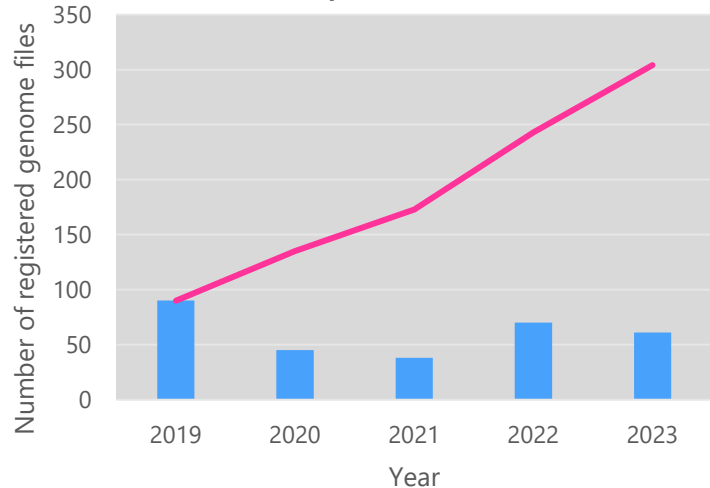
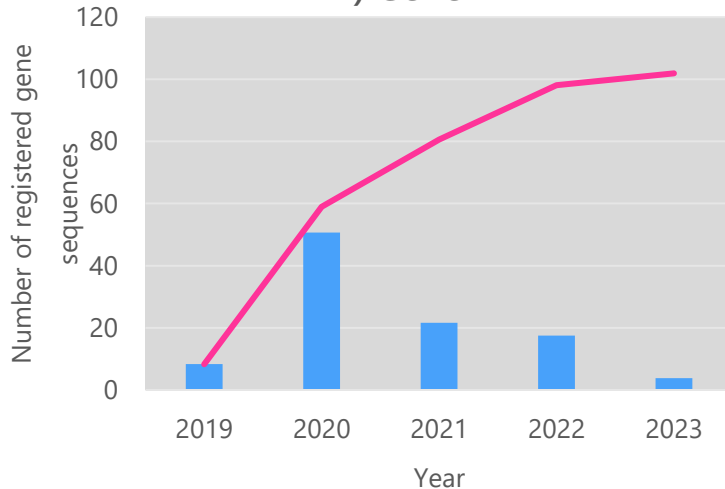
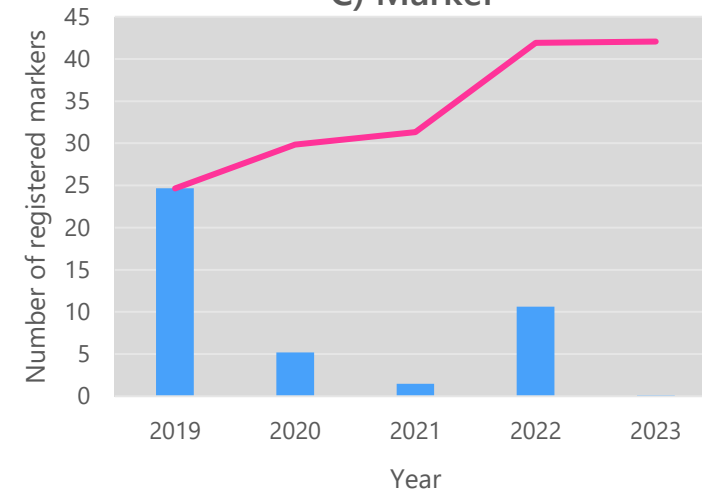
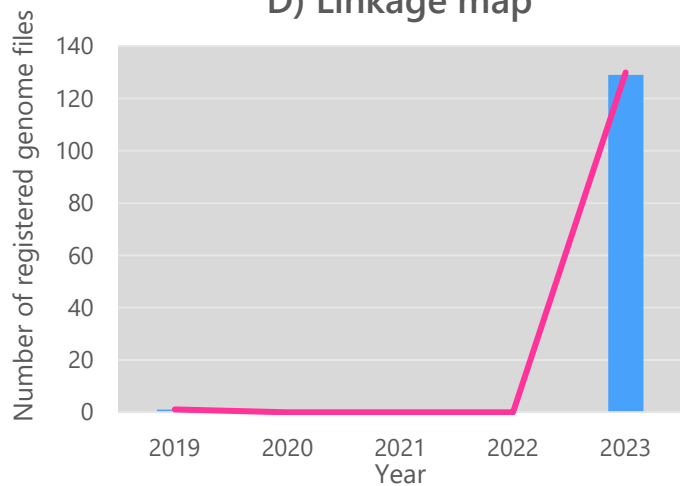
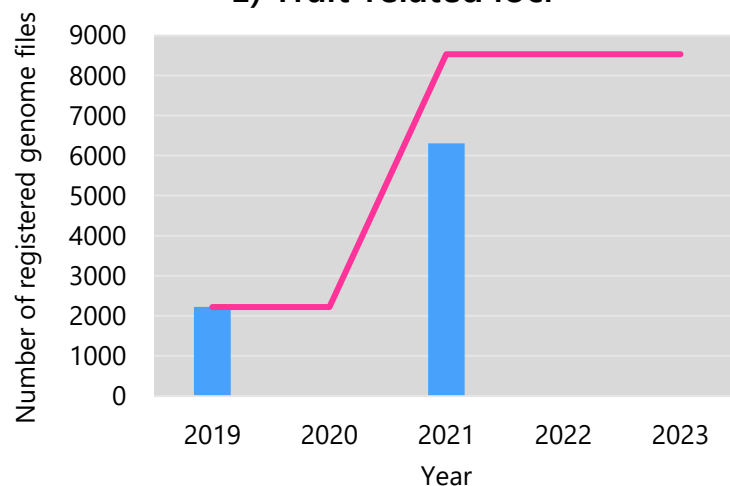


Supplementary Fig. S1.

Structure of *pages*, the developed keyword search system. Blue and green boxes indicate external and developed search systems, respectively. Gray boxes indicate contents developed for the keyword search.

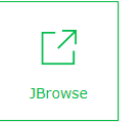
A) Genome**B) Gene****C) Marker****D) Linkage map****E) Trait-related loci****Supplementary Fig. S2.**

Numbers of registered data in Plant GARDEN since 2019. The data is as of March every year. A) genome files, B) gene sequences, C) Marker. D) linkage map, E) trait related loci.

Blue bars and pink lines indicate the annual registration number and cumulative number, respectively.

Lotus japonicus

Sequence Name : Lj3.0



Details of the Assembled Genome Sequences

Sequence Name	Lj3.0	Biological Sample	Miyakojima MG-20
Number of Sequences	9	Number of Chromosomes	2n = 2x = 12
Total Length (bp)	447,416,816	N50 Length (bp)	62,285,374
Number of Genes	48,105	Number of Genes Source File	Lj3.0_pep.fna
Number of Genes Annotated by Hayai-annotation	48,105	Hayai-Annotation Version	zen_v2.0
Sequencing Method	Sanger, Illumina, 454	Read Depth	35x
Assembly Method	Paracel Genome Assembler	Estimated Genome Size (Mb)	465
Sequencing Method Comments		Comments	
DOI/PMID	10.1093/dnares/dsn008	Corresponding author	Satoshi TABATA (Kazusa DNA Research Institute)
Data Source	Lotus japonicus Genome Sequencing Project	Data Source URL	http://www.kazusa.or.jp/lotus/
BUSCO Version	5.1.0	BUSCO Dataset	embryophyta_odb10
BUSCO Genome	C:93.5%[S:86.9%,D:6.6%],F:3.7%,M:2.8%,n:1614	BUSCO Gene (pep/cds)	C:79.8%[S:59.5%,D:20.3%],F:11.9%,M:8.3%,n:1614

Supplementary Fig. S3.

A screen view of the assembled stats table on a genome sequence page of Lj3.0 in *Lotus japonicus*. We performed a test of the quality of the assembled genome and gene sequences by using BUSCOs.

A)

Lotus japonicus

Assembly Name:Lj3.0

Gene File:Lj3.0_pep.fna.gz



Detail of the Gene Sequence

Position on the Genome	Gene Name	CDS	Lj3g3v0303780.2
		PEP	Lj3g3v0303780.2
Position on the Genome	Chromosome	Lj3.0_chr3	
	Start Position	2207888	
	End Position	2214202	
	Strand	+	
Annotation (Hayai Annotation ZEN)	KusakiDB	KusakiDB Accession	KPRO00028977
		KusakiDB version	2
		Evidence is present	Yes
		Databases intersection (the sequence exists in multiple databases)	orthodb-refseq-uniprot
OrthoDB	Database version	10.1	
	Description	Protein kinase domain	
	Gene ID	3885_0:00328b	
	Ortholog group unique ID	28179at33090	
Functional annotation	Source DB	refseq	
	Protein name	inactive protein kinase SELMODRAFT_444075-like	
	Accession	XP_027344439 Details	
	CrossRef Refseq from UniProt	NA	
	EC	NA	
	KEGG entry	NA	
	KO ID	NA	
	Pfam ID	PF00069	
	Pfam Description	Details	
	InterPro ID	IPR000719	
	InterPro Description	Details	

B)

Annotation Details

ID	Group/Do...	Name	Link
Source Annotation (1 item)			
<input type="checkbox"/> XP_027344439		inactive protein kinase SELMODRAFT_444075-like	UniProt
OrthoDB (1 item)			
<input type="checkbox"/> 3885_0:00328b	28179at33090	Protein kinase domain	OrthoDB(SIB)
Pfam (1 item)			
<input type="checkbox"/> PF00069		Protein kinase domain	Pfam
InterPro (1 item)			
<input type="checkbox"/> IPR000719		Protein kinase domain	InterPro(EBI)
Gene ontology (3 items)			
<input type="checkbox"/> GO:0004672	MF	protein kinase activity	QuickGO(EBI)
<input type="checkbox"/> GO:0005524	MF	ATP binding	QuickGO(EBI)
<input type="checkbox"/> GO:0006468	BP	protein phosphorylation	QuickGO(EBI)
GO slim (5 items)			
<input type="checkbox"/> GO:0006793	BP	phosphorus metabolic process	QuickGO(EBI)
<input type="checkbox"/> GO:0006464	BP	cellular protein modification process	QuickGO(EBI)
<input type="checkbox"/> GO:0000166	MF	nucleotide binding	QuickGO(EBI)
<input type="checkbox"/> GO:0043167	MF	ion binding	QuickGO(EBI)
<input type="checkbox"/> GO:0016740	MF	transferase activity	QuickGO(EBI)

Search Checked ID

Supplementary Fig. S4.

A screen view of the functional annotation in a gene sequence page, Lj3g3v0303780.2, on the Lj3.0 genome. Re-annotation of all genes registered in Plant GARDEN was performed by our group using Hayai-Annotation. A) A main gene table. B) A detailed table of the functional annotations displayed below the main table. The IDs shown in the detailed annotations table are linked to the external database.

A)



Lotus japonicus

ID	Population Name	Line List	Variant Type	Reference Sequence	Sequence Type	Variant Counts	Data Source	Comments	Download		TASUKE+	JBrowse
									Table	Vcf file		
t34305.SNP000001	Lotus_japonicus_SRA_9_lines_20191022		SNPs, In/dels	Lj3.0	WGS	354,881	Plant GARDEN	Bwa/bcftools 1.9, (QUAL≥200, 10≤DP≤200, max-missing=0.7)				



B)



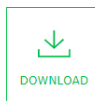
Lotus japonicus

Bio Sample	Sequence Name	Accession	JBrowse	gVCF	Comment
Gifu B129	SRA799662	SRX4941819			
Miyakojima MG-20	DRA001236	DRX013250			
Miyakojima MG-20	DRA001236	DRX013249			
Miyakojima MG-20 (EMS-mutagenised)	SRA188542	SRX729747			
Miyakojima MG-20 (EMS-mutagenised)	SRA188542	SRX719550			
nrsym1-2	DRA005940	DRX090748			
nrsym1-2	DRA005940	DRX090747			

Supplementary Fig. S5.

A screen view of base variant lists in *L. japonicus*. A) A vcf file list on the “Find Variants” page. The conditions of the variant call are described in the comments file. A vcf and a text table, which show the variant bases with the letters A, G, T, and C, are available for download. The variant positions are displayed on the two browsers, TASUKE+ and JBrowse. B) A list of gvcf files and SRAs. The list is displayed by clicking the Line list button in the vcf file list.

A)

TOP > Species list > *Vitis vinifera* > Search by Marker Type*Vitis vinifera*

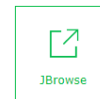
1 2 3 4 5 ... ▶

Number of Hit Markers : 487

1-50 件表示 ▼

Marker ID ↓	Marker Name ↓	Type ↓	Fw Primer Start Position		
			Reference Genome ↓	Chromosome ↓	Start Position ↓
t29760.M000373.1	FAM79	SSR	12X	1	579169
t29760.M000443.1	VChr1a	SSR	12X	1	2819297
t29760.M000012.1	vmc8A7	SSR	12X	1	3423317
t29760.M000171.1	scu04vv	SSR	12X	1	4261254
t29760.M000342.1	FAM47	SSR	12X	1	5326620
t29760.M000445.1	VChr1c	SSR	12X	1	11408586
t29760.M000444.1	VChr1b	SSR	12X	1	11457785
t29760.M000380.1	FAM86	SSR	12X	1	11610088
t29760.M000433.1	FAM141	SSR	12X	1	16536955
t29760.M000469.1	VChr13b	SSR	12X	13_random	2689217
t29760.M000402.1	FAM108	SSR	12X	2	1574031
t29760.M000447.1	VChr2b	SSR	12X	2	3888472

B)

Vitis vinifera

Marker ID	t29760.M000443.1	
Marker Name	VChr1a	
Type	SSR	
Position on the Genome	Reference Genome	12X
	Chromosome	1
	Fw Primer	TTCATACCTTGCAGGGAGCTA
	Start Position	2819297
	End Position	2819317
	Rv Primer	TGATTTCCATTCCCAAATTCA
	Start Position	2819515
End Position	2819495	
Target Sequences	NA	
Allele [Sample Name]	7 [Chardonnay VCR 4]; 7 [Merlot VCR 494]; 7 [PN40024]	
Restriction Enzyme	NA	
Comment		
DOI	10.1186/1471-2229-8-127	
PubMed	19087321	

Supplementary Fig. S6.

A screen view of the PCR-based DNA marker lists. A) A partial view of the DNA marker list in *Vitis vinifera*. Marker names, types, and positions on the reference genome and the name of the reference genome are shown. B) The detailed information of the selected marker. The table is shown by clicking the marker ID in the marker list. The marker name, type, primer or target sequences and their positions on the genome, and source manuscript information are available. Allele information was derived from the source manuscript by manual curation. The restriction enzyme is for CAPS or dCAPS markers.



B) *Brassica rapa*

Results : 642 Hit(s)

Trait ↓	Category ↓	Nearest Marker 1	Nearest Marker 2	Trait / Analysis Method / Population Name / Population Type			Other Data	Locus ID ↓
		Reference Genome ↓	Nearest Marker 1 ↓	Chromosome ↓	Start Position ↓	End Position ↓		
Bolting time	Morphology/Growth	BrapaV3.0	cnu_m616a	A02	721260	721528	t3711.T000124	
Bolting time	Morphology/Growth	BrapaV3.0	cnu_m335a	A08	19606371	19606574	t3711.T000125	
Bolting time	Morphology/Growth	BrapaV3.0	cnu_m372a	A09	34123484	34123659	t3711.T000126	
Bolting time	Morphology/Growth	BrapaV3.0	ACMP00598	A10	15798743	15799010	t3711.T000127	
Bolting time	Morphology/Growth	BrapaV3.0	cnu_m056a	A07	26030383	26030580	t3711.T000128	
Bolting time	Morphology/Growth	BrapaV3.0	SNP-CKX3a	A02	6286170	6286372	t3711.T000131	
Bolting time	Morphology/Growth	BrapaV3.0	cnu_m288a	A03	9986707	9986860	t3711.T000132	

C)

Locus ID	t3711.T000124	
Locus Name	qDB1	
Trait	Bolting time G+	
Trait Category	[4]Morphology/Growth	
Analysis Method	QTL analysis	
Population Name	CRF3	
Population Type	F2:3	
Position on the Genome	Reference Genome	BrapaV3.0
	Nearest Marker 1	cnu_m616a G+
Chromosome	A02	
Start Position	721260	
End Position	721528	
Nearest Marker 2	At5g12290 G+	
Chromosome	NA	
Start Position	0	
End Position	0	
Position(cM)	Linkage Group	CRF3 ChrA02
	LOD Peak Position(cM)	0
Max LOD	4.8	
P Value		
DOI/PMID	10.1093/dnares/dss029	
Comment	Chifu 401-42:long flowering time after vernalization, high plant height, large leaf, many seeds per siliqua, better seed weight; RCB:rapid cycling, short flowering time after vernalization, low plant height, small leaf, low seeds per siliqua, lower seed weight	

Supplementary Fig. S7.

A screen view of trait-related loci lists in *Brassica rapa*. A) Graphical view of registered locus positions of the reference genome. B) A part of the list of the registered trait-related loci. The displayed information is changed by selecting the tabs. C) The detailed information of the selected locus. The table is shown by clicking the locus ID in the trait-related loci list. The locus name, trait name, trait category, analysis method, population name, population type, position on the genome estimated via nearest markers, position on the linkage map (if available in the source manuscript), and source manuscript are shown in the table.

A)

Plant GARDEN

TOP > Run BLAST

Search by Sequence
BLAST

Select BLAST program

- BLASTN (Search for nucleotide sequence against nucleotide sequences)
- BLASTP (Search for protein sequence against protein sequences)
- BLASTX (Search for nucleotide sequence against protein sequences)
- TBLASTN (Search for protein sequence against translated nucleotide sequences)
- TBLASTX (Search for translated nucleotide sequence against translated nucleotide sequences)

Select reference sequences

Plant Species(example:Tomato)

- Acer_truncatum:version2_pep
- Actinidia_chinensis:female_of_cv.Hong_Yang:v3.0_update_pep
- Actinidia_chinensis_Red5_PS1_1.69.0_pep
- Actinidia_eriantha_t165200.G001_pep
- Aegilops_tauschii_Aet_v4.0_pep

Select All

Clear

Enter sequence to search
FASTA Format

Recognize by OCR

Convert

Sequence Input

Enter sequence to search

Number of Search Results to Display
(optional)

Search results MAX

500

Sequence alignments MAX

250

Other Settings
(optional)

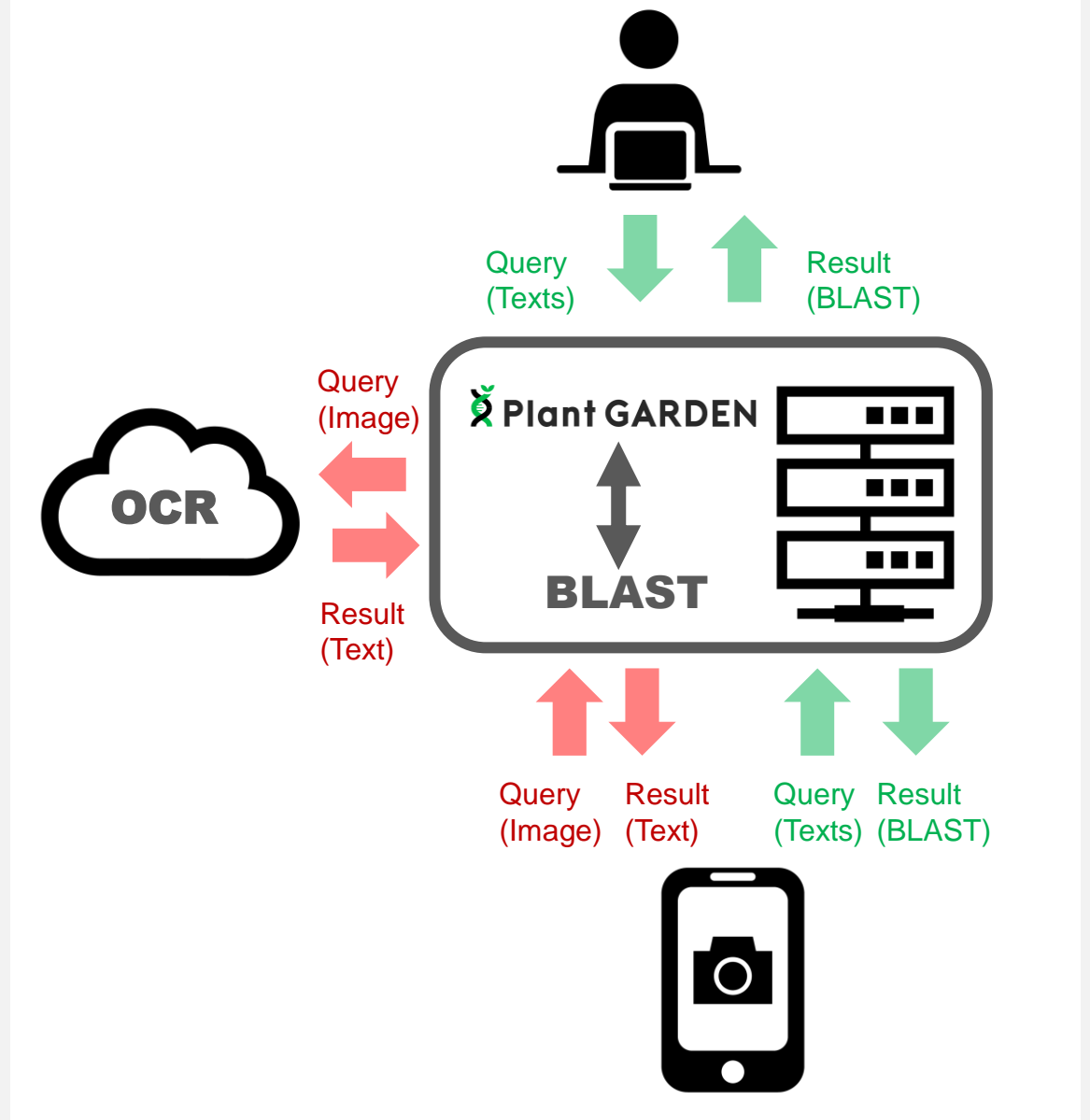
- Filtering of Query Sequences (DUST for BLASTN, SEG for others)
- Do not perform gap alignment

E-value

0.1

Submit

B)



Supplementary Fig. S8.

BLAST analysis in Plant GARDEN. A) A screen view of BLAST analysis in the tablet version. B) The data flow of BLAST analysis in Plant GARDEN with the PC and tablet versions. Red and green represent the flow of OCR and BLAST, respectively.