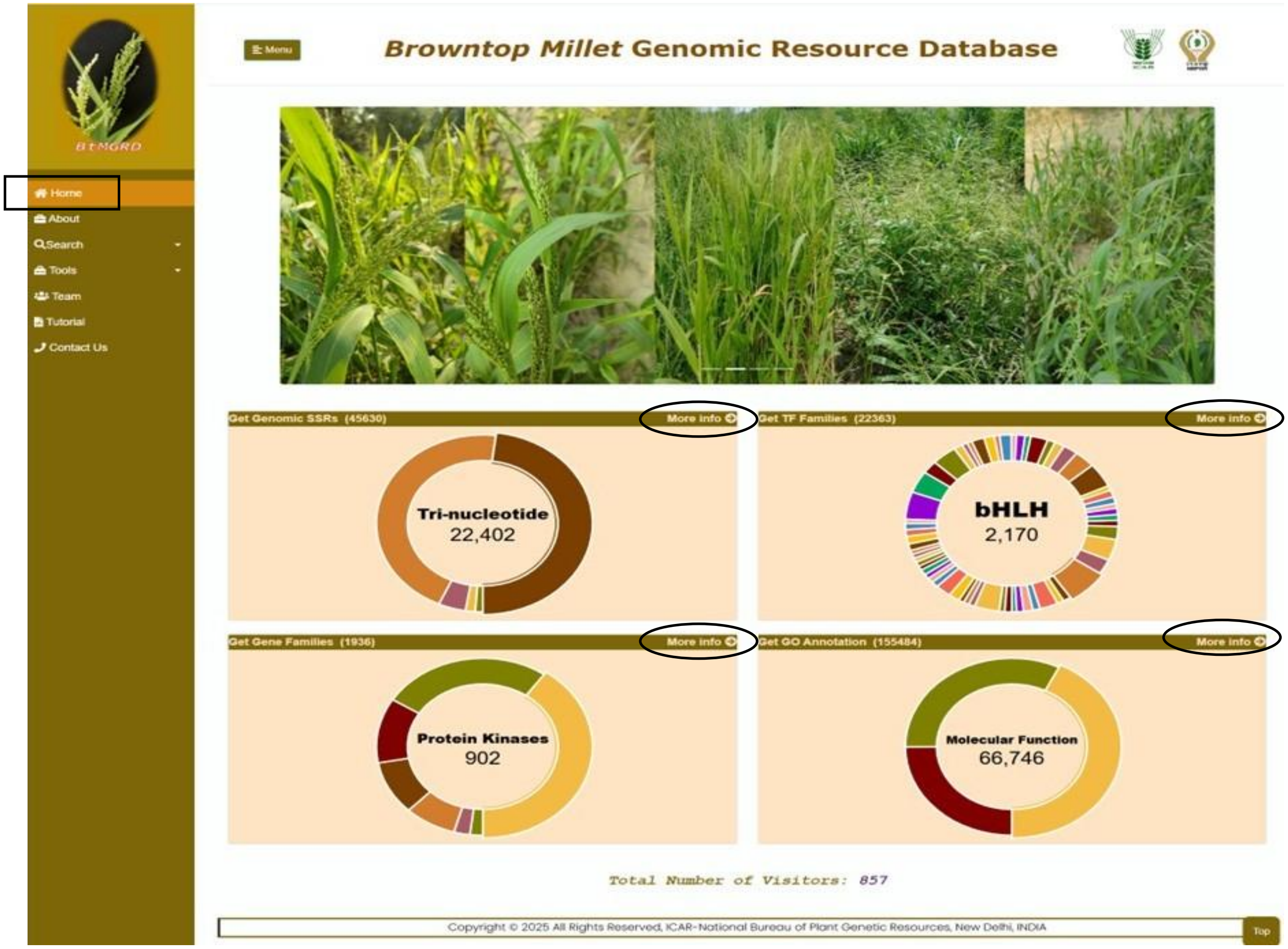
Tutorials of Browntop Millet Genomic Resource Database

1. **Home:** The Home page provides an overview of the **Browntop Millet Genomic Resource Database**. It highlights key features, quick access to tools, visitor count, and statistical summaries of the genomic data resources available.



Total Number of Visitors: 857

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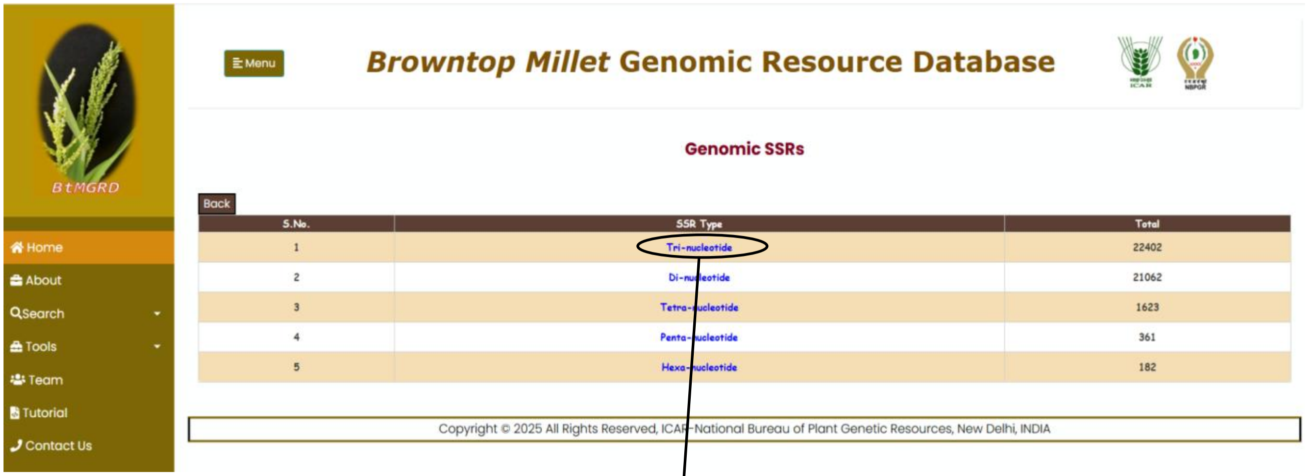
User can get information about Genomic SSRs, Transcription Factors, Gene Families, and Gene Ontology annotation of the genes predicted in *Brachiaria ramosa* genome by clicking on the More info tag or circular diagrams of that category.

- By clicking on "More info" tag, under Get Genomic SSRs block, user will get all SSR categories information with the number details.



Browntop Millet Genomic Resource Database

Genomic SSRs

S.No.	SSR Type	Total
1	Tri-nucleotide	22402
2	Di-nucleotide	21062
3	Tetra-nucleotide	1623
4	Penta-nucleotide	361
5	Hexa-nucleotide	182

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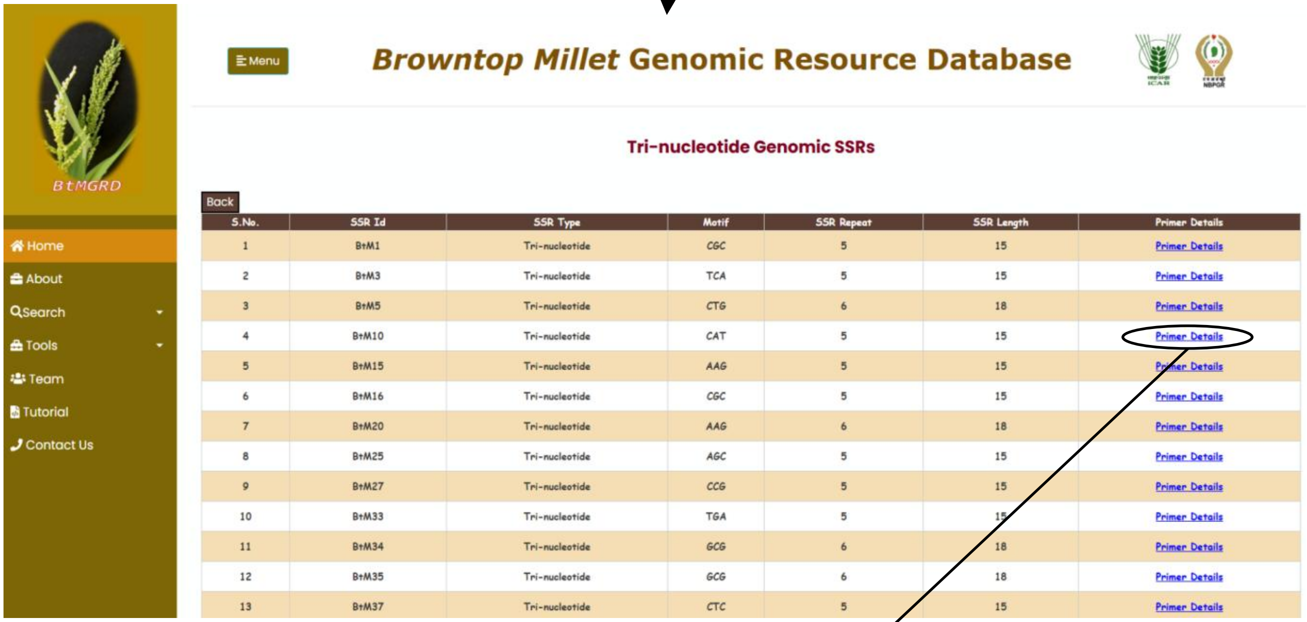
By clicking on particular category link, user will get list of SSRs predicted in that particular category with the link to get their primers details. User can also get the similar details by clicking on that SSR categories displayed on the circular diagram. eg. Tri-Nucleotide

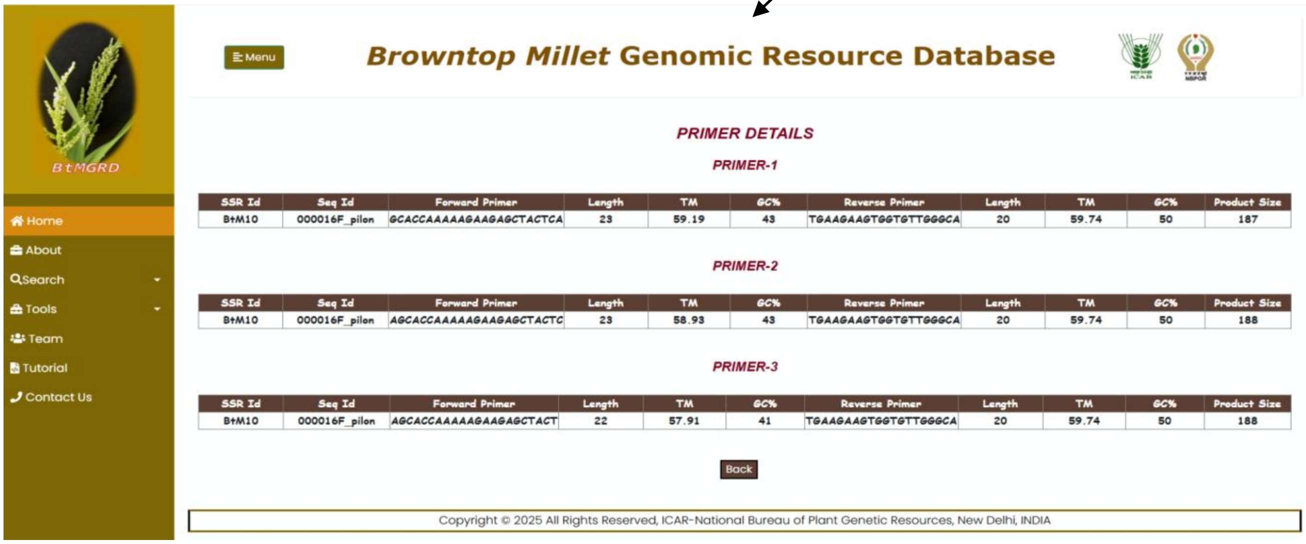


Browntop Millet Genomic Resource Database

Tri-nucleotide Genomic SSRs

S.No.	SSR Id	SSR Type	Motif	SSR Repeat	SSR Length	Primer Details
1	BtM1	Tri-nucleotide	CGC	5	15	Primer Details
2	BtM3	Tri-nucleotide	TCA	5	15	Primer Details
3	BtM5	Tri-nucleotide	CTG	6	18	Primer Details
4	BtM10	Tri-nucleotide	CAT	5	15	Primer Details
5	BtM15	Tri-nucleotide	AAG	5	15	Primer Details
6	BtM16	Tri-nucleotide	CGC	5	15	Primer Details
7	BtM20	Tri-nucleotide	AAG	6	18	Primer Details
8	BtM25	Tri-nucleotide	AGC	5	15	Primer Details
9	BtM27	Tri-nucleotide	CCG	5	15	Primer Details
10	BtM33	Tri-nucleotide	TGA	5	15	Primer Details
11	BtM34	Tri-nucleotide	GCG	6	18	Primer Details
12	BtM35	Tri-nucleotide	GCG	6	18	Primer Details
13	BtM37	Tri-nucleotide	CTC	5	15	Primer Details

By clicking on the Primer Details link, it will give three primer pair information of selected genomic SSR.



Browntop Millet Genomic Resource Database

PRIMER DETAILS

PRIMER-1

SSR Id	Seq Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
BtM10	000016F_pilon	GCACCAAAAAGAAGAGCTACTCA	23	59.19	43	TGAAGAAGTGGTGTTGGGCA	20	59.74	50	187

PRIMER-2

SSR Id	Seq Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
BtM10	000016F_pilon	AGCACCAAAAAGAAGAGCTACTC	23	58.93	43	TGAAGAAGTGGTGTTGGGCA	20	59.74	50	188

PRIMER-3

SSR Id	Seq Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
BtM10	000016F_pilon	AGCACCAAAAAGAAGAGCTACT	22	57.91	41	TGAAGAAGTGGTGTTGGGCA	20	59.74	50	188

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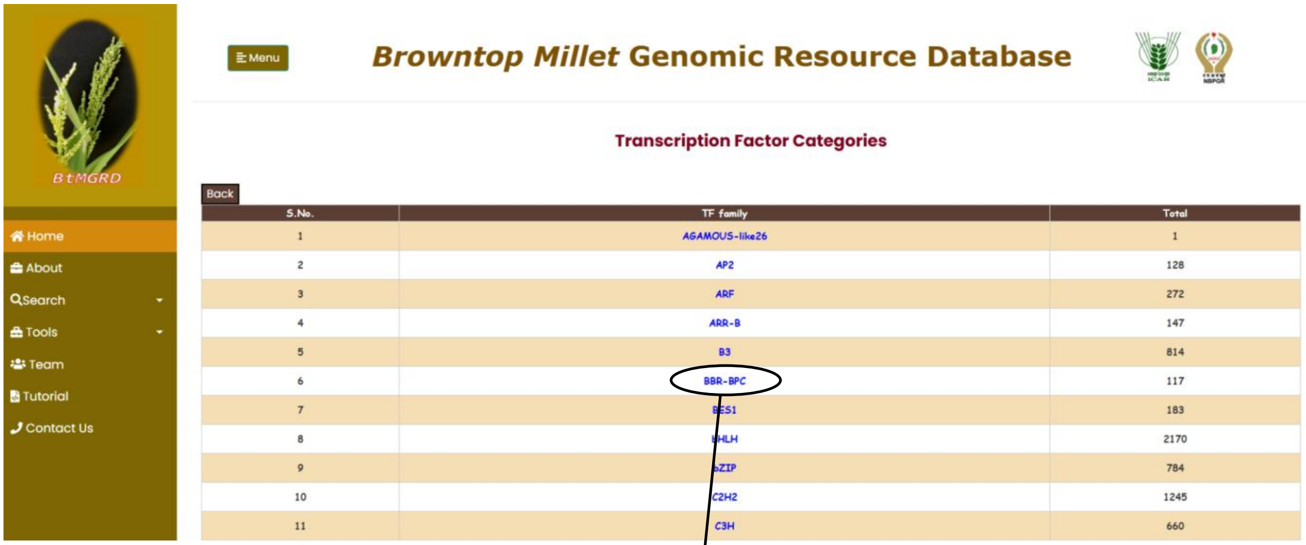
- By clicking on “More info” tag, under Get TF Families block, user will get all TF categories information with the number details.

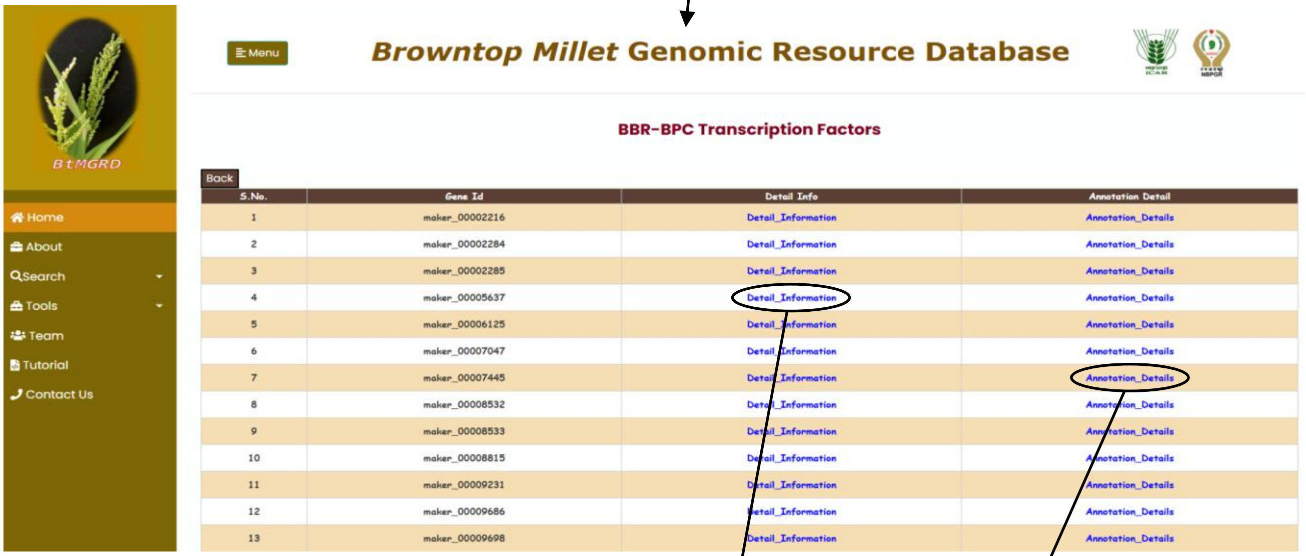


Browntop Millet Genomic Resource Database

Transcription Factor Categories

S.No.	TF family	Total
1	AGAMOUS-like26	1
2	AP2	128
3	ARF	272
4	ARR-B	147
5	B3	814
6	BBR-BPC	117
7	BES1	183
8	bHLH	2170
9	bZIP	784
10	C2H2	1245
11	C3H	660

By clicking on particular category link, user will get list of TFs in that particular category. User can also get the similar details by clicking on that TF category displayed on the circular diagram. eg. BBR-BPC

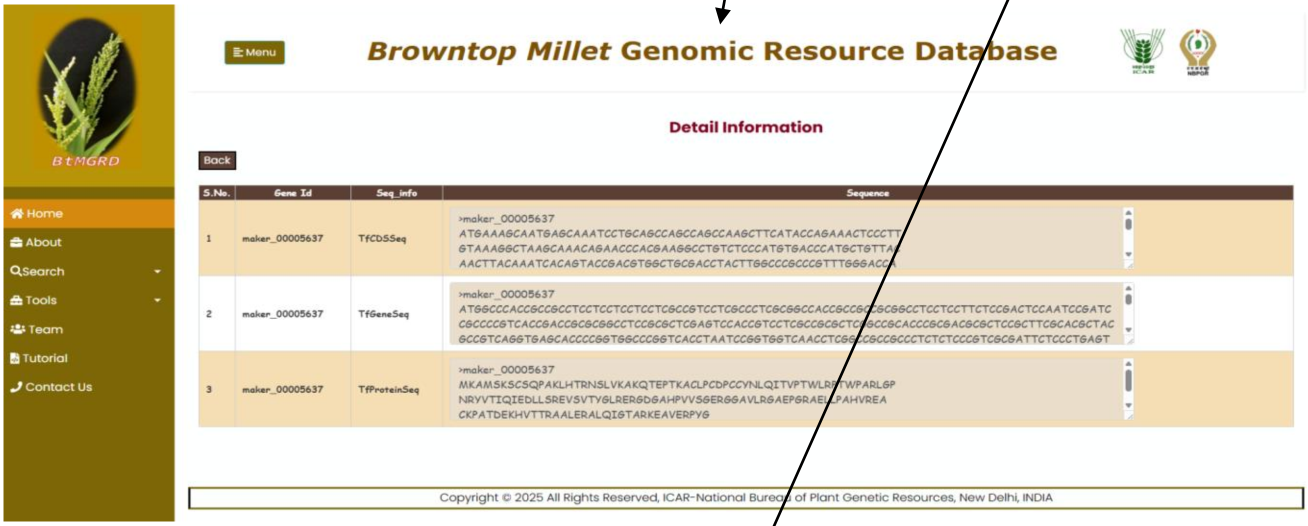


Browntop Millet Genomic Resource Database

BBR-BPC Transcription Factors

S.No.	Gene Id	Detail Info	Annotation Detail
1	maker_00002216	Detail_Information	Annotation_Details
2	maker_00002284	Detail_Information	Annotation_Details
3	maker_00002285	Detail_Information	Annotation_Details
4	maker_00005637	Detail_Information	Annotation_Details
5	maker_00006125	Detail_Information	Annotation_Details
6	maker_00007047	Detail_Information	Annotation_Details
7	maker_00007445	Detail_Information	Annotation_Details
8	maker_00008532	Detail_Information	Annotation_Details
9	maker_00008533	Detail_Information	Annotation_Details
10	maker_00008815	Detail_Information	Annotation_Details
11	maker_00009231	Detail_Information	Annotation_Details
12	maker_00009686	Detail_Information	Annotation_Details
13	maker_00009698	Detail_Information	Annotation_Details

By clicking on the Detail_Information link, it will give protein, CDS, and gene sequences of selected TF.

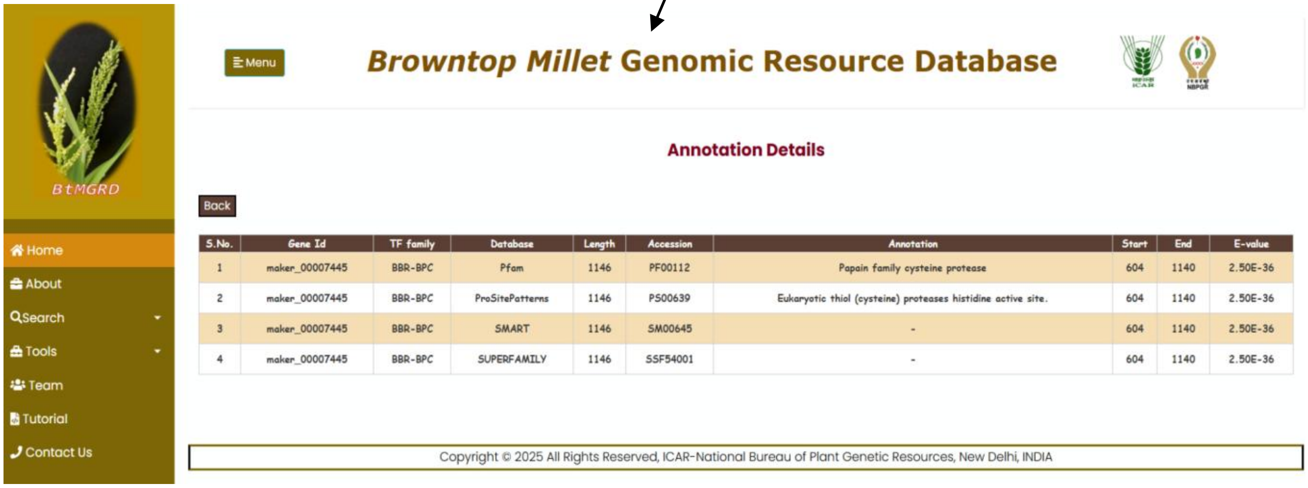


Browntop Millet Genomic Resource Database

Detail Information

S.No.	Gene Id	Seq_info	Sequence
1	maker_00005637	TfCDSSeq	>maker_00005637 ATGAAAGCAATGAGCAAATCCTGCAGCCAGCCAGCCAAGCTTCATACCAGAAACTCCCTT GTAAAGGCTAAGCAAACAGAACCCACGAAGGCCTGTCTCCCATGTGACCCATGCTGTTAC AACTTACAAATCACAGTACCGACGTGGCTGCGACCTACTTGGCCCGCCCGTTTGGGACCA
2	maker_00005637	TfGeneSeq	>maker_00005637 ATGGCCCACCGCCGCCTCCTCCTCCTCCTCGCCGTCCTCGCCCTCGCGGCCACCGCCGCCGCGGCCTCCTCCTTCTCCGACTCCAATCCGATC CGCCCCGTCACCGACCGCGCGGCCTCCGCGCTCGAGTCCACCGTCCTCGCCGCGCTCGGCCGCACCCGCGACGCGCTCCGCTTCGCACGCTAC GCCGTCAGGTGAGCACCCCGGTGGCCCGGTCACCTAATCCGGTGGTCAACCTCGGCCGCCGCCCTCTCTCCCGTCGCGATTCTCCCTGAGT
3	maker_00005637	TfProteinSeq	>maker_00005637 MKAMSKSCSQPAKLHTRNSLVKAKQTEPTKACLPCDPCCYNLQITVPTWLRPTWPARLGP NRYVTIQIEDLLSREVSVTYGLRERGDGAHPVVSGERGGAVLRGAEPGRAELLPAHVREA CKPATDEKHVTTRAALERALQIGTARKEAVERPYG

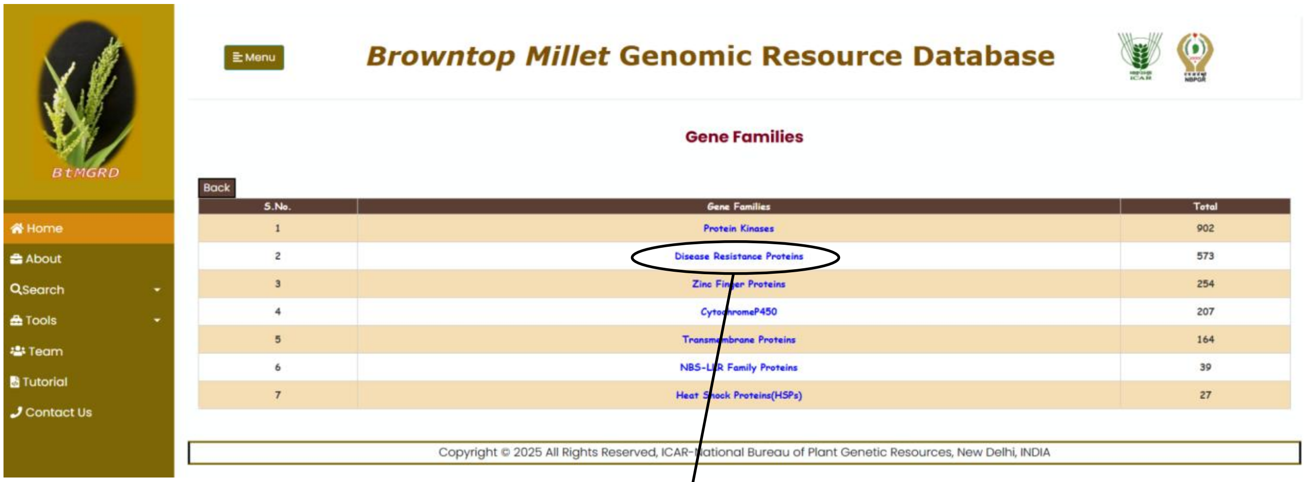
By clicking on the Annotation_Details link, user will get annotation information of selected TF with InterProScan databases.



Annotation Details

S.No.	Gene Id	TF family	Database	Length	Accession	Annotation	Start	End	E-value
1	maker_00007445	BBR-BPC	Pfam	1146	PF00112	Papain family cysteine protease	604	1140	2.50E-36
2	maker_00007445	BBR-BPC	ProSitePatterns	1146	PS00639	Eukaryotic thiol (cysteine) proteases histidine active site.	604	1140	2.50E-36
3	maker_00007445	BBR-BPC	SMART	1146	SM00645	-	604	1140	2.50E-36
4	maker_00007445	BBR-BPC	SUPERFAMILY	1146	SSF54001	-	604	1140	2.50E-36

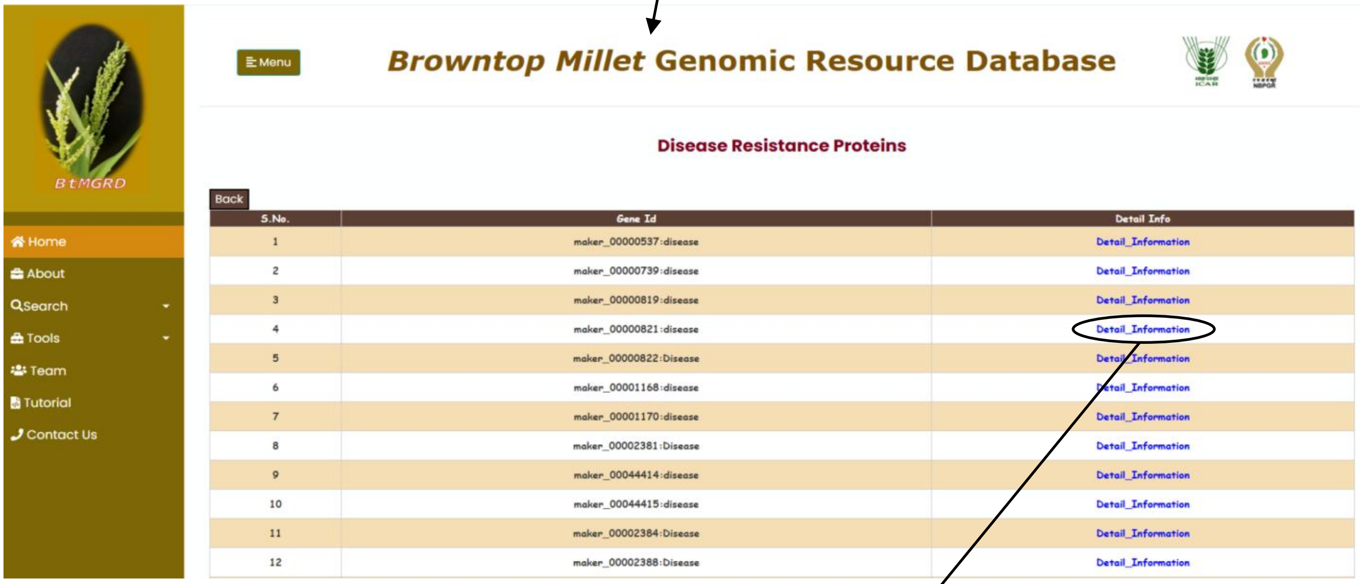
- By clicking on "More info" tag, under Get Gene Families block, user will get important gene families information with the number details.



Gene Families

S.No.	Gene Families	Total
1	Protein Kinases	902
2	Disease Resistance Proteins	573
3	Zinc Finger Proteins	254
4	CytochromeP450	207
5	Transmembrane Proteins	164
6	NBS-LRR Family Proteins	39
7	Heat Shock Proteins(HSPs)	27

By clicking on the selected gene family link, user will get list of genes belongs to this category. User can also get the similar details by clicking on that gene families displayed on the circular diagram. eg. Disease Resistance Proteins



Disease Resistance Proteins

S.No.	Gene Id	Detail Info
1	maker_00000537:disease	Detail_Information
2	maker_00000739:disease	Detail_Information
3	maker_00000819:disease	Detail_Information
4	maker_00000821:disease	Detail_Information
5	maker_00000822:Disease	Detail_Information
6	maker_00001168:disease	Detail_Information
7	maker_00001170:disease	Detail_Information
8	maker_00002381:Disease	Detail_Information
9	maker_00044414:disease	Detail_Information
10	maker_00044415:disease	Detail_Information
11	maker_00002384:Disease	Detail_Information
12	maker_00002388:Disease	Detail_Information

By clicking on the Detail_Information link, user will get protein sequence information of that gene.

Browntop Millet Genomic Resource Database

Detail Information

S.No.	Gene Id	Gene Family	Sequence
1	maker_00000821:disease	Disease Resistance Proteins	>maker_00000821:disease MQCFVFNNLRNRYFVIIDDIWSTQSWKDIQCAFPQDKNASRIMTTTRIHGVAESCCFPNNIYVVPMKPLDNDDSKRLFMKRTFGHED DCPLELQEITDDIVRKCDGLPLALVNIASLLATKQPSRKEWEGVHKSIGSTLEQDQELGVVKGILFLSYYDLPYYLKICLLDLSIFPEDHQID RLRLIRRWMAEGLIIEQQGRSLEDTGESYISELINKNMIQPVGIDYSGRPACRVHNIMLDLIVLLSTKENFATILGNQKLTPSAHKIRRL

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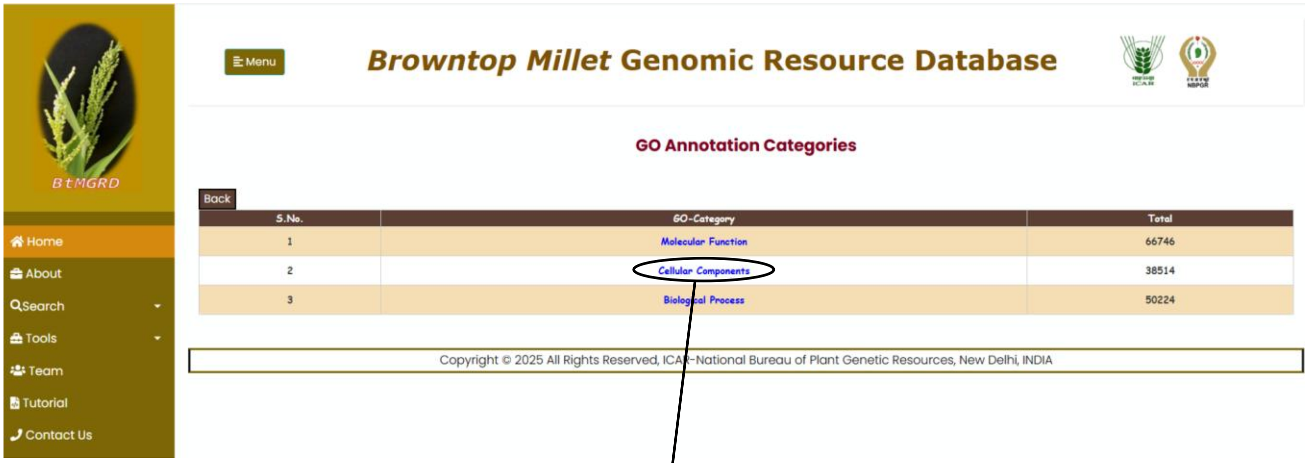
❖ By clicking on "More info" tag, under Get GO Annotation block, user will get three categories information with the number details.



Browntop Millet Genomic Resource Database

GO Annotation Categories

S.No.	GO-Category	Total
1	Molecular Function	66746
2	Cellular Components	38514
3	Biological Process	50224

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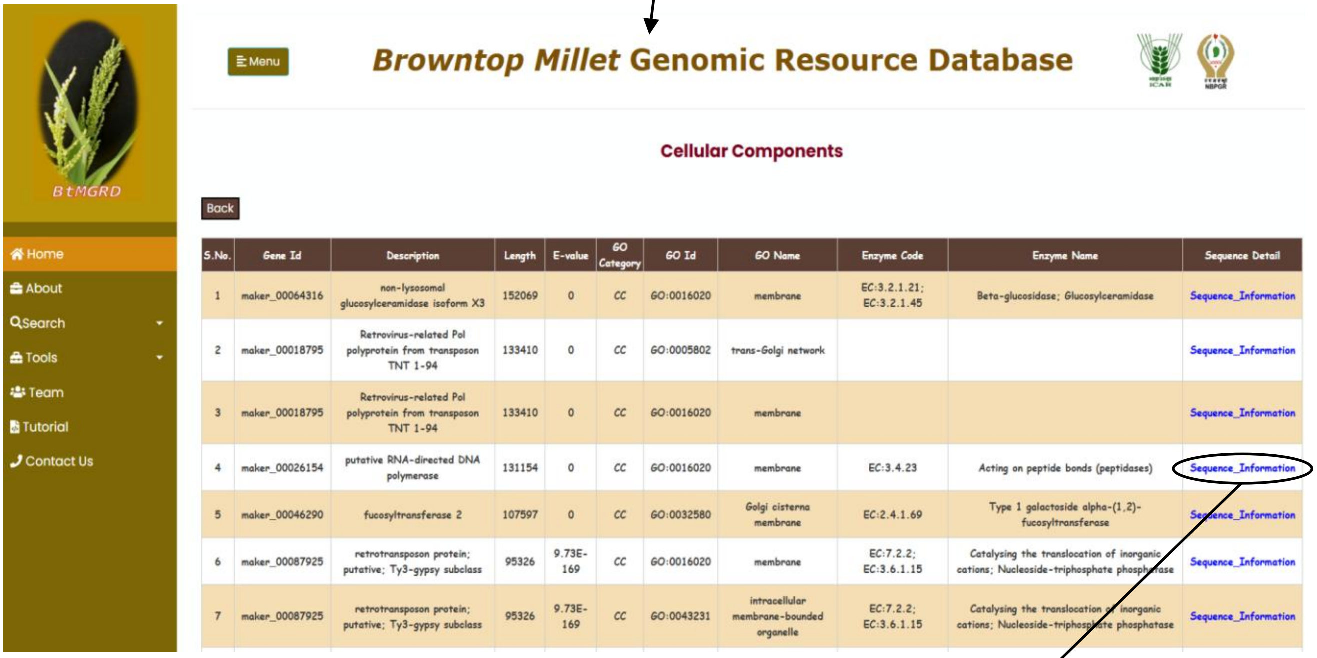
By clicking on the selected category link, user will get list of annotated gene information of this category. User can also get the similar details by clicking on that GO categories displayed on the circular diagram. eg. Cellular Components

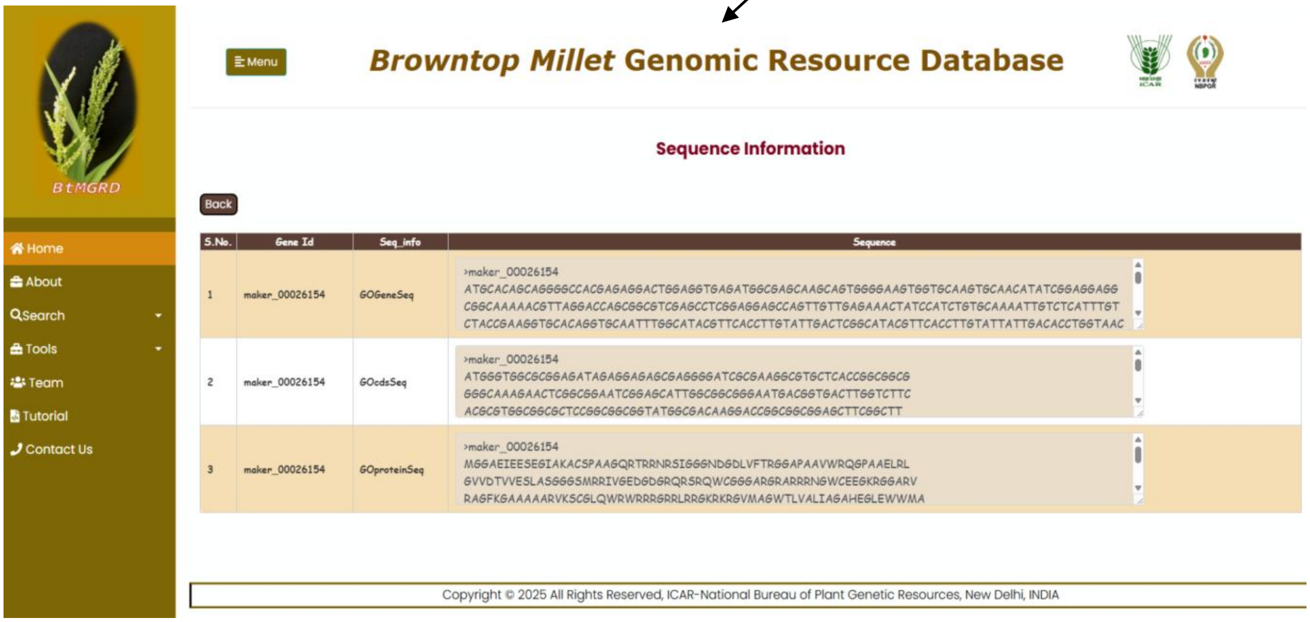


Browntop Millet Genomic Resource Database

Cellular Components

S.No.	Gene Id	Description	Length	E-value	GO Category	GO Id	GO Name	Enzyme Code	Enzyme Name	Sequence Detail
1	maker_00064316	non-lysosomal glucosylceramidase isoform X3	152069	0	CC	GO:0016020	membrane	EC:3.2.1.21; EC:3.2.1.45	Beta-glucosidase; Glucosylceramidase	Sequence_Information
2	maker_00018795	Retrovirus-related Pol polyprotein from transposon TNT 1-94	133410	0	CC	GO:0005802	trans-Golgi network			Sequence_Information
3	maker_00018795	Retrovirus-related Pol polyprotein from transposon TNT 1-94	133410	0	CC	GO:0016020	membrane			Sequence_Information
4	maker_00026154	putative RNA-directed DNA polymerase	131154	0	CC	GO:0016020	membrane	EC:3.4.23	Acting on peptide bonds (peptidases)	Sequence_Information
5	maker_00046290	fucosyltransferase 2	107597	0	CC	GO:0032580	Golgi cisterna membrane	EC:2.4.1.69	Type 1 galactoside alpha-(1,2)-fucosyltransferase	Sequence_Information
6	maker_00087925	retrotransposon protein; putative; Ty3-gypsy subclass	95326	9.73E-169	CC	GO:0016020	membrane	EC:7.2.2; EC:3.6.1.15	Catalysing the translocation of inorganic cations; Nucleoside-triphosphate phosphatase	Sequence_Information
7	maker_00087925	retrotransposon protein; putative; Ty3-gypsy subclass	95326	9.73E-169	CC	GO:0043231	intracellular membrane-bounded organelle	EC:7.2.2; EC:3.6.1.15	Catalysing the translocation of inorganic cations; Nucleoside-triphosphate phosphatase	Sequence_Information

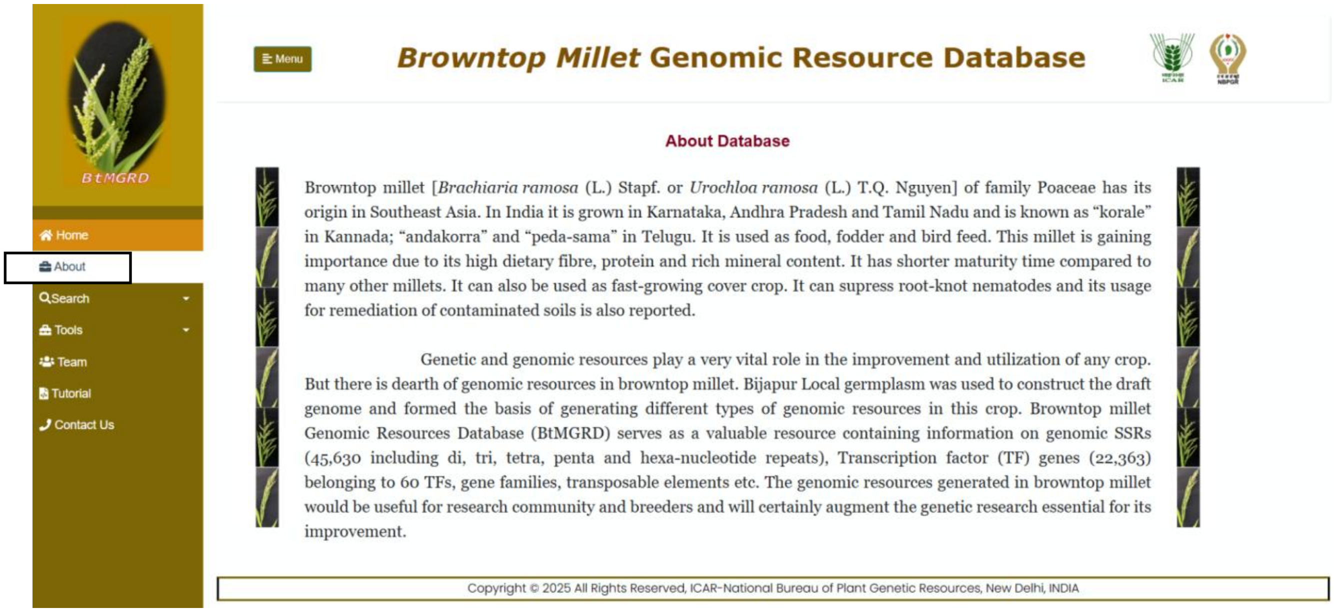
By clicking on the Sequence_Information link, user will get protein, CDS, and gene sequence information.



Sequence Information

S.No.	Gene Id	Seq_info	Sequence
1	maker_00026154	GOGeneSeq	>maker_00026154 ATGCACAGCAGGGGCCACGAGAGGACTGGAGGTGAGATGGCGAGCAAGCAGTGGGGAAGTGGTGCAAGTGCAACATATCGGAGGAGG CGGCAAAAACGTTAGGACCAGCGGCGTCGAGCCTCGGAGGAGCCAGTTGTTGAGAAACTATCCATCTGTGCAAAATTGTCTCATTTGT CTACCGAAGGTGCACAGGTGCAATTTGGCATACGTTCACCTTGTATTGACTCGGCATACGTTCACCTTGTATTATTGACACCTGGTAAC
2	maker_00026154	GOcdsSeq	>maker_00026154 ATGGGTGGCGCGGAGATAGAGGAGAGCGAGGGGATCGCGAAGGCGTGCTCACCGGCGGCG GGGCAAAGAACTCGGCGGAATCGGAGCATTGGCGGCGGGAATGACGGTGACTTGGTCTTC ACGCGTGGCGGCGCTCCGGCGGCGGTATGGCGACAAGGACCGGCGGCGGAGCTTCGGCTT
3	maker_00026154	GOproteinSeq	>maker_00026154 MGGAEIEESEGIAKACSPAAGQRTRRNRSIGGGNDGDLVFTRGGAPAAVWRQGPAAELRL GVVDTVVESLASGGGSMRRIVGEDGDGRQRSRQWCGGGARGRARRRNGWCEEGKRGGARV RAGFKGAAAAARVKSCGLQWRWRRRGRRLRRGKRKRGVMAGWTLVALIAGAHEGLEWWMA

2. **About:** The About page describes the **purpose and background of the database**. It includes details on the project objectives, data source, and the significance of the developed genomic resource for research and crop improvement.

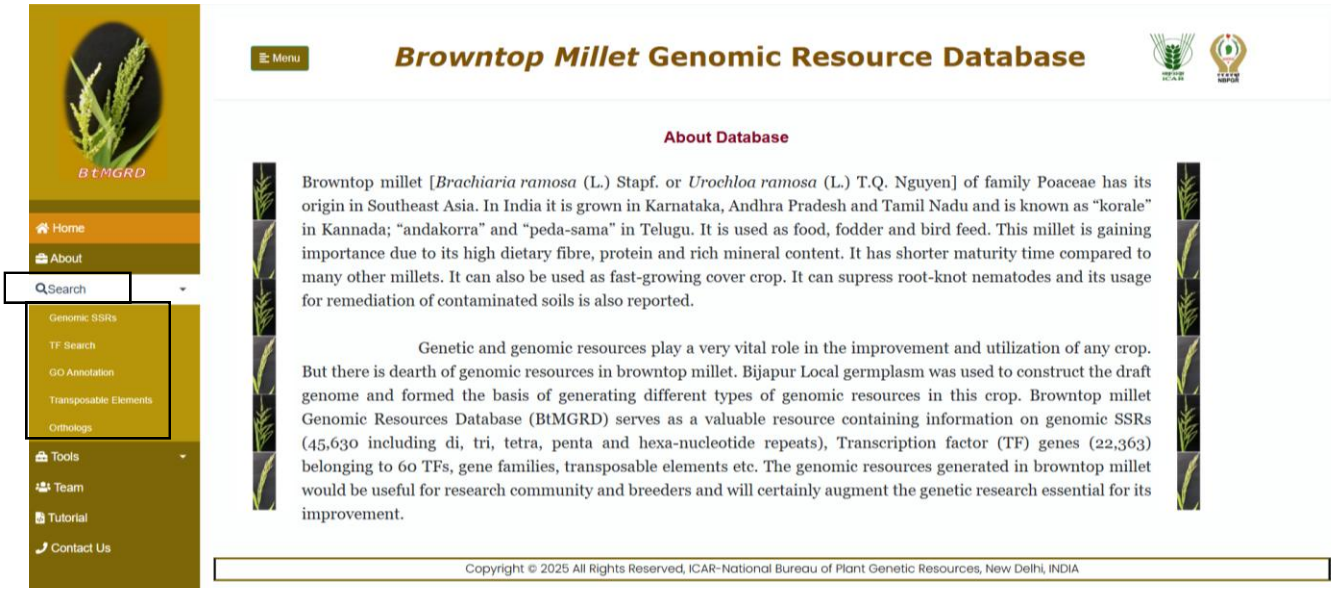


About Database

Browntop millet [*Brachiaria ramosa* (L.) Stapf. or *Urochloa ramosa* (L.) T.Q. Nguyen] of family Poaceae has its origin in Southeast Asia. In India it is grown in Karnataka, Andhra Pradesh and Tamil Nadu and is known as "korale" in Kannada; "andakorra" and "peda-sama" in Telugu. It is used as food, fodder and bird feed. This millet is gaining importance due to its high dietary fibre, protein and rich mineral content. It has shorter maturity time compared to many other millets. It can also be used as fast-growing cover crop. It can supress root-knot nematodes and its usage for remediation of contaminated soils is also reported.

Genetic and genomic resources play a very vital role in the improvement and utilization of any crop. But there is dearth of genomic resources in browntop millet. Bijapur Local germplasm was used to construct the draft genome and formed the basis of generating different types of genomic resources in this crop. Browntop millet Genomic Resources Database (BtMGRD) serves as a valuable resource containing information on genomic SSRs (45,630 including di, tri, tetra, penta and hexa-nucleotide repeats), Transcription factor (TF) genes (22,363) belonging to 60 TFs, gene families, transposable elements etc. The genomic resources generated in browntop millet would be useful for research community and breeders and will certainly augment the genetic research essential for its improvement.

3. **Search:** The Search section allows users to query based search for different datasets such as **Genomic SSRs, Transcription Factors (TFs),** and **GO annotation, Transposable Elements, and Orthologs** search.



About Database

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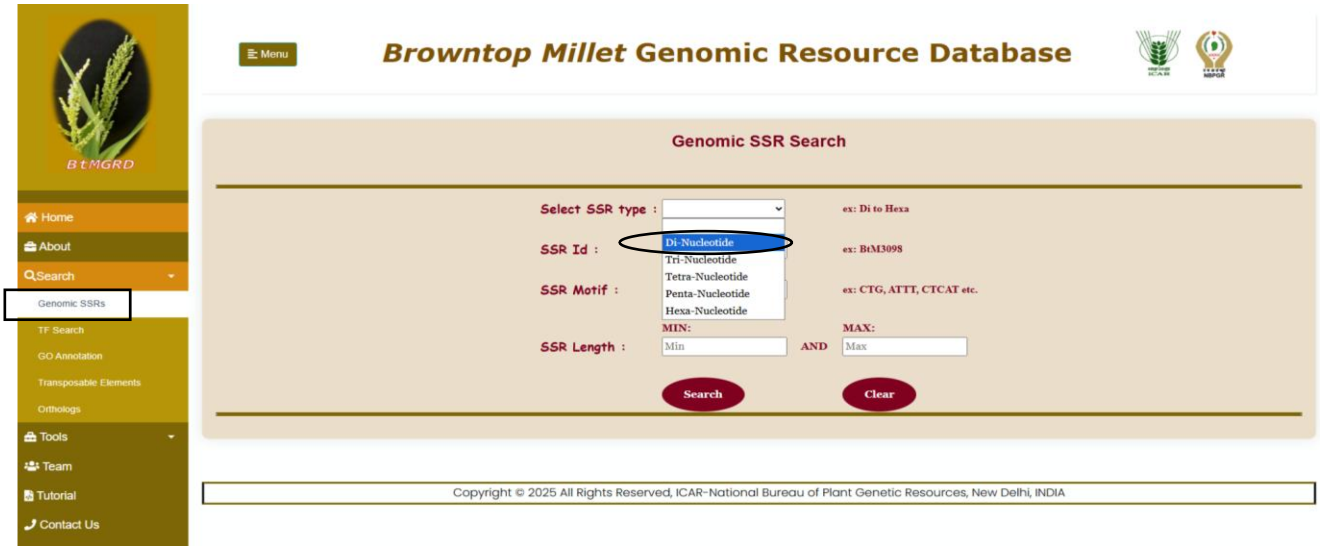
- **Genomic SSR Search:** Search for genomic SSRs using different search parameters such as by selecting SSR Type; search by SSR Id, Sequence motif, Min and Max sequence lengths etc. eg. Select SSR Type from dropdown list



Genomic SSR Search

Select SSR type : ex: Di to Hexa

SSR Id : ex: BtM3098

SSR Motif : ex: CTG, ATTT, CTCAT etc.

SSR Length : MIN: AND MAX:

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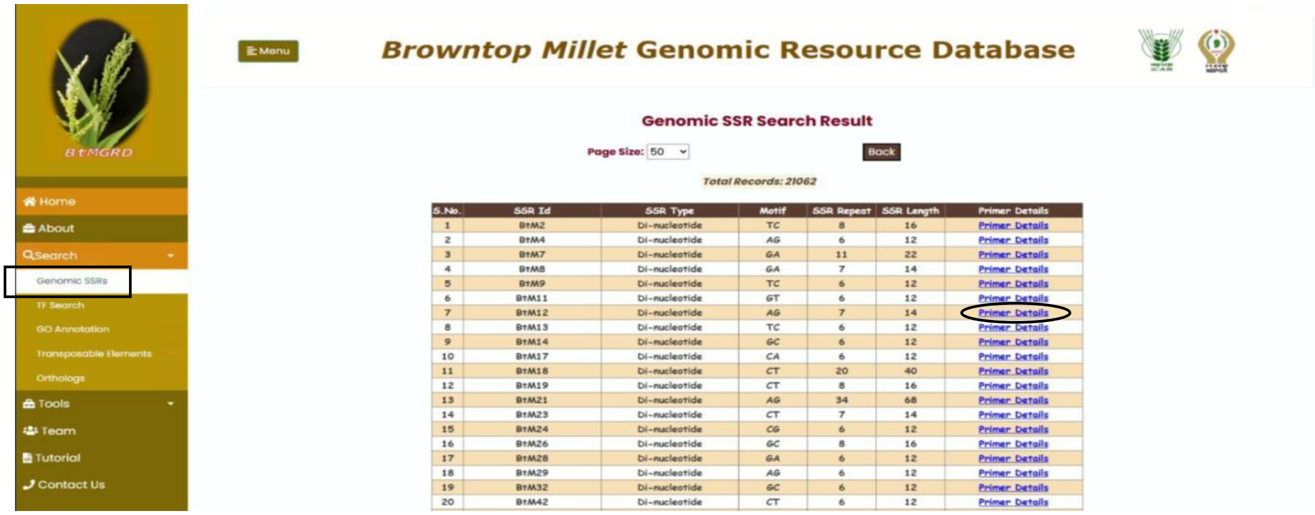
By selecting Di-Nucleotide from dropdown list and click on search button, it will display list of Di-Nucleotide type of genomic SSRs with a link of Primer_Details.



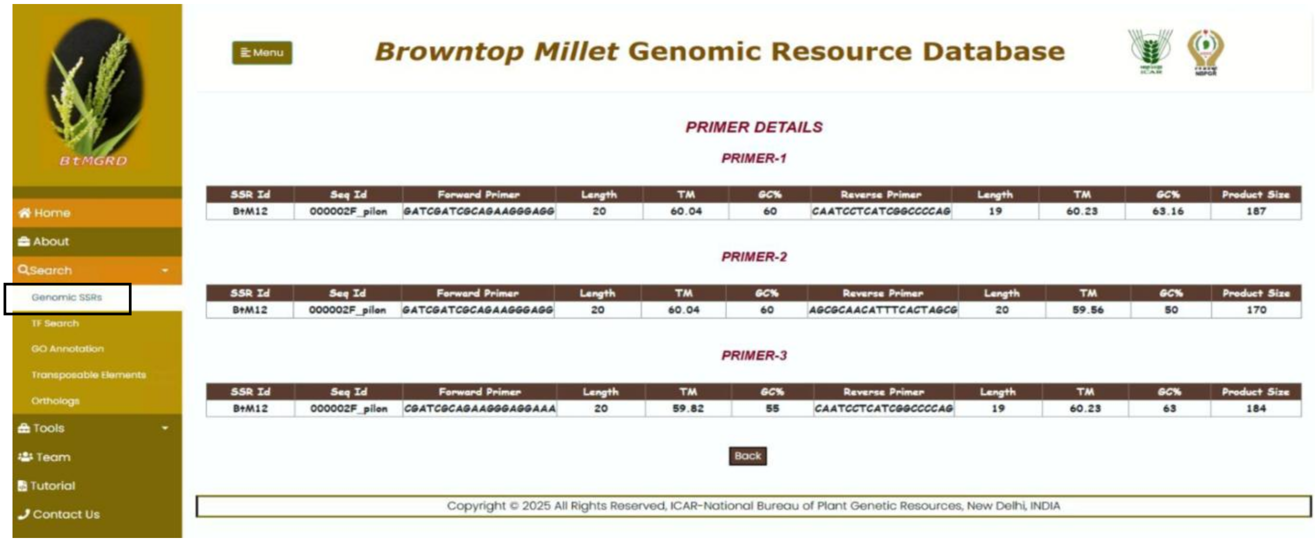
Genomic SSR Search Result

Page Size: 50

Total Records: 21062

S.No.	SSR Id	SSR Type	Motif	SSR Repeat	SSR Length	Primer Details
1	BtM2	Di-nucleotide	TC	8	16	Primer Details
2	BtM4	Di-nucleotide	AG	6	12	Primer Details
3	BtM7	Di-nucleotide	GA	11	22	Primer Details
4	BtM8	Di-nucleotide	GA	7	14	Primer Details
5	BtM9	Di-nucleotide	TC	6	12	Primer Details
6	BtM11	Di-nucleotide	GT	6	12	Primer Details
7	BtM12	Di-nucleotide	AG	7	14	Primer Details
8	BtM13	Di-nucleotide	TC	6	12	Primer Details
9	BtM14	Di-nucleotide	GC	6	12	Primer Details
10	BtM17	Di-nucleotide	CA	6	12	Primer Details
11	BtM18	Di-nucleotide	CT	20	40	Primer Details
12	BtM19	Di-nucleotide	CT	8	16	Primer Details
13	BtM21	Di-nucleotide	AG	34	68	Primer Details
14	BtM23	Di-nucleotide	CT	7	14	Primer Details
15	BtM24	Di-nucleotide	CG	6	12	Primer Details
16	BtM26	Di-nucleotide	GC	8	16	Primer Details
17	BtM28	Di-nucleotide	GA	6	12	Primer Details
18	BtM29	Di-nucleotide	AG	6	12	Primer Details
19	BtM32	Di-nucleotide	GC	6	12	Primer Details
20	BtM42	Di-nucleotide	CT	6	12	Primer Details

By clicking on the Primer Details link, it will give three primer pair information of the selected genomic SSR.



PRIMER DETAILS

PRIMER-1

SSR Id	Seq Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
BtM12	000002F_pilon	GATCGATCGCAGAAGGGAGG	20	60.04	60	CAATCCTCATCGGCCCCAG	19	60.23	63.16	187

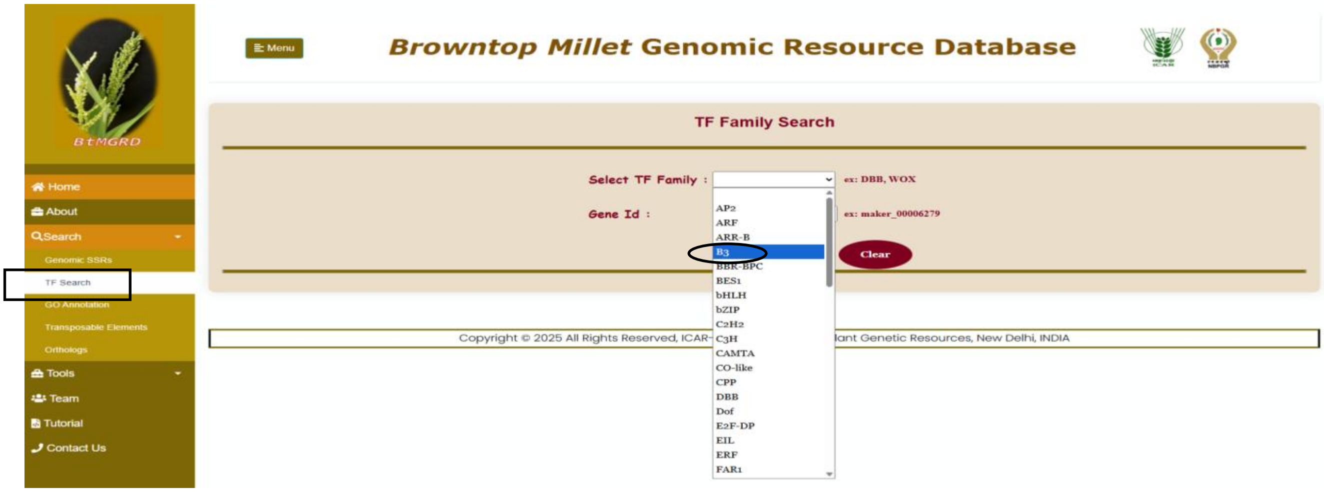
PRIMER-2

SSR Id	Seq Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
BtM12	000002F_pilon	GATCGATCGCAGAAGGGAGG	20	60.04	60	AGCGCAACATTTCACTAGCG	20	59.56	50	170

PRIMER-3

SSR Id	Seq Id	Forward Primer	Length	TM	GC%	Reverse Primer	Length	TM	GC%	Product Size
BtM12	000002F_pilon	CGATCGCAGAAGGGAGGAAA	20	59.82	55	CAATCCTCATCGGCCCCAG	19	60.23	63	184

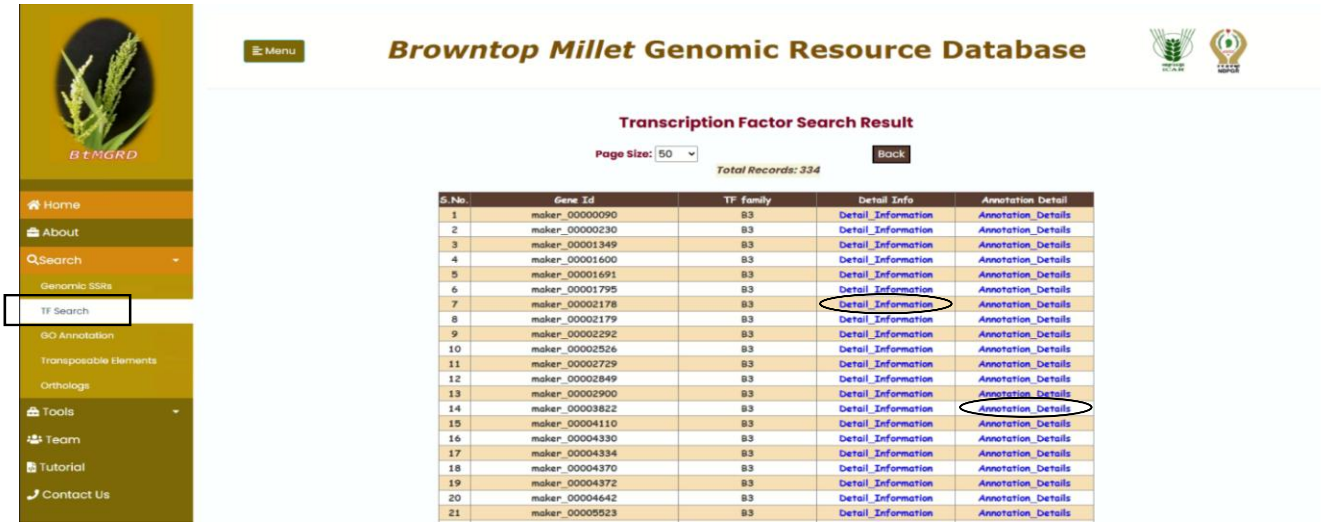
- **Transcription Factors (TFs) Search:** Search for TFs using different search parameters such as by selecting TF family and search by Gene Id.



Select TF Family : B3 ex: DBB, WOX

Gene Id : ex: maker_00006279

By selecting TF family from dropdown list and click on search button, it will display list of TFs in that selected category with a links Detail_Information and Annotation_Details. eg. B3



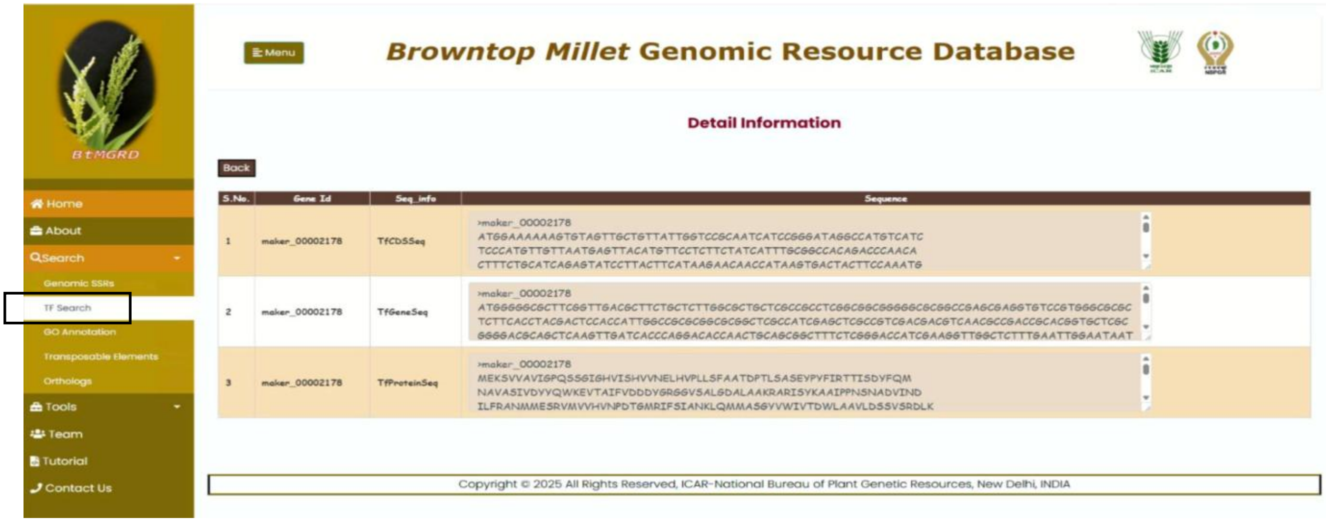
Transcription Factor Search Result

Page Size: 50

Total Records: 334

S.No.	Gene Id	TF family	Detail Info	Annotation Detail
1	maker_00000090	B3	Detail_Information	Annotation_Details
2	maker_00000230	B3	Detail_Information	Annotation_Details
3	maker_00001349	B3	Detail_Information	Annotation_Details
4	maker_00001600	B3	Detail_Information	Annotation_Details
5	maker_00001691	B3	Detail_Information	Annotation_Details
6	maker_00001795	B3	Detail_Information	Annotation_Details
7	maker_00002178	B3	Detail_Information	Annotation_Details
8	maker_00002179	B3	Detail_Information	Annotation_Details
9	maker_00002292	B3	Detail_Information	Annotation_Details
10	maker_00002526	B3	Detail_Information	Annotation_Details
11	maker_00002729	B3	Detail_Information	Annotation_Details
12	maker_00002849	B3	Detail_Information	Annotation_Details
13	maker_00002900	B3	Detail_Information	Annotation_Details
14	maker_00003822	B3	Detail_Information	Annotation_Details
15	maker_00004110	B3	Detail_Information	Annotation_Details
16	maker_00004330	B3	Detail_Information	Annotation_Details
17	maker_00004334	B3	Detail_Information	Annotation_Details
18	maker_00004370	B3	Detail_Information	Annotation_Details
19	maker_00004372	B3	Detail_Information	Annotation_Details
20	maker_00004642	B3	Detail_Information	Annotation_Details
21	maker_00005523	B3	Detail_Information	Annotation_Details

By clicking on the Detail_Information link, it will give protein, CDS, and gene sequence of selected TF.



Detail Information

S.No.	Gene Id	Seq_info	Sequence
1	maker_00002178	TfCDSSeq	>maker_00002178 ATGGAAAAAAGTGTAGTTGCTGTTATTGGTCCGCAATCATCCGGGATAGGCCATGTCATC TCCCATGTTGTTAATGAGTTACATGTTCCTCTTCTATCATTTGCGGCCACAGACCCAACA CTTTCTGCATCAGAGTATCCTTACTTCATAAGAACAACCATAAGTGACTACTTCCAAATG
2	maker_00002178	TfGeneSeq	>maker_00002178 ATGGGGGCGCTTCGGTTGACGCTTCTGCTCTTGGCGCTGCTCGCCGCCTCGGCGGCGGGGGCGCGGCCGAGCGAGGTGTCCGTGGGCGCGC TCTTCACCTACGACTCCACCATTGGCCGCGCGGCGCGGCTCGCCATCGAGCTCGCCGTCGACGACGTCAACGCCGACCGCACGGTGCTCGC GGGGACGCAGCTCAAGTTGATCACCCAGGACACCAACTGCAGCGGCTTTCTCGGGACCATCGAAGGTTGGCTCTTTGAATTGGAATAAT
3	maker_00002178	TfProteinSeq	>maker_00002178 MEKSVVAVIGPQSSGIGHVISHVVNELHVPLLSFAATDPTLSASEYPYFIRTTISDYFQM NAVASIVDYYQWKEVTAIFVDDDYGRGGVSALGDALAAKRARISYKAAIPPNSNADVIND ILFRANMMESRVMVVHVNPDTGMRIFSIANKLQMMASGYVWIVTDWLAAVLDSSVSRDLK

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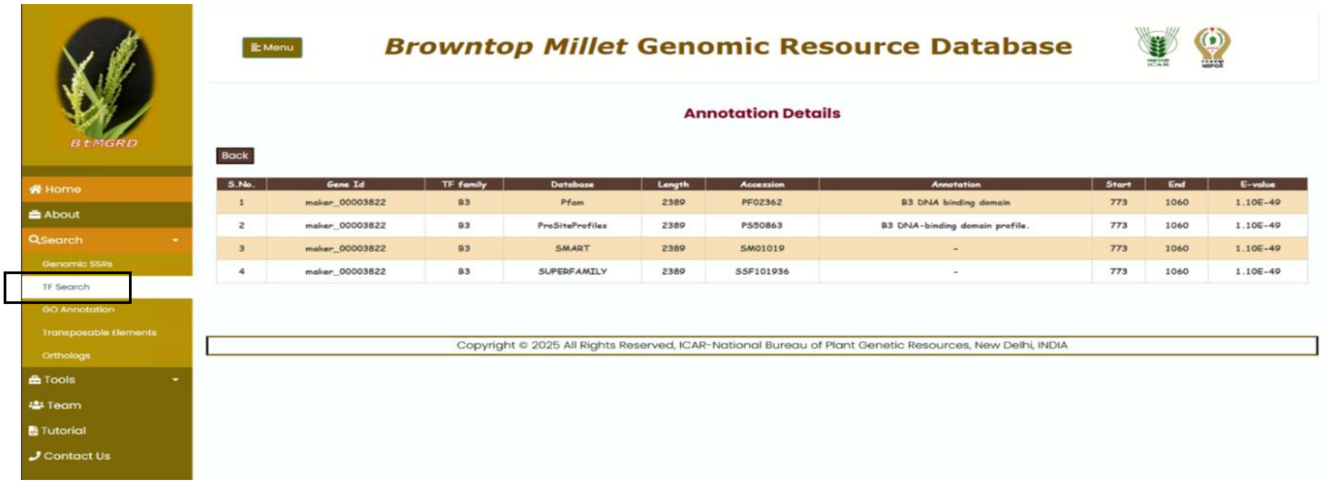
By clicking on the Annotation_Details link, user will get annotation information of the selected TF with InterProScan databases.



Annotation Details

S.No.	Gene Id	TF family	Database	Length	Accession	Annotation	Start	End	E-value
1	maker_00003822	B3	Pfam	2389	PF02362	B3 DNA binding domain	773	1060	1.10E-49
2	maker_00003822	B3	ProSiteProfiles	2389	PS50863	B3 DNA-binding domain profile.	773	1060	1.10E-49
3	maker_00003822	B3	SMART	2389	SM01019	-	773	1060	1.10E-49
4	maker_00003822	B3	SUPERFAMILY	2389	SSF101936	-	773	1060	1.10E-49

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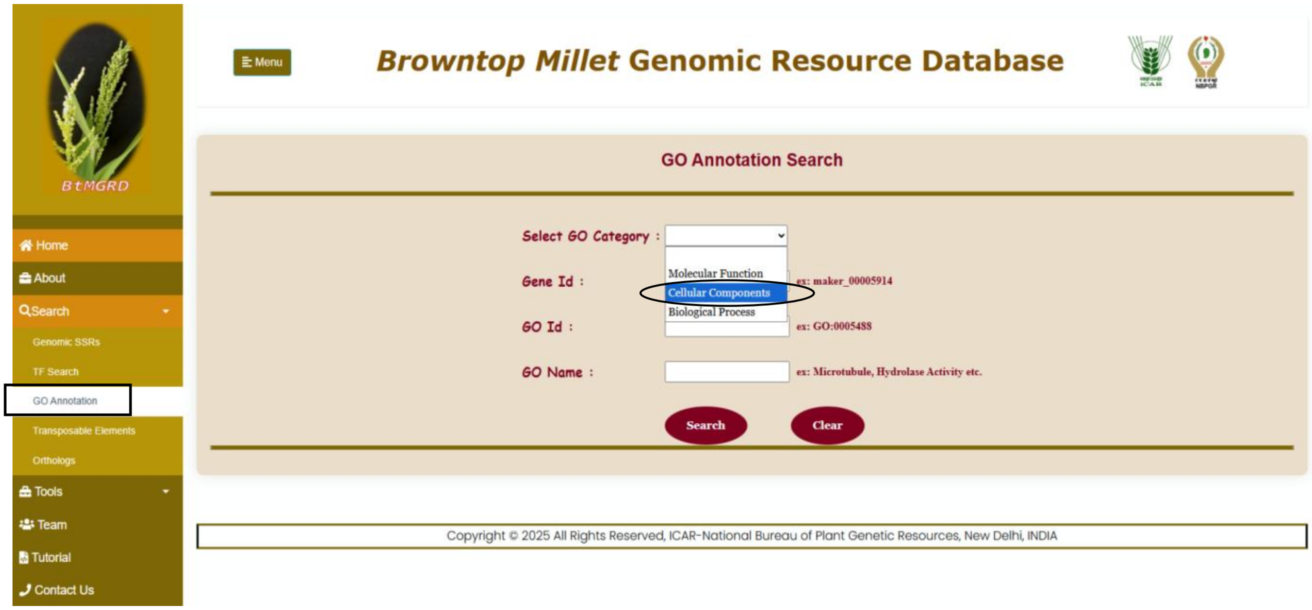
- **Gene Ontology (GO) Search:** Search gene ontology based functional annotation using different search parameters such as by selecting GO category, search by Gene Id, GO Id, and GO names.



GO Annotation Search

Select GO Category :
Gene Id : ex: maker_00005914
GO Id : ex: GO:0005488
GO Name : ex: Microtubule, Hydrolase Activity etc.

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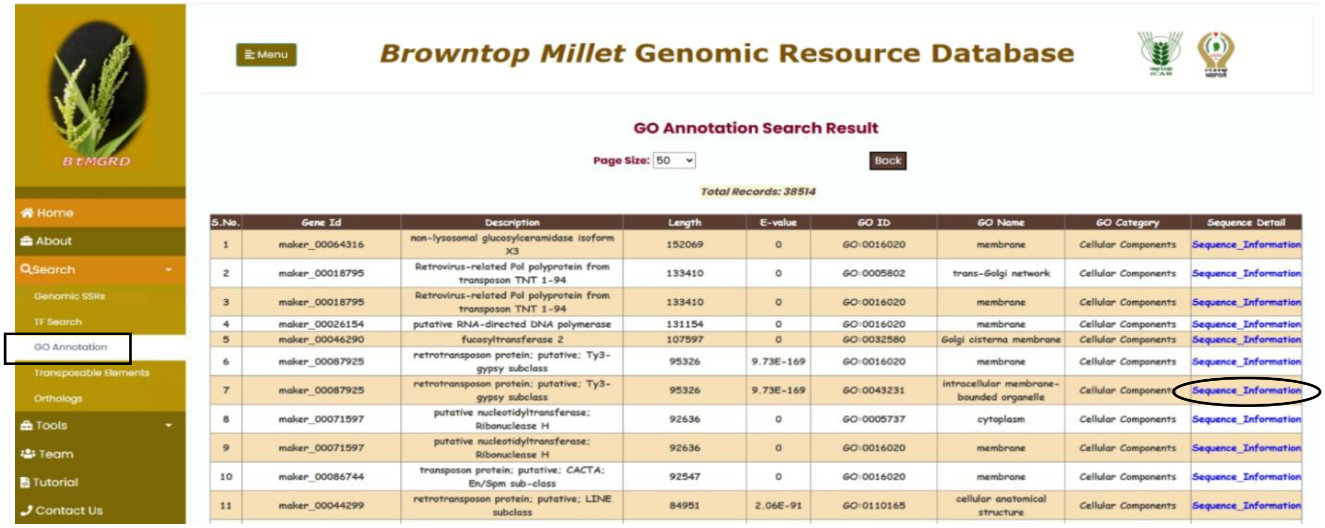
By selecting GO category from the dropdown list and click on search button, it will display list of genes functionally annotated in that selected category with a link of Sequence_Information. eg. Cellular Components



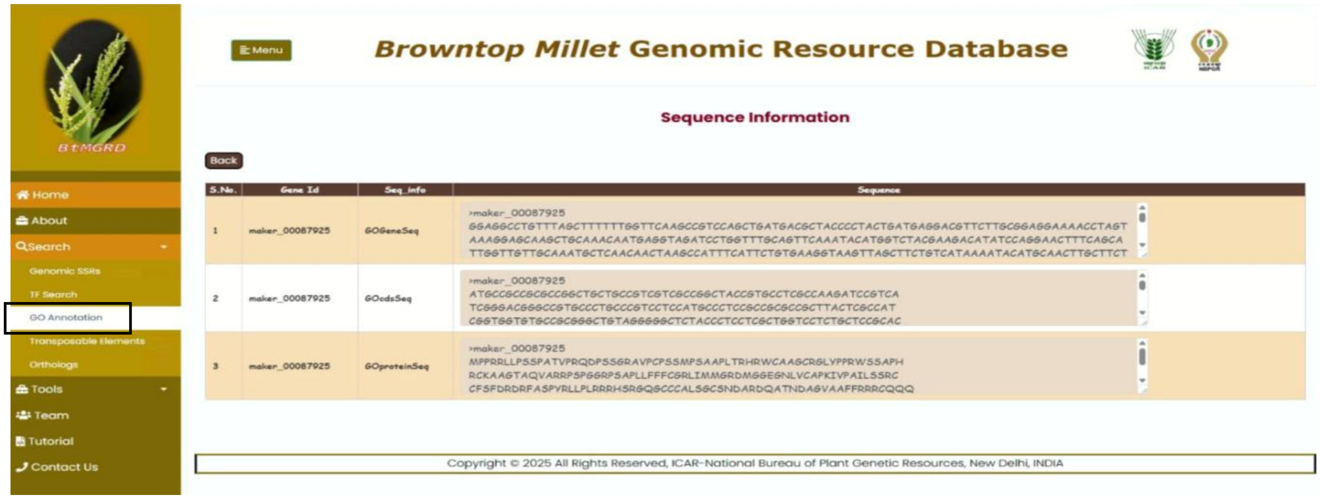
GO Annotation Search Result

Page Size: 50

Total Records: 38514

S.No.	Gene Id	Description	Length	E-value	GO ID	GO Name	GO Category	Sequence Detail
1	maker_00064316	non-lysosomal glucosylceramidase isoform X3	152069	0	GO:0016020	membrane	Cellular Components	Sequence_Information
2	maker_00018795	Retrovirus-related Pol polyprotein from transposon TNT 1-94	133410	0	GO:0005802	trans-Golgi network	Cellular Components	Sequence_Information
3	maker_00018795	Retrovirus-related Pol polyprotein from transposon TNT 1-94	133410	0	GO:0016020	membrane	Cellular Components	Sequence_Information
4	maker_00026154	putative RNA-directed DNA polymerase	131154	0	GO:0016020	membrane	Cellular Components	Sequence_Information
5	maker_00046290	fucosyltransferase 2	107597	0	GO:0032580	Golgi cisterna membrane	Cellular Components	Sequence_Information
6	maker_00087925	retrotransposon protein; putative; Ty3-gypsy subclass	95326	9.73E-169	GO:0016020	membrane	Cellular Components	Sequence_Information
7	maker_00087925	retrotransposon protein; putative; Ty3-gypsy subclass	95326	9.73E-169	GO:0043231	intracellular membrane-bounded organelle	Cellular Components	Sequence_Information
8	maker_00071597	putative nucleotidyltransferase; Ribonuclease H	92636	0	GO:0005737	cytoplasm	Cellular Components	Sequence_Information
9	maker_00071597	putative nucleotidyltransferase; Ribonuclease H	92636	0	GO:0016020	membrane	Cellular Components	Sequence_Information
10	maker_00086744	transposon protein; putative; CACTA; En/Spm sub-class	92547	0	GO:0016020	membrane	Cellular Components	Sequence_Information
11	maker_00044299	retrotransposon protein; putative; LINE subclass	84951	2.06E-91	GO:0110165	cellular anatomical structure	Cellular Components	Sequence_Information

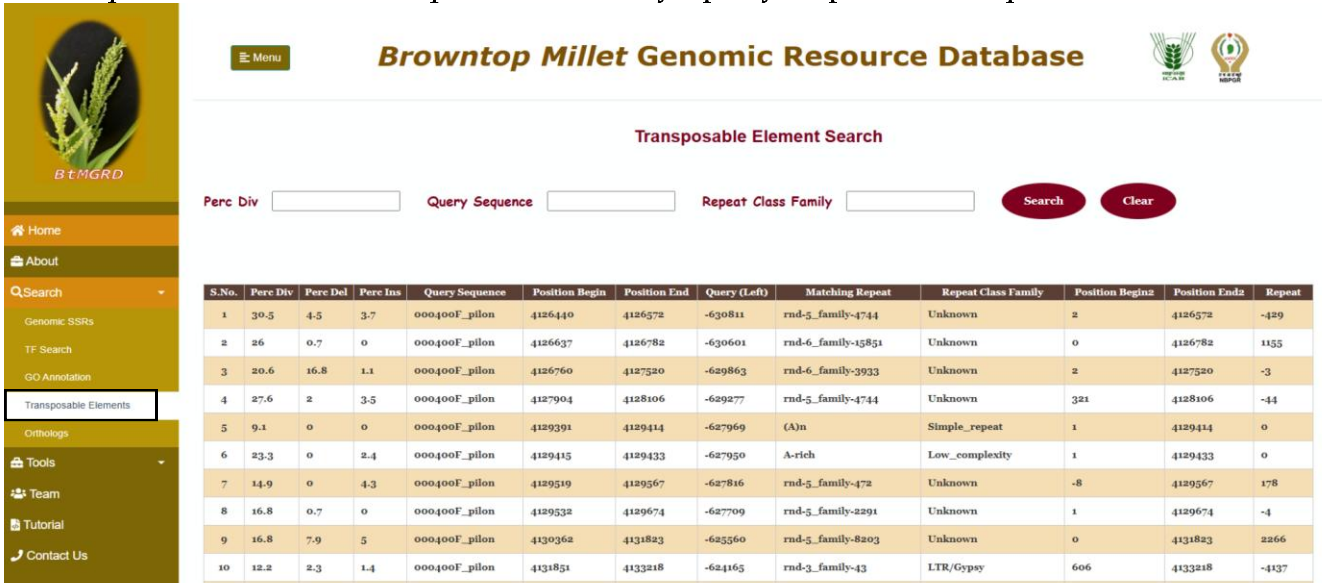
By clicking on the Sequence_Information link, user will get protein, CDS, and gene sequence information.



Sequence Information

S.No.	Gene Id	Seq_info	Sequence
1	maker_00087925	GOGeneSeq	>maker_00087925 GGAGGCCTGTTTAGCTTTTTTGGTTCAAGCCGTCCAGCTGATGACGCTACCCCTACTGATGAGGACGTTCTTGCGGAGGAAAACCTAGT AAAGGAGCAAGCTGCAAACAATGAGGTAGATCCTGGTTTGCAGTTCAAATACATGGTCTACGAAGACATATCCAGGAACTTTCAGCA TTGGTTGTTGCAAATGCTCAACAACTAAGCCATTTCATTCTGTGAAGGTAAGTTAGCTTCTGTCATAAAATACATGCAACTTGCTTCT
2	maker_00087925	GOcdsSeq	>maker_00087925 ATGCCGCCGCGCCGGCTGCTGCCGTCGTCGCCGGCTACCGTGCCTCGCCAAGATCCGTCA TCGGGACGGGCCGTGCCCTGCCCGTCCTCCATGCCCTCCGCCGCGCCGCTTACTCGCCAT CGGTGGTGTGCCGCGGGCTGTAGGGGGCTCTACCCTCCTCGCTGGTCCTCTGCTCCGCAC
3	maker_00087925	GOproteinSeq	>maker_00087925 MPPRRLLPSSPATVPRQDPSSGRAVPCPSSMPSAAPLTRHRWCAAGCRGLYPPRWSSAPH RCKAAGTAQVARRPSPGGRPSAPLLFFFCGRLIMMGRDMGGEGNLVCAPKIVPAILSSRC CFSFDRDRFASPYRLLPLRRRHSRGQGCCCALSGCSNDARDQATNDAGVAAFFRRRCQQQ

- **Transposable Elements Search:** Search transposable elements based on different search parameters such as repeat class family, query sequence, and per div.

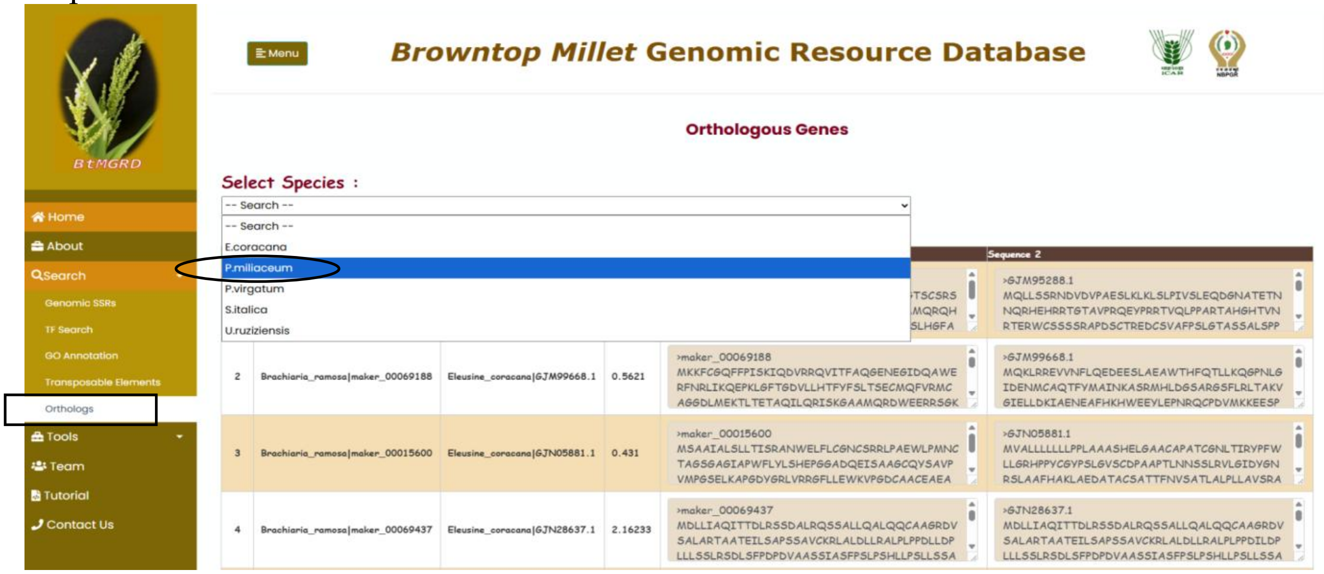


Transposable Element Search

Perc Div ☐ Query Sequence ☐ Repeat Class Family ☐

S.No.	Perc Div	Perc Del	Perc Ins	Query Sequence	Position Begin	Position End	Query (Left)	Matching Repeat	Repeat Class Family	Position Begin2	Position End2	Repeat
1	30.5	4.5	3.7	000400F_pilon	4126440	4126572	-630811	rnd-5_family-4744	Unknown	2	4126572	-429
2	26	0.7	0	000400F_pilon	4126637	4126782	-630601	rnd-6_family-15851	Unknown	0	4126782	1155
3	20.6	16.8	1.1	000400F_pilon	4126760	4127520	-629863	rnd-6_family-3933	Unknown	2	4127520	-3
4	27.6	2	3.5	000400F_pilon	4127904	4128106	-629277	rnd-5_family-4744	Unknown	321	4128106	-44
5	9.1	0	0	000400F_pilon	4129391	4129414	-627969	(A)n	Simple_repeat	1	4129414	0
6	23.3	0	2.4	000400F_pilon	4129415	4129433	-627950	A-rich	Low_complexity	1	4129433	0
7	14.9	0	4.3	000400F_pilon	4129519	4129567	-627816	rnd-5_family-472	Unknown	-8	4129567	178
8	16.8	0.7	0	000400F_pilon	4129532	4129674	-627709	rnd-5_family-2291	Unknown	1	4129674	-4
9	16.8	7.9	5	000400F_pilon	4130362	4131823	-625560	rnd-5_family-8203	Unknown	0	4131823	2266
10	12.2	2.3	1.4	000400F_pilon	4131851	4133218	-624165	rnd-3_family-43	LTR/Gypsy	606	4133218	-4137

- **Gene Orthologs Search:** Search orthologous genes in the selected species with respect to *Brachiaria ramosa*.



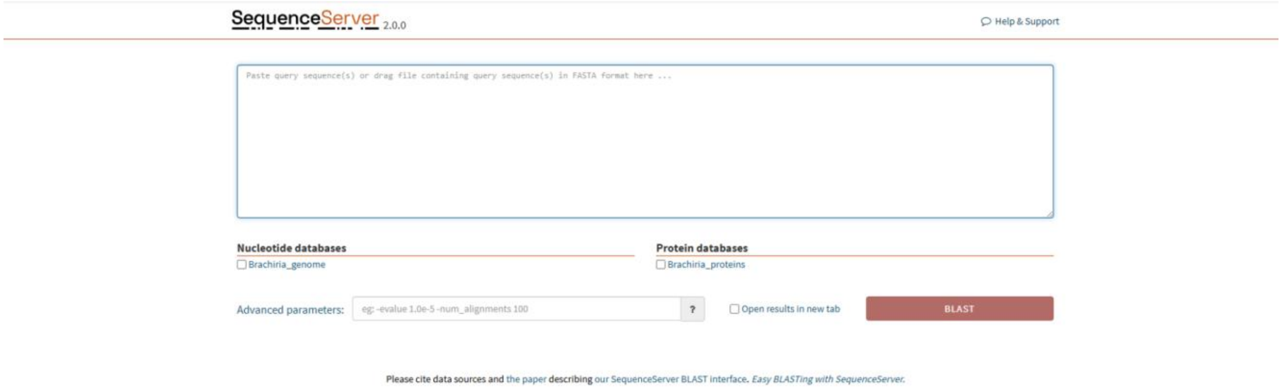
					Sequence 2
				TSCSRS MQRQH SLHGFA	>GJM95288.1 MQLLSSRNDVDVPAESLKLKLSLPIVSLEQDGNATETN NQRHEHRRTGTAVPRQEYPRRTVQLPPARTAHGHTVN RTERWCSSSSRAPDSCTREDCSVAFPSLGTASSALSPP
2	Brachiaria_ramosa|maker_00069188	Eleusine_coracana|GJM99668.1	0.5621	>maker_00069188 MKKFCGQFFPISKIQDVRRQVITFAQGENEGIDQAWE RFNRLIKQEPKLGFTGDVLLHTFYFSLTSECMQFVRMC AGGDLMEKTLTETAQILQRISKGAAMQRDWEERRSGK	>GJM99668.1 MQKLRREVVNFLQEDEESLAEAWTHFQTLLKQGPNLG IDENMCAQTFYMAINKASRMHLDGSARGSFLRLTAKV GIELLDKIAENEAFHKHWEEYLEPNRQCPDVMKKEESP
3	Brachiaria_ramosa|maker_00015600	Eleusine_coracana|GJN05881.1	0.431	>maker_00015600 MSAAIALSLLTISRANWELFLCGNCSRRLPAEWLPMNC TAGSGAGIAPWFLYLSHEPGGADQEISAAGCQYSAVP VMPGSELKAPGDYGRLVRRGFLLEWKVPGDCAACEAEA	>GJN05881.1 MVALLLLLLLPPLAAASHELGAACAPATCGNLTIRYPFW LLGRHPPYCGYPSLGVSCDPAAPTLNNSSLRVLGIDYGN RSLAAFHAKLAEDATACSATTFNVSATLALPLLAVSRA
4	Brachiaria_ramosa|maker_00069437	Eleusine_coracana|GJN28637.1	2.16233	>maker_00069437 MDLLIAQITTDLRSSDALRQSSALLQALQQCAAGRDV SALARTAATEILSAPSSAVCKRLALDLLRALPLPPDLLDP LLLSSLRSDLSFPDPDVAASSIASFPSLPSHLLPSLLSSA	>GJN28637.1 MDLLIAQITTDLRSSDALRQSSALLQALQQCAAGRDV SALARTAATEILSAPSSAVCKRLALDLLRALPLPPDILDP LLLSSLRSDLSFPDPDVAASSIASFPSLPSHLLPSLLSSA

By selecting the species name from the dropdown list, it will display list of orthologous genes in selected species with sequence information.

S.No.	Species 1	Species 2	%Orthology	Sequence 1	Sequence 2
1	Brachiaria_ramosa|maker_00018883	Panicum_miliaceum|RLN00837.1	0.3668	>maker_00018883 MSGWDDFARAHGLHENDLLIFTCSGNYSFDVQIFDAS GCEKVPCFFTSKMGPCTHKHLDGIMDQHTEHCILSDSD DSGMLLPLLGSPNKASTSKKMSGKTKPSKLKNEFVVSS	>RLN00837.1 MVRKTLSAHMNPMVEKGCESCREWQEHYYREHMDVT KIRFFKLMTGDFALGISMPAKFVKNFNGRITKGLDLKVP SGETWHVCVDKRDDELLLTSGWKDFVKIVPSRFAADHL
2	Brachiaria_ramosa|maker_00023216	Panicum_miliaceum|RLM57966.1	0.4876	>maker_00023216 MQEPSRAMRQDNDGEAAGVVLSSHDDPEHGHGTIRG RADAGMGTEEDEERGGGGQESFFLCLDQDDDGDGDDA RFSFATAVGDRLLEEQSELDLDVEEEEEEDTSRYDYVT	>RLM57966.1 MQEPSQTMSQENGDGEVAGVVNSHGVQEHDHGTTR GGRAGAGASAEEDEERGGGQEPFYQCLDQEQPSGMVH LDDARAEFLSDDEDGGGDSDDVRCSFATAVGDGDRLLE
3	Brachiaria_ramosa|maker_00017577	Panicum_miliaceum|RLN23467.1	0.4961	>maker_00017577 MVAGRVKAAMGFQRSPKSPASPPRTPTRAPSSGSASAS PCGSAPSSKASALARSFGAYFPRSSAQVRPAAARAPPQ VAELLRAIEQLQEREARLRVELLEHKILKETVAIVPFLEA	>RLN23467.1 MVAGRVKAAMGFQRSPKSPAPAPEPASPSLTPGRAPPPG SASPCGPAPSKASALARSFGSYFPRSSAQVRPAAARAPP QVAELLRAIEQLQEREARLRVELLEHKILKETVAIVPFLE
4	Brachiaria_ramosa|maker_00033739	Panicum_miliaceum|RLN17617.1	0.2308	>maker_00033739 MHPHLRSAVDNALAIPLHWAAPRLQARWFIDHYARDAE ADQVMLHFAKLDFNNVQKLHQQELSRITW	>RLN17617.1 MESLEAANKCDGNPADPSSFDKLKFRVRHLLHHEIELLP KLRVIDTVQRLGVAYHFDEEIHAILNSVSMEGQDVGR MDDAHLMTLLFRLLRQNKSPTSPELLLRSLKDGTGGFKK

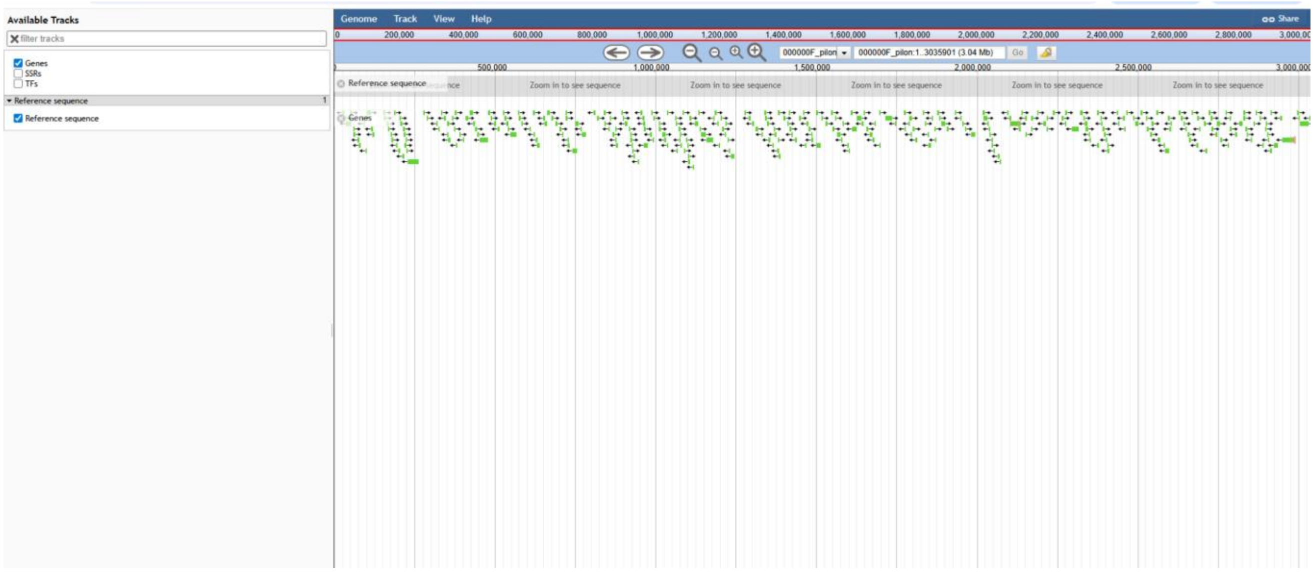
4. **Tools:** The Tools page integrates external bioinformatics applications with the database such as BLAST Search and Genome Browser (JBrowse).

- **BLAST Search:** It performs sequence similarity searches against *Luffa acutangula* genome and proteome datasets.

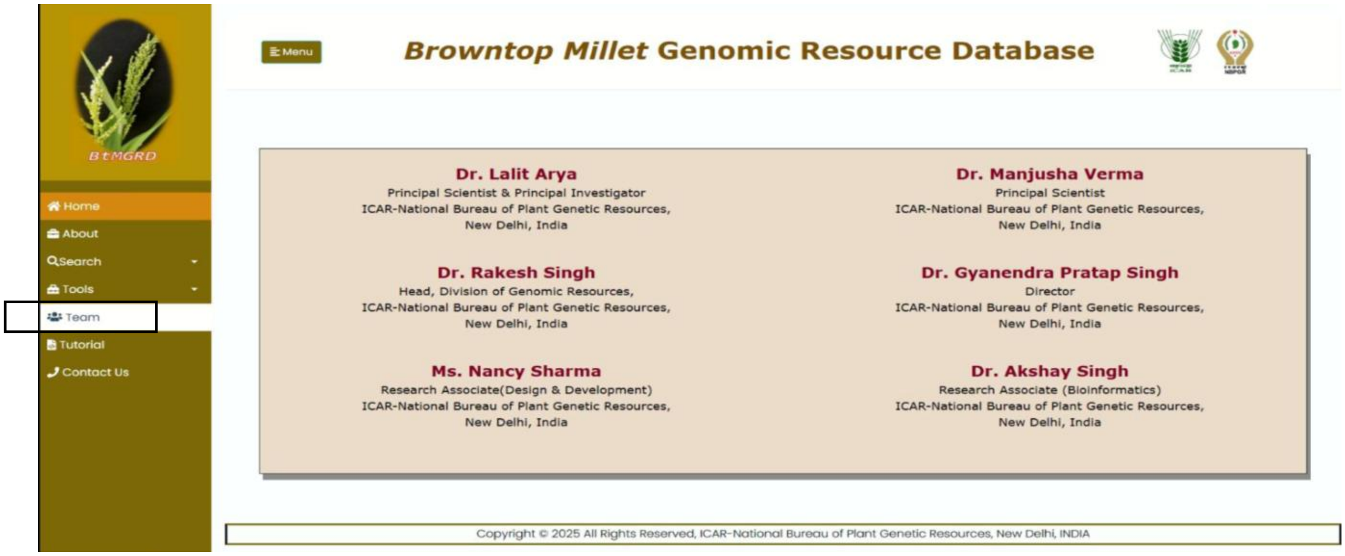


Please cite data sources and the paper describing our SequenceServer BLAST interface. *Easy BLASTing with SequenceServer.*

- **Genome Browser:** It visualizes genomic regions, genes, genomic SSRs, TFs interactively.



5. **Team:** The Download section provides direct access to datasets, including genomic SSRs, TFs, and GO annotations. User can download curated files for offline analysis and their research use.



Browntop Millet Genomic Resource Database

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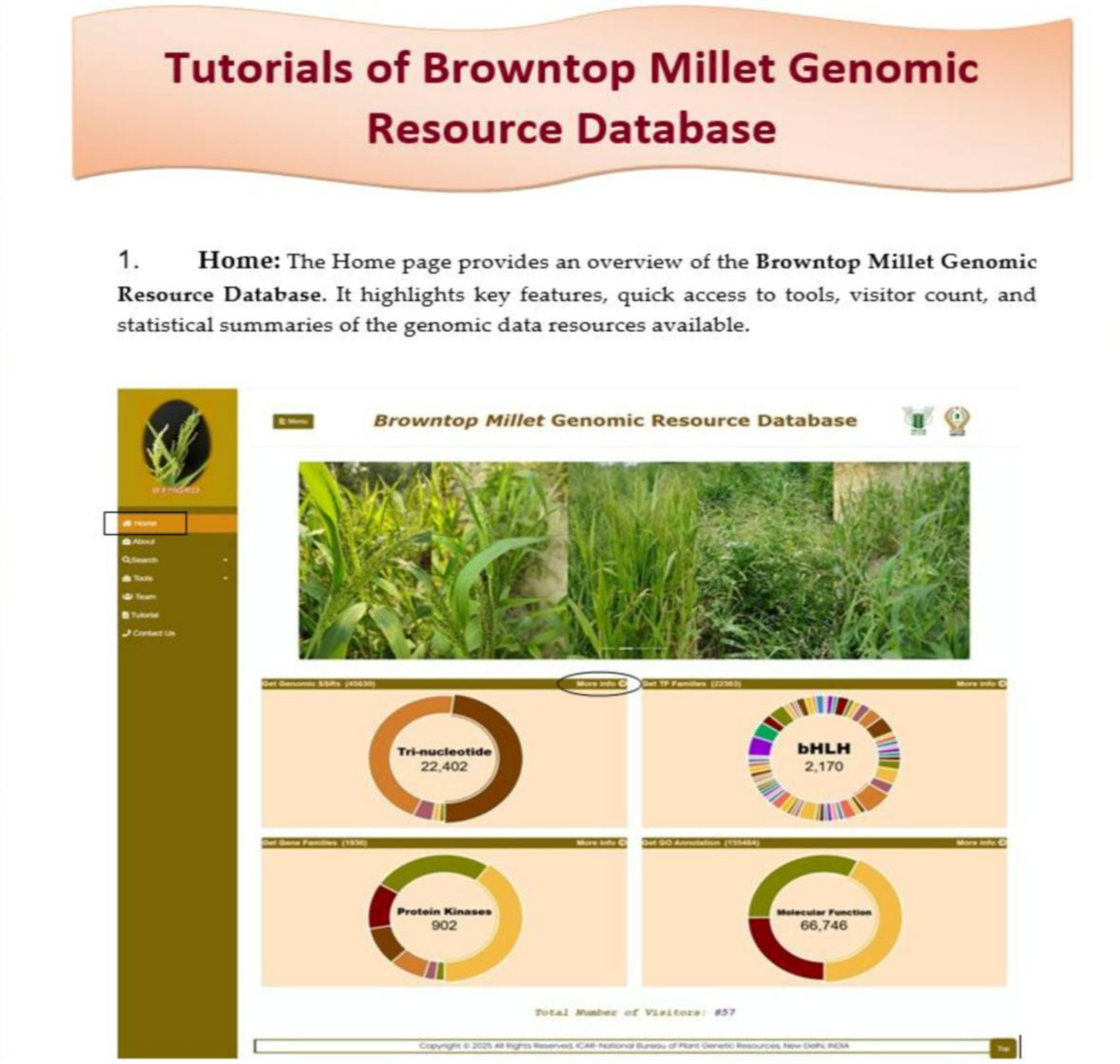
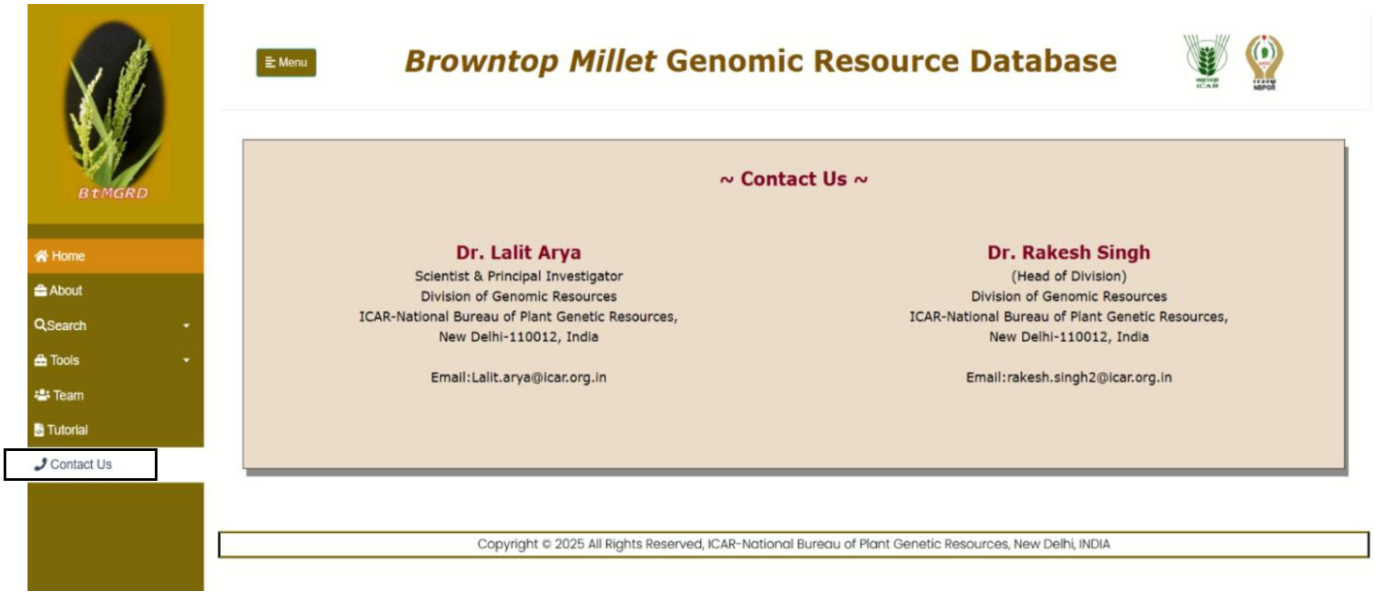
6. **Tutorials:** The Tutorial page offers a step-by-step guide on how to use the database effectively. It includes instructions with screenshots or examples for searching, browsing, downloading data, and using integrated tools like BLAST.



Tutorials of Browntop Millet Genomic Resource Database

1. **Home:** The Home page provides an overview of the **Browntop Millet Genomic Resource Database.** It highlights key features, quick access to tools, visitor count, and statistical summaries of the genomic data resources available.

7. **Contact Us:** The Contact page provides the contact information on how to reach the database administrators and research team.



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