

4 records were returned

#	Map Name	Maternal Parent	Paternal Parent	Pop size	Pop Type	Species
1	Kana-Ck17×SAK_F1	Kana-Ck17	Sayamakaori	54	F1	Camellia sinensis
2	Fushun×Kemaui_F1	'Fushun'	'Kemaui'	79	F1	Camellia sinensis
3	LJ43×BHZ1_F1_LJ43	Longjing43	Baihaozao	327	F1	Camellia sinensis
4	LJ43×BHZ2_F1_XHFD	Longjing43	Baihaozao	170	F1	Camellia sinensis

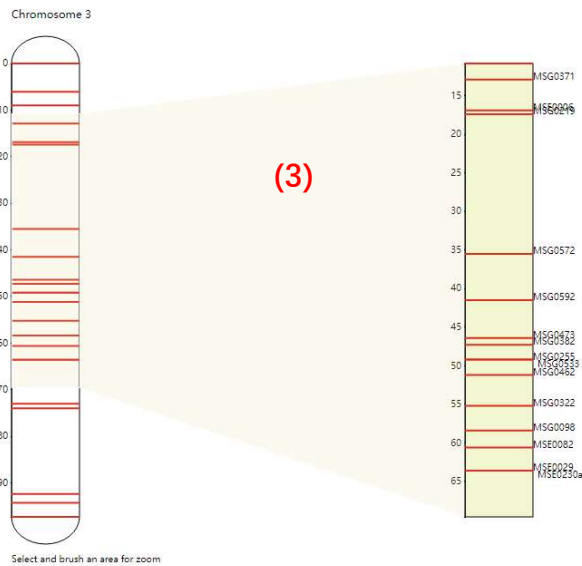
### Map Overview

Click on any linkage group to explore this map further; you will be taken to MapViewer and leave this page.



Map Name	Kana-Ck17×SAK_F1
Species	Camellia sinensis
Software	ArifMap
Map Type	genetic
Population Type	F1
Map Unit	cM
Maternal Parent	Kana-Ck17
Paternal Parent	Sayamakaori
Number of LGs	15
Number of Loci	278
Reference	Taniguchi F., et al., 2012

### Genetic map - Kana-Ck17×SAK\_F1



■ SSR ■ RAPD ■ AFLP ■ CAPS ■ STS

- (1) Select your interested genetic map.
- (2) Overview the genetic map and select the chromosome to view the detail
- (3) click and slide your mouse to view the marker on this chromosome.

## 9.Synteny Visualization

Go to “Synteny Visualization” under the ‘tools’ page

**SynVisio** An Interactive Multiscale Synteny Visualization Tool for McScanX.  
Please follow the steps below to visualize the synteny analysis result.

Step 1. Choose Species Pair

Camellia sinensis var. sinen

Camellia sinensis var. sinensis(YK10)\_Camellia sinensis var. assamica(CSA)  
Camellia sinensis var. sinensis(YK10)\_Camellia sinensis var. sinensis(CSS)(GS2002008)  
Camellia sinensis var. sinensis(YK10)\_Camellia sinensis var. sinensis(longjing43)


Multi-Level Analysis  Single Analysis

Default Dashboard  Dot Plot  Linear Plot


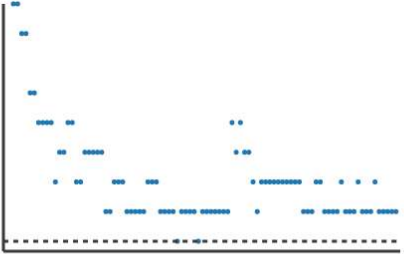
Step 3. Choose Chromosomes

Source Chromosomes: 7

Target Chromosomes: 4



Count  
Match Score  
E value



Refer to the page tutorial for online analysis, currently provides three sets of data sources

## 10.Download

Go to “Download”

Jump to section	Genome Assembly and Annotation	Transcriptome sequencing data	Resequencing raw data	1KGT Raw data	
	VCF files	Metagenome Raw Data	Pan-genome	Reference	
Genome Assembly and Annotation ^					
Transcriptome sequencing data ^					
Resequencing raw data ^					
1KGT Raw data ^					
VCF files ^					
Metagenome Raw Data ^					
Pan-genome ^					
Item	Format	Data size	Release Date	Files	Files
Pan-genome assembly	fasta	3.39GB	10/1/2022	Chashu.panGenome.gene.fasta.gz	Chashu.panGenome.gene.fasta.gz
Pan-genome annotation	gff3	164.4MB	10/1/2022	Chashu.panGenome.gene.gff3	Chashu.panGenome.gene.gff3
Pan-genome statistics	txt	8KB	10/1/2022	Tea_N50_Total_Depth_group.txt	Tea_N50_Total_Depth_group.txt

Showing 1 to 3 filtered from 3 total entries

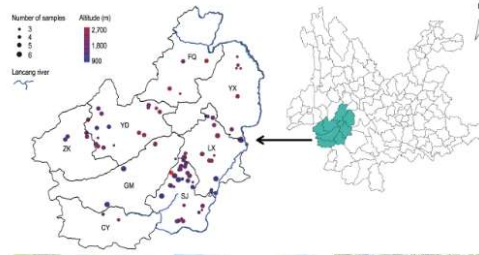
Reference ^

View the file details and click file link to download.

## 11. Additional information

### Projects

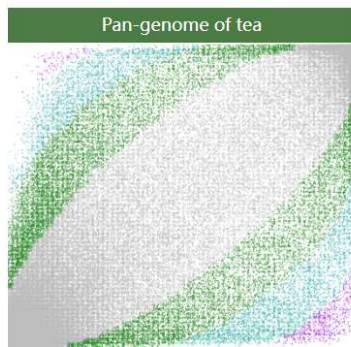
Based on the sequencing of the tea plant genome, some projects related tea genome and biological questions about tea also product massive data. We hope to use the genome sequence to diet a series of scientific issues such as the genetic diversity, origin and migration of tea trees, and the mechanism of quality formation. At present, we have included three relatively complete projects in the tea database, including tea pan-genome, research on genetic diversity of thousands of tea trees in the central region of tea origin, and research on tea soil metagenomics. This database accepts third-party complete project data related to tea genome and genetics for quick access by users. If you have data that needs to be displayed, please do not hesitate to contact us.



(1)

(2)

(3)



Pan-genome of tea



1KGT in Yunnan



Soil metagenomics of tea garden

The Project module contains three individual projects of the *Camellia*: (1) One unpublished pangenome was constructed from 206 globally representative individuals, (2) 1,350 unpublished whole genome sequences of ancient tea trees from Lincang, China, (3) and 448 soil metagenomes from the same region.

Click any one project and view the preliminary results of all three projects are summarized in three subpages. And then jump to the Download get the complete data for this module.

### Submit data

#### Submitting Data to Teabase

Teabase is a community resource dedicated to making research results broadly available. Researchers can help us meet this objective by submitting their data directly. Our curators can also help to clean up and properly present data at Teabase prior to publication. It will be helpful if you contact us before submitting your data so that we can help you through the process.

We currently accept genome assembly, germplasm, phenotype, maps and markers, and QTLs (see below). Please contact us if you have a different type of data you would like Teabase to host and we will work with you to make that happen.

#### All data types use the same spreadsheet template.

Download the Excel spreadsheet template

#### Assembly and Annotation

A total of 5 tea genome assemblies are currently included in the Teabase. If you have a genome assembly you would like to share with Teabase, please contact us and download the submission template above. You will need to fill in the worksheets describing your publication and assembly: Pub and Assembly. Tools for available assemblies are JBrowse, BLAST, Downloads, and Synteny Visualization.

#### Germplasm

Based on sequencing data, we are working with the grape research community to deal with the issue of mislabeling or incorrect pedigree documentation of tea varieties. To submit your sequenced accession(s), please fill in the datasheets describing your publication (Pub), detailed information on accessions and sequencing methods (Germplasm). 497 sequenced germplasm can be seen here.

#### Phenotypes

At present, the phenotype module in Teabase is not complete because of less data. If you have any phenotypic data to complement Teabase, please fill in the datasheets Pub and Phenotype, which describe your publication and detailed data for your traits.

#### Markers and Maps

Teabase is collecting maps for Camellia. If you have a map you would like loaded into Teabase, download the submission template above. You will need to fill in the worksheets describing your publication and map(s): Pub and Map\_description, and the worksheet describing the markers, Map\_markers. Available maps in Teabase are presented in View Genetic Maps.

#### QTL

To submit your QTL data, the current template is available at the link above. We would like to work with you to load your QTL data so that it is available online at or shortly after publication. The template asks for basic information about your publication (Pub), information about the phenotypic traits (QTL\_Traits), association analysis result (marker\_trait\_asso) and the QTL themselves (QTL\_pos).

## Publication

<b>Title</b> <input type="text" value="Title"/>	<b>Authors</b> <input type="text" value="Authors"/>	<b>Abstract</b> <input type="text" value="Abstract"/>	<b>Year</b> start <input type="text"/> - end <input type="text"/>
<input type="button" value="Submit"/>		<input type="button" value="Reset"/>	



Title	Year	Authors	Url	Resource	Operate
Inducing apoptosis of cancer cells using small-molecule plant compounds that bind to GRP78	2013	Martin S, Lamb HK, Brady C, Lefkove B, Bonner MY, Thompson P, Lovat PE, Arbiser JL, Hawkins AR, Redfern CP.	<a href="https://www.ncbi.nlm.nih.gov/pubmed/17434991">https://www.ncbi.nlm.nih.gov/pubmed/17434991</a>	PubMed	
Epigallocatechin-3-gallate prevents disruption of connective tissue in periodontium and salivary glands of rats during systemic inflammation	2018	Yelin 'ka AM, Shvaykov 'ka OO, Kostenko VO.	<a href="https://www.ncbi.nlm.nih.gov/pubmed/23807168">https://www.ncbi.nlm.nih.gov/pubmed/23807168</a>	PubMed	
Quercetin potentiates antiradical properties of epigallocatechin-3-gallate in periodontium of rats under systemic and local administration of lipopolisaccharide of salmonella typhi	2019	Yelins' ka AM, Liashenko LI, Kostenko VO.	<a href="https://www.ncbi.nlm.nih.gov/pubmed/30099426">https://www.ncbi.nlm.nih.gov/pubmed/30099426</a>	PubMed	
Adverse effects of plant food supplements and botanical preparations: a systematic review with critical evaluation of causality	2015	Di Lorenzo C, Ceschi A, Kupferschmidt H, Lude S, De Souza Nascimento E, Dos Santos A, Colombo F, Frigerio G, Narby K, Plumb J, Finglas P, Restani P.	<a href="https://www.ncbi.nlm.nih.gov/pubmed/25251944">https://www.ncbi.nlm.nih.gov/pubmed/25251944</a>	PubMed	

## External link

**The Genomics, Genetics and Breeding Resource for Cacao Improvement**

A collaboration among MARRS, USDA/ARS, IBM, NCGR, Clemson University, HudsonAlpha Institute for Biotechnology, Indiana University and Washington State University

Database: CGD  
 Full name: Cacao Genome Database  
 Webtag: Non-alcoholic crops database  
 Abstract:  
 The release of the cacao genome sequence will provide researchers with access to the latest genomic tools, enabling more efficient research and accelerating the breeding process, thereby expediting the release of superior cacao cultivars. The sequenced genotype, Matina 1-6, is representative of the genetic background most commonly found in the cacao producing countries, enabling results to be applied immediately and broadly to current commercial cultivars. Matina 1-6 is highly homozygous which greatly reduces the complexity of the sequence assembly process. While the sequence provided is a preliminary release, it already covers 92% of the genome, with approximately 35,000 genes.

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**Coffee Genome Hub**  
 a genomics and genetics resource for coffee

Database: CGH  
 Full name: Coffee Genome Hub  
 Webtag: Non-alcoholic crops database  
 Abstract:  
 The Coffee Genome Hub is an integrated web-based database providing centralized access to coffee community genomics, genetics and breeding data and analysis tools to facilitate basic, translational and applied research in coffee. Data available are the complete genome sequence of *C. canephora* along with gene structure, gene product information, metabolism, gene families, transcriptomics (ESTs, RNA-Seq), genetic markers and genetic maps. The hub provides also tools for easy querying, visualizing and downloading research data.

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**CoffeebEST**

Database: CoffeebEST  
 Full name: CoffeebEST  
 Webtag: Non-alcoholic crops database  
 Abstract:  
 A comparative analysis of the transcriptomes of *Coffea arabica* and *Coffea canephora* with a focus on fruit development using publicly available expressed sequence tags (ESTs). Most of the fruit and seed EST data has been obtained from *C. canephora*. Therefore, we performed a fruit EST analysis of the 5 developmental stages of this species (18, 22, 30, 42, and 46 weeks after flowering) comprising 29,009 sequences. We compared *C. canephora* fruit ESTs to reference unigenes of *C. canephora* (7710 contigs and 8955 singletons) and *C. arabica* (15,656 contigs and 16,351 singletons). Additional analyses included functional annotation based on Gene Ontology, as well as an annotation using PlantCyc, a curated plant protein database. The Coffee Bean EST (CoffeebEST) is a public database

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## News

[2020/9/7 Population sequencing enhances understanding of tea plant evolution](#)  
Nat Commun. 2020 Sep 7;11(1):4447. doi: 10.1038/s41467-020-18228-8.

[2020/7/6 The Reference Genome of Tea Plant and Resequencing of 81 Diverse Accessions Provide Insights into Its Genome Evolution and Adaptation](#)  
Mol Plant. 2020 Jul 6;13(7):1013-1026. doi: 10.1016/j.molp.2020.04.010. Epub 2020 Apr 27.

[2020/1/2 SMRT sequencing yields the chromosome-scale reference genome of tea tree, \*Camellia sinensis\* var. \*sinensis\*](#)  
bioRxiv. 2020 Jan 2; doi: <https://doi.org/10.1101/2020.01.02.892430>

[2020/7/24 Genome assembly of wild tea tree DASZ reveals pedigree and selection history of tea varieties](#)  
Nat Commun 11, 3719 (2020). <https://doi.org/10.1038/s41467-020-17498-6>

[2021/7/15 Haplotype-resolved genome assembly provides insights into evolutionary history of the tea plant \*Camellia sinensis\*](#)  
Nat Genet 53, 1250–1259 (2021). <https://doi.org/10.1038/s41588-021-00895-y>

[2021/5/1 Genetic basis of high aroma and stress tolerance in the oolong tea cultivar genome](#)  
Horticulture Research, Volume 8, 2021, 107, <https://doi.org/10.1038/s41438-021-00542-x>

[2021/3/19 Chromosome-level genome reference and genome editing of the tea geometrid](#)  
Molecular Ecology Resource 19 March 2021 <https://doi.org/10.1111/1755-0998.13385>

[2022/1/25 The reference genome of \*Camellia chekiangoleosa\* provides insights into \*Camellia\* evolution and tea oil biosynthesis](#)  
Horticulture Research, Volume 9, 2022, uhab083, <https://doi.org/10.1093/hr/uhab083>

[2019/7/15 The tea plant reference genome and improved gene annotation using long-read and paired-end sequencing data](#)  
Sci Data 6, 122 (2019). <https://doi.org/10.1038/s41597-019-0127-1>

## About us

<a href="#">Jump to section</a>	<a href="#">Global Tea Genome Project</a>	<a href="#">Funding</a>	<a href="#">Principal Investigators</a>	<a href="#">Visiting statistics</a>	<a href="#">Contact us</a>
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### [Global Tea Genome Project](#)

For thousands of years, tea, this kind of oriental magical leaf, has been famous all over the world. The application and dissemination of tea is a model of the harmonious and sustainable development of man and plant. In the past two decades, the development of genomics technology has allowed us to explore the characteristics of plants and the course of their domestication from the perspective of heredity and genes. Yunnan is the region with the richest tea resources and is also considered the center of the origin of tea. Based on the protection, development, utilization of tea resources, and the responsibility for the sustainable development of tea, in the past ten years, our team has been committed to the research on the diversity and genome of tea genetic resources, and together with domestic and foreign counterparts, we have achieved a lot in tea genomes. However, the origin of global tea and the process of domestication of tea are still not fully understood. Here, we have completed the sequencing of thousands of tea genetic resources, especially the genome analysis of important tea resources around the world. These massive amounts of data are not only important for us to understand the origin and domestication of tea, but also for the breeding and protection of tea resources. This database not only includes the above-mentioned genomic information, but also information about tea and its related species. We hope that this database can become an important comprehensive database in the field of tea research.

### [Funding](#)

Yunnan provincial key programs of Yunnan Eco-friendly Food International Cooperation Research Center project under grant 2019ZG00908  
Yunnan Provincial Department of Science and Technology Biological Resources Digital Development and Application Project Number 202002AA100007

### [Principal Investigators](#)



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### [Visiting statistics](#)



30 visits  
REVOLVERMAPS

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