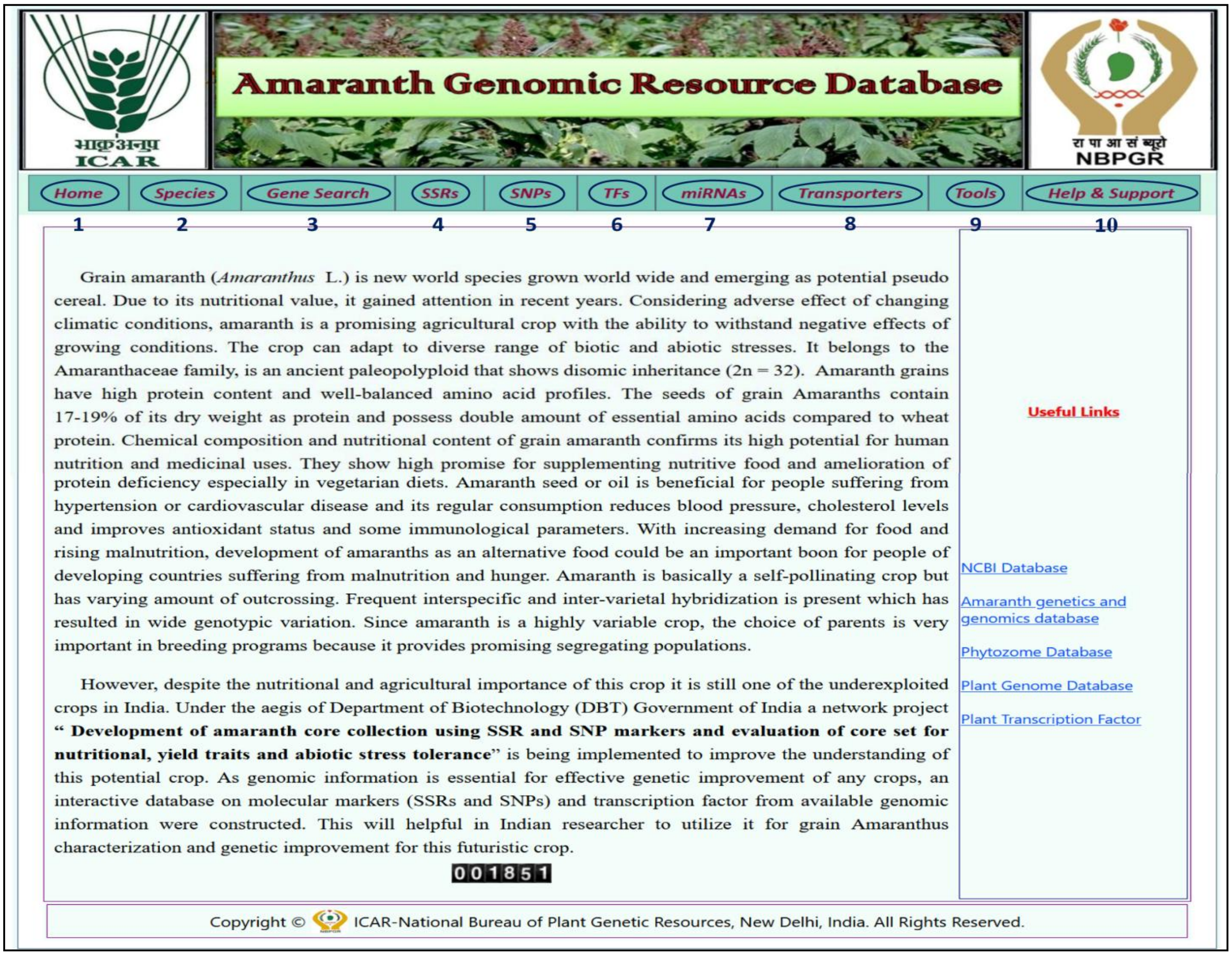
HELP-TUTORIALS

Amaranth Genomic Resource Database

1: Home (Information about the Database)



Grain amaranth (*Amaranthus* L.) is new world species grown world wide and emerging as potential pseudo cereal. Due to its nutritional value, it gained attention in recent years. Considering adverse effect of changing climatic conditions, amaranth is a promising agricultural crop with the ability to withstand negative effects of growing conditions. The crop can adapt to diverse range of biotic and abiotic stresses. It belongs to the Amaranthaceae family, is an ancient paleopolyploid that shows disomic inheritance (2n = 32). Amaranth grains have high protein content and well-balanced amino acid profiles. The seeds of grain Amaranths contain 17-19% of its dry weight as protein and possess double amount of essential amino acids compared to wheat protein. Chemical composition and nutritional content of grain amaranth confirms its high potential for human nutrition and medicinal uses. They show high promise for supplementing nutritive food and amelioration of protein deficiency especially in vegetarian diets. Amaranth seed or oil is beneficial for people suffering from hypertension or cardiovascular disease and its regular consumption reduces blood pressure, cholesterol levels and improves antioxidant status and some immunological parameters. With increasing demand for food and rising malnutrition, development of amaranths as an alternative food could be an important boon for people of developing countries suffering from malnutrition and hunger. Amaranth is basically a self-pollinating crop but has varying amount of outcrossing. Frequent interspecific and inter-varietal hybridization is present which has resulted in wide genotypic variation. Since amaranth is a highly variable crop, the choice of parents is very important in breeding programs because it provides promising segregating populations.

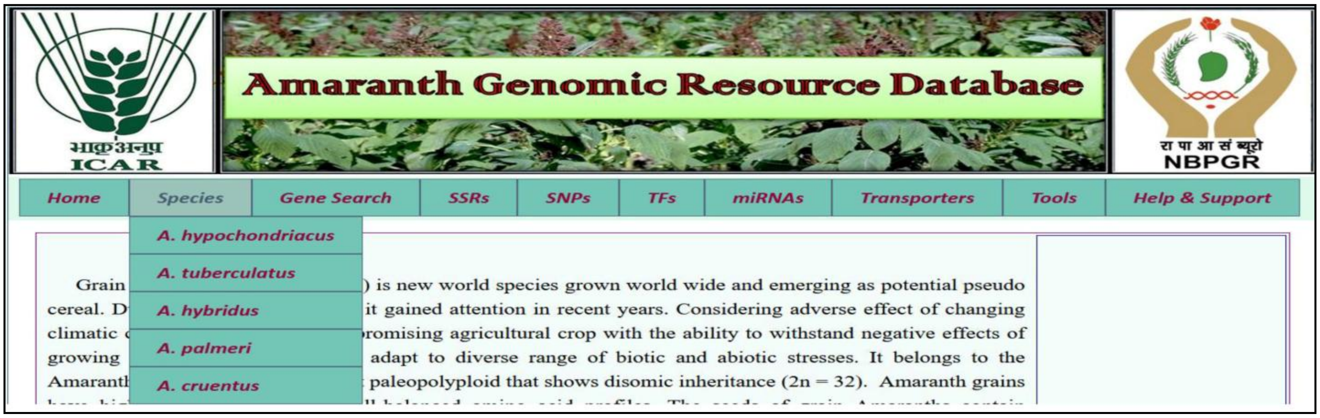
However, despite the nutritional and agricultural importance of this crop it is still one of the underexploited crops in India. Under the aegis of Department of Biotechnology (DBT) Government of India a network project **" Development of amaranth core collection using SSR and SNP markers and evaluation of core set for nutritional, yield traits and abiotic stress tolerance"** is being implemented to improve the understanding of this potential crop. As genomic information is essential for effective genetic improvement of any crops, an interactive database on molecular markers (SSRs and SNPs) and transcription factor from available genomic information were constructed. This will helpful in Indian researcher to utilize it for grain Amaranthus characterization and genetic improvement for this futuristic crop.

001851

Useful Links

- NCBI Database
- Amaranth genetics and genomics database
- Phytozome Database
- Plant Genome Database
- Plant Transcription Factor

2: Species (Information of five Amaranth species in separate tabs with their respective search buttons)



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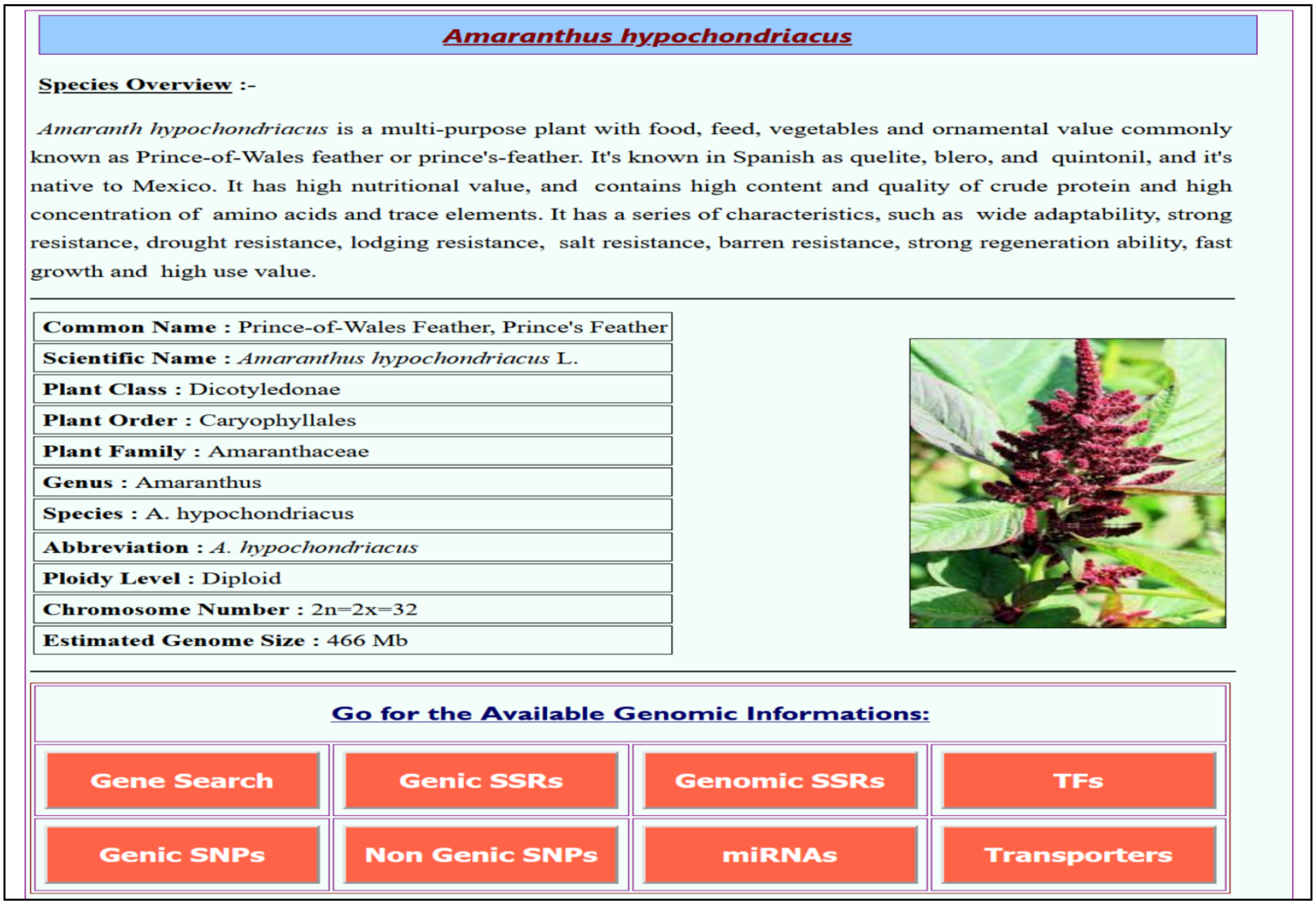
Amaranth paleopolyploid that shows disomic inheritance (2n = 32). Amaranth grains

(i) ***A.hypochondriacus***



Amaranthus hypochondriacus

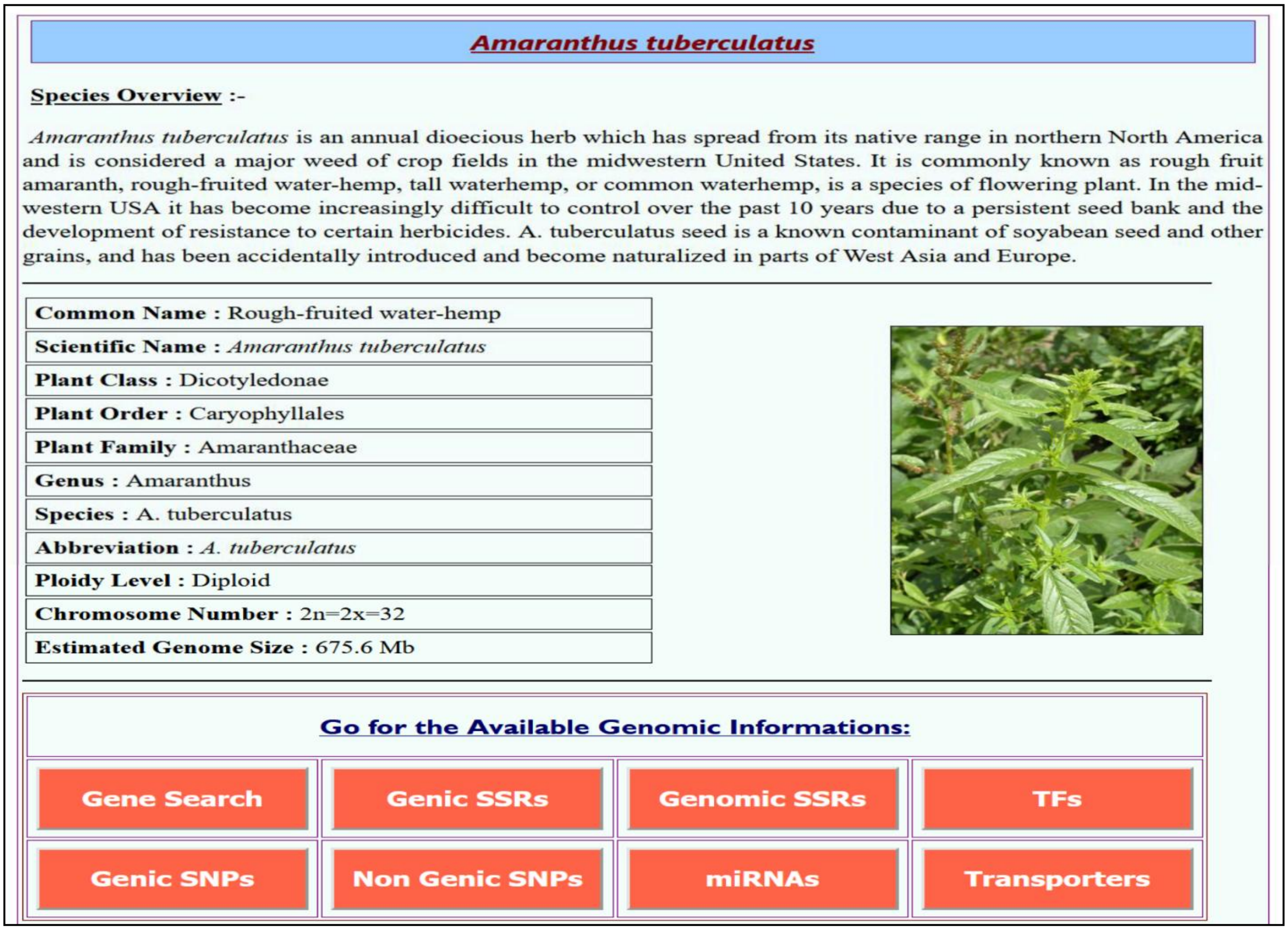
Species Overview :-

Amaranth hypochondriacus is a multi-purpose plant with food, feed, vegetables and ornamental value commonly known as Prince-of-Wales feather or prince's-feather. It's known in Spanish as quelite, blero, and quintonil, and it's native to Mexico. It has high nutritional value, and contains high content and quality of crude protein and high concentration of amino acids and trace elements. It has a series of characteristics, such as wide adaptability, strong resistance, drought resistance, lodging resistance, salt resistance, barren resistance, strong regeneration ability, fast growth and high use value.

Common Name : Prince-of-Wales Feather, Prince's Feather
Scientific Name : *Amaranthus hypochondriacus* L.
Plant Class : Dicotyledonae
Plant Order : Caryophyllales
Plant Family : Amaranthaceae
Genus : Amaranthus
Species : A. hypochondriacus
Abbreviation : *A. hypochondriacus*
Ploidy Level : Diploid
Chromosome Number : 2n=2x=32
Estimated Genome Size : 466 Mb

Go for the Available Genomic Informations:

(ii) ***A. tuberculatus***



Amaranthus tuberculatus

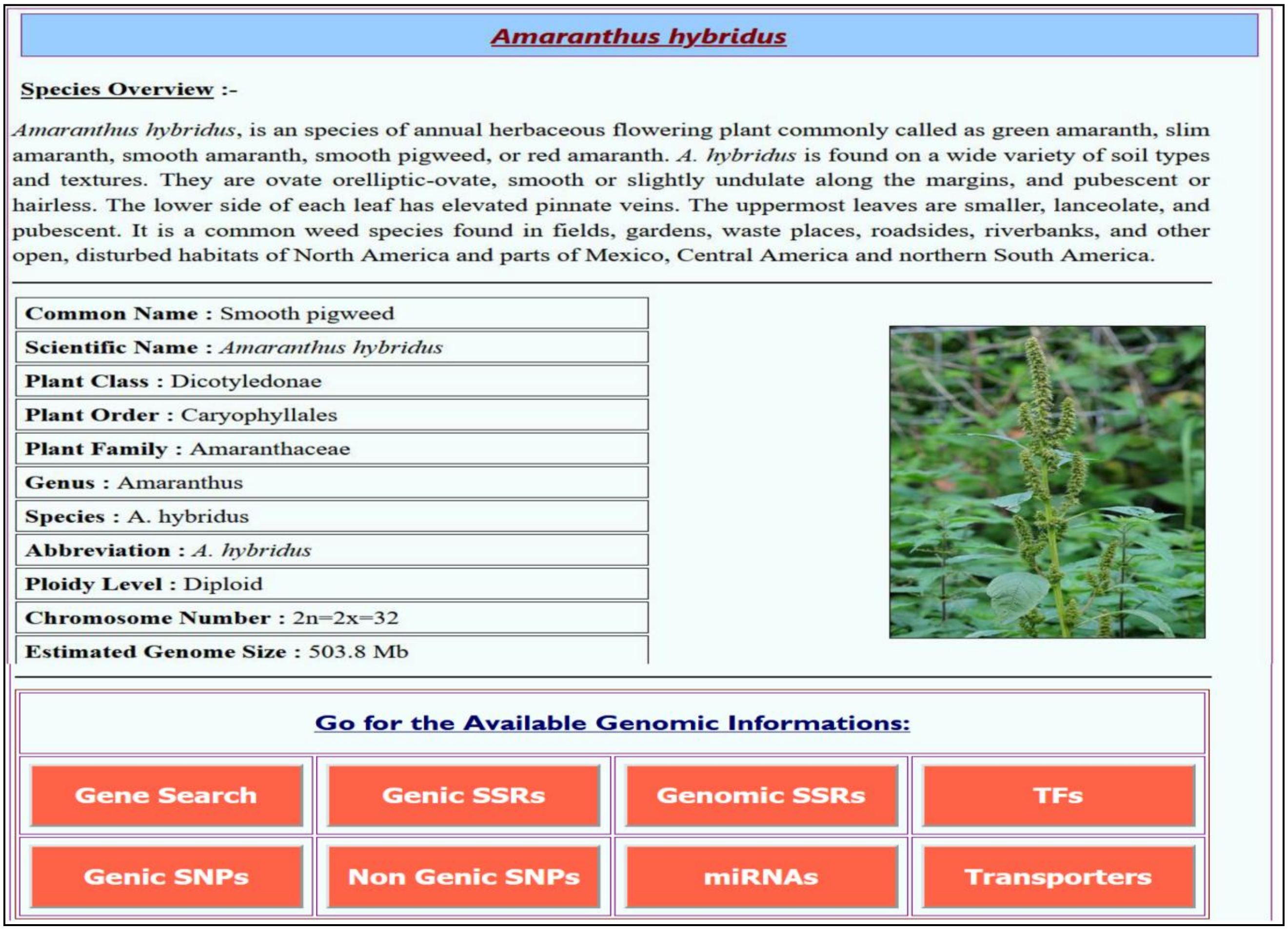
Species Overview :-

Amaranthus tuberculatus is an annual dioecious herb which has spread from its native range in northern North America and is considered a major weed of crop fields in the midwestern United States. It is commonly known as rough fruit amaranth, rough-fruited water-hemp, tall waterhemp, or common waterhemp, is a species of flowering plant. In the mid-western USA it has become increasingly difficult to control over the past 10 years due to a persistent seed bank and the development of resistance to certain herbicides. A. tuberculatus seed is a known contaminant of soyabean seed and other grains, and has been accidentally introduced and become naturalized in parts of West Asia and Europe.

Common Name : Rough-fruited water-hemp
Scientific Name : *Amaranthus tuberculatus*
Plant Class : Dicotyledonae
Plant Order : Caryophyllales
Plant Family : Amaranthaceae
Genus : Amaranthus
Species : A. tuberculatus
Abbreviation : *A. tuberculatus*
Ploidy Level : Diploid
Chromosome Number : 2n=2x=32
Estimated Genome Size : 675.6 Mb

Go for the Available Genomic Informations:

(iii) *A. hybridus*



Amaranthus hybridus

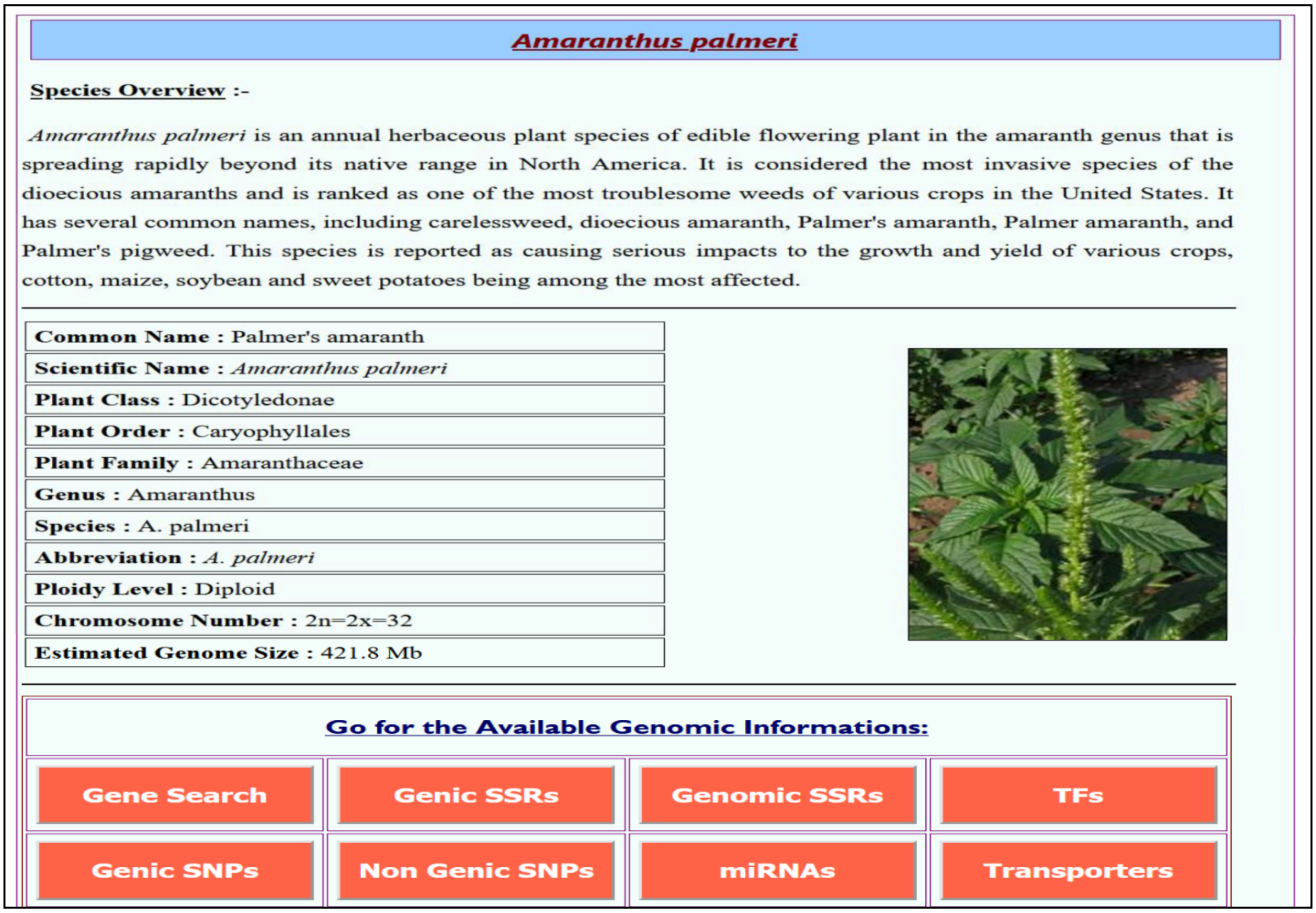
Species Overview :-

Amaranthus hybridus, is an species of annual herbaceous flowering plant commonly called as green amaranth, slim amaranth, smooth amaranth, smooth pigweed, or red amaranth. *A. hybridus* is found on a wide variety of soil types and textures. They are ovate orelliptic-ovate, smooth or slightly undulate along the margins, and pubescent or hairless. The lower side of each leaf has elevated pinnate veins. The uppermost leaves are smaller, lanceolate, and pubescent. It is a common weed species found in fields, gardens, waste places, roadsides, riverbanks, and other open, disturbed habitats of North America and parts of Mexico, Central America and northern South America.

Common Name : Smooth pigweed
Scientific Name : *Amaranthus hybridus*
Plant Class : Dicotyledonae
Plant Order : Caryophyllales
Plant Family : Amaranthaceae
Genus : Amaranthus
Species : A. hybridus
Abbreviation : *A. hybridus*
Ploidy Level : Diploid
Chromosome Number : 2n=2x=32
Estimated Genome Size : 503.8 Mb

Go for the Available Genomic Informations:

(iv) *A. palmeri*



Amaranthus palmeri

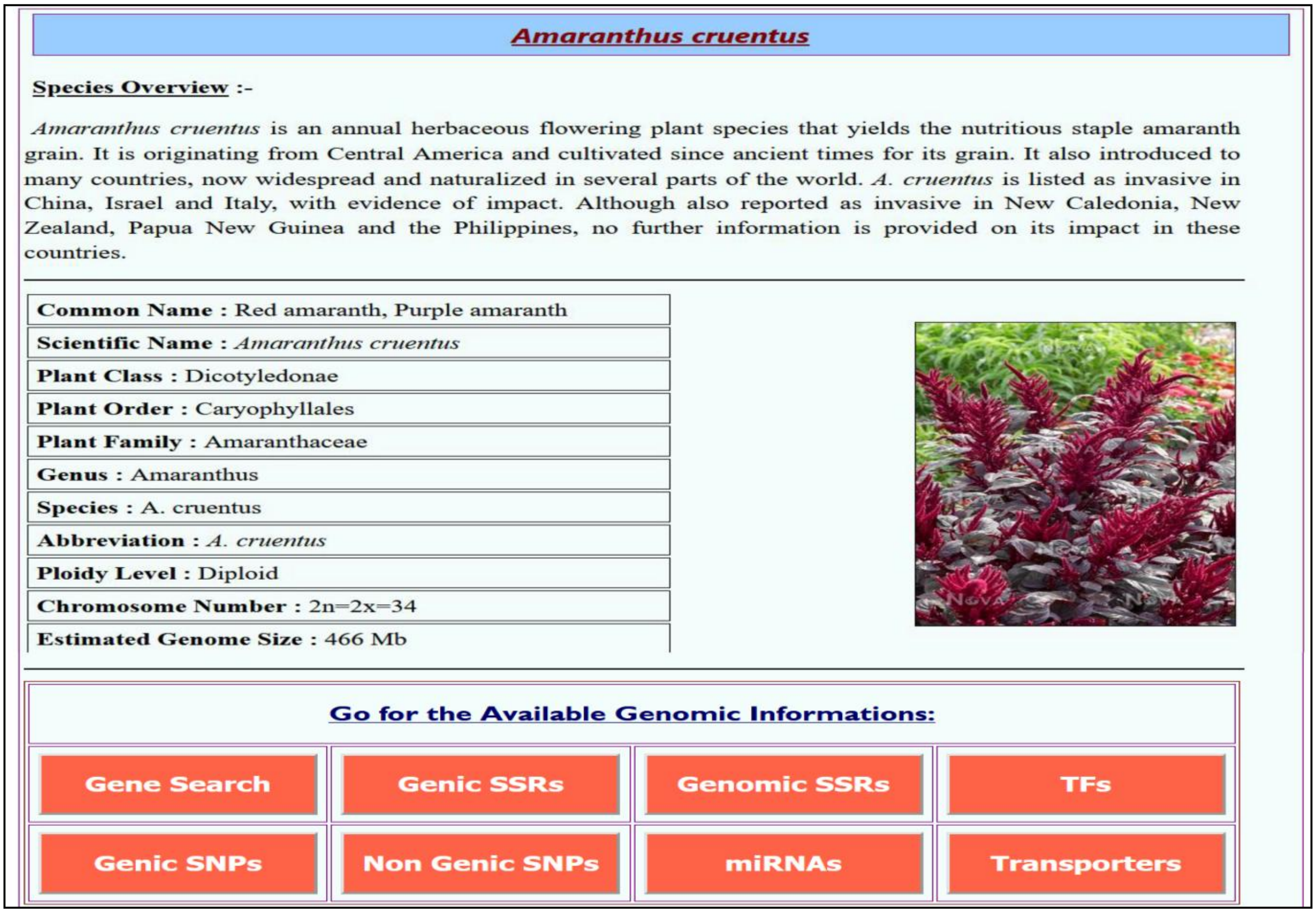
Species Overview :-

Amaranthus palmeri is an annual herbaceous plant species of edible flowering plant in the amaranth genus that is spreading rapidly beyond its native range in North America. It is considered the most invasive species of the dioecious amaranths and is ranked as one of the most troublesome weeds of various crops in the United States. It has several common names, including carelessweed, dioecious amaranth, Palmer's amaranth, Palmer amaranth, and Palmer's pigweed. This species is reported as causing serious impacts to the growth and yield of various crops, cotton, maize, soybean and sweet potatoes being among the most affected.

Common Name : Palmer's amaranth
Scientific Name : *Amaranthus palmeri*
Plant Class : Dicotyledonae
Plant Order : Caryophyllales
Plant Family : Amaranthaceae
Genus : Amaranthus
Species : A. palmeri
Abbreviation : *A. palmeri*
Ploidy Level : Diploid
Chromosome Number : 2n=2x=32
Estimated Genome Size : 421.8 Mb

Go for the Available Genomic Informations:

(v) *A. cruentus*



Amaranthus cruentus

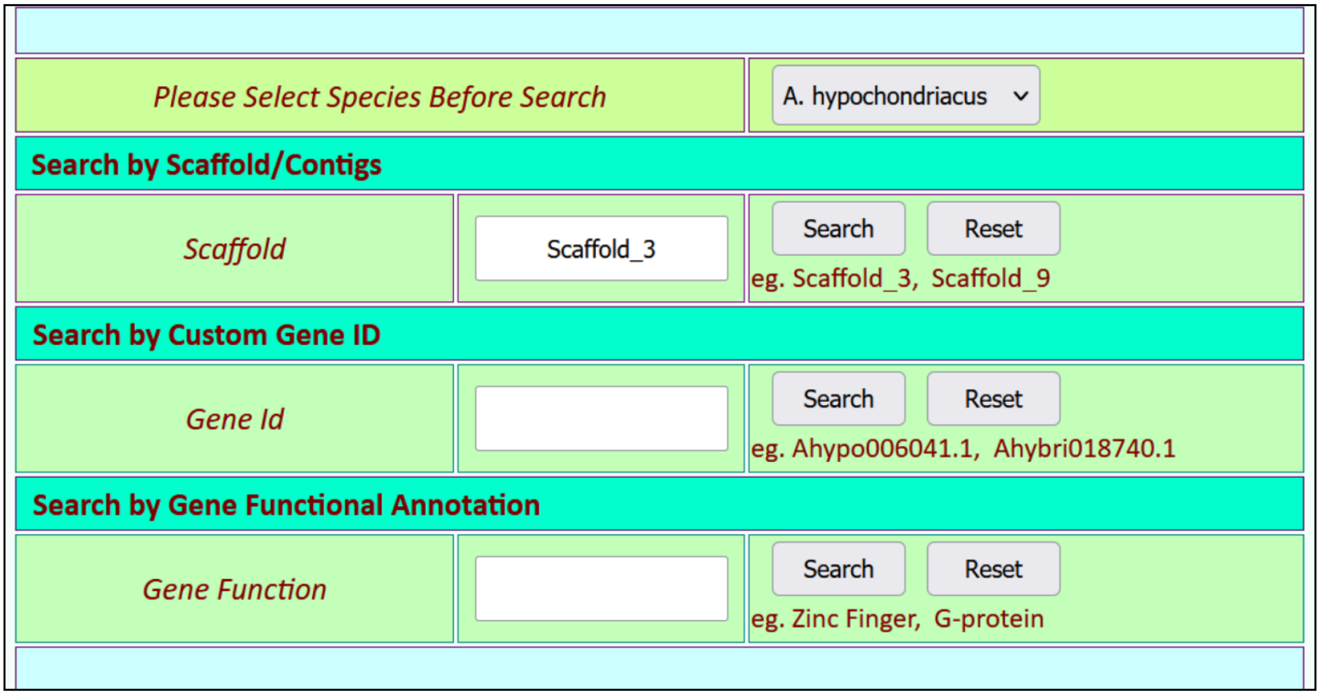
Species Overview :-

Amaranthus cruentus is an annual herbaceous flowering plant species that yields the nutritious staple amaranth grain. It is originating from Central America and cultivated since ancient times for its grain. It also introduced to many countries, now widespread and naturalized in several parts of the world. *A. cruentus* is listed as invasive in China, Israel and Italy, with evidence of impact. Although also reported as invasive in New Caledonia, New Zealand, Papua New Guinea and the Philippines, no further information is provided on its impact in these countries.

Common Name : Red amaranth, Purple amaranth
Scientific Name : *Amaranthus cruentus*
Plant Class : Dicotyledonae
Plant Order : Caryophyllales
Plant Family : Amaranthaceae
Genus : Amaranthus
Species : A. cruentus
Abbreviation : *A. cruentus*
Ploidy Level : Diploid
Chromosome Number : 2n=2x=34
Estimated Genome Size : 466 Mb

Go for the Available Genomic Informations:

3: Gene Search (First selects the species from dropdown, and then choose any of the search criteria given below for gene search)



Please Select Species Before Search: A. hypochondriacus

Search by Scaffold/Contigs

Scaffold: Scaffold_3
eg. Scaffold_3, Scaffold_9

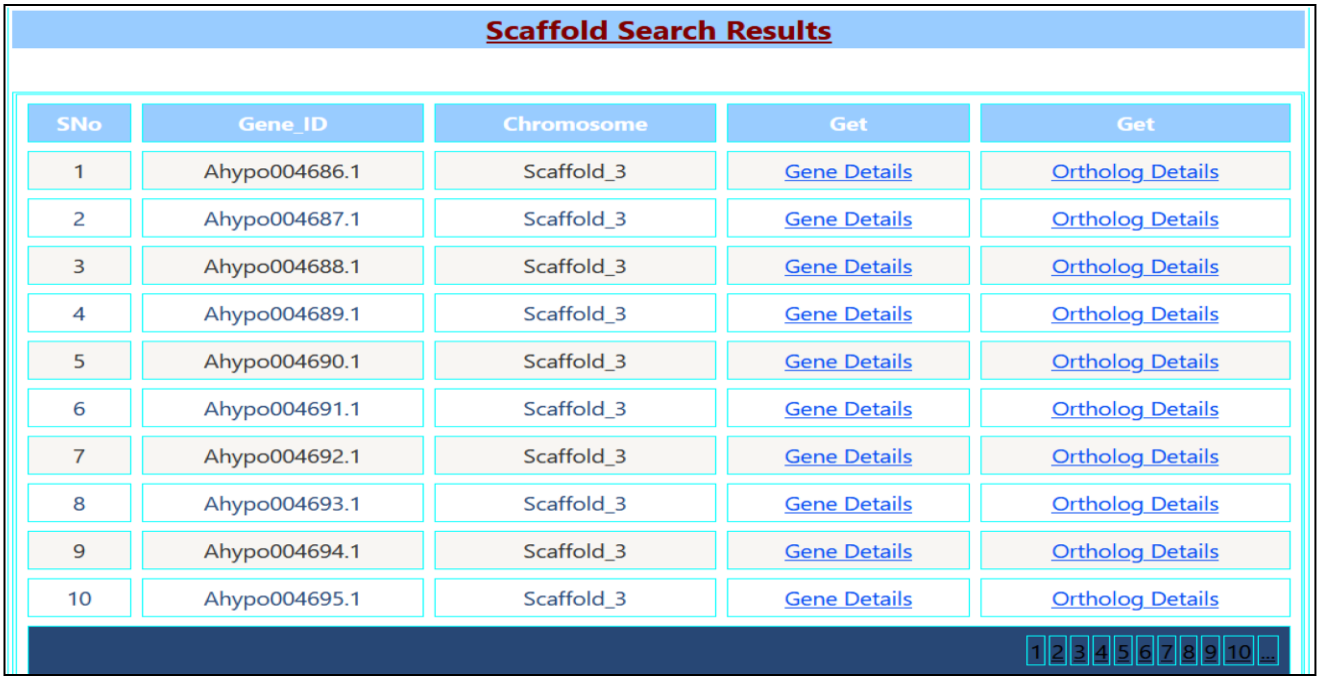
Search by Custom Gene ID

Gene Id
eg. Ahypo006041.1, Ahybri018740.1

Search by Gene Functional Annotation

Gene Function
eg. Zinc Finger, G-protein

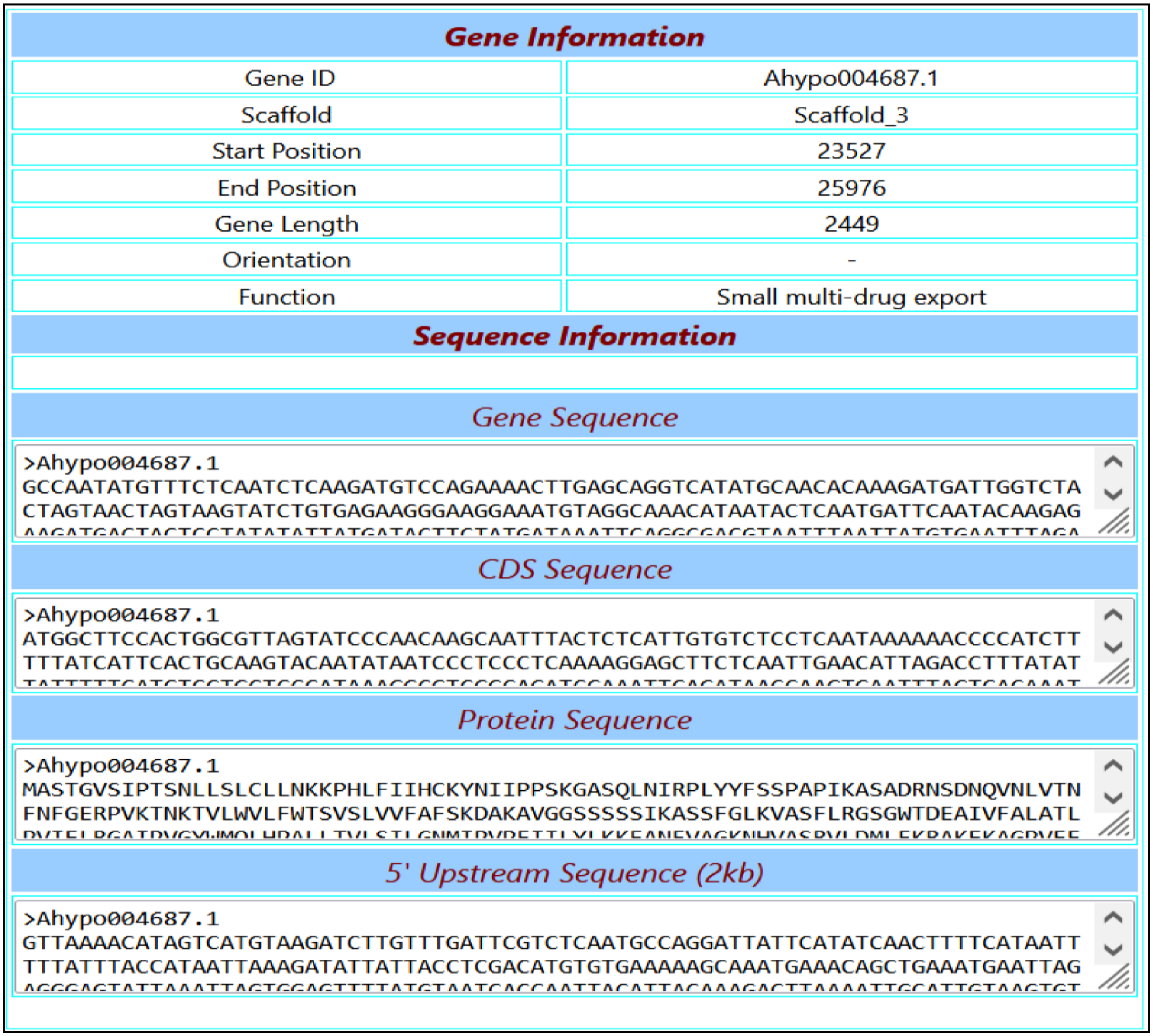
Search by Scaffold: (It gives scaffold wise list of genes)



Scaffold Search Results

SNo	Gene_ID	Chromosome	Get	Get
1	Ahypo004686.1	Scaffold_3	Gene Details	Ortholog Details
2	Ahypo004687.1	Scaffold_3	Gene Details	Ortholog Details
3	Ahypo004688.1	Scaffold_3	Gene Details	Ortholog Details
4	Ahypo004689.1	Scaffold_3	Gene Details	Ortholog Details
5	Ahypo004690.1	Scaffold_3	Gene Details	Ortholog Details
6	Ahypo004691.1	Scaffold_3	Gene Details	Ortholog Details
7	Ahypo004692.1	Scaffold_3	Gene Details	Ortholog Details
8	Ahypo004693.1	Scaffold_3	Gene Details	Ortholog Details
9	Ahypo004694.1	Scaffold_3	Gene Details	Ortholog Details
10	Ahypo004695.1	Scaffold_3	Gene Details	Ortholog Details

Gene Details: (It gives gene information as well as sequence information)



Gene Information

Gene ID	Ahypo004687.1
Scaffold	Scaffold_3
Start Position	23527
End Position	25976
Gene Length	2449
Orientation	-
Function	Small multi-drug export

Sequence Information

Gene Sequence

```
>Ahypo004687.1
GCCAATATGTTTCTCAATCTCAAGATGTCCAGAAAACTTGAGCAGGTCATATGCAACACAAAGATGATTGGTCTA
CTAGTAACTAGTAAGTATCTGTGAGAAGGGAAGGAAATGTAGGCAAACATAATACTCAATGATTCAATACAAGAG
```

CDS Sequence

```
>Ahypo004687.1
ATGGCTTCCACTGGCGTTAGTATCCCAACAAGCAATTTACTCTCATTGTGTCTCCTCAATAAAAAACCCCATCTT
TTTATCATTCACTGCAAGTACAATATAATCCCTCCCTCAAAAGGAGCTTCTCAATTGAACATTAGACCTTTATAT
```

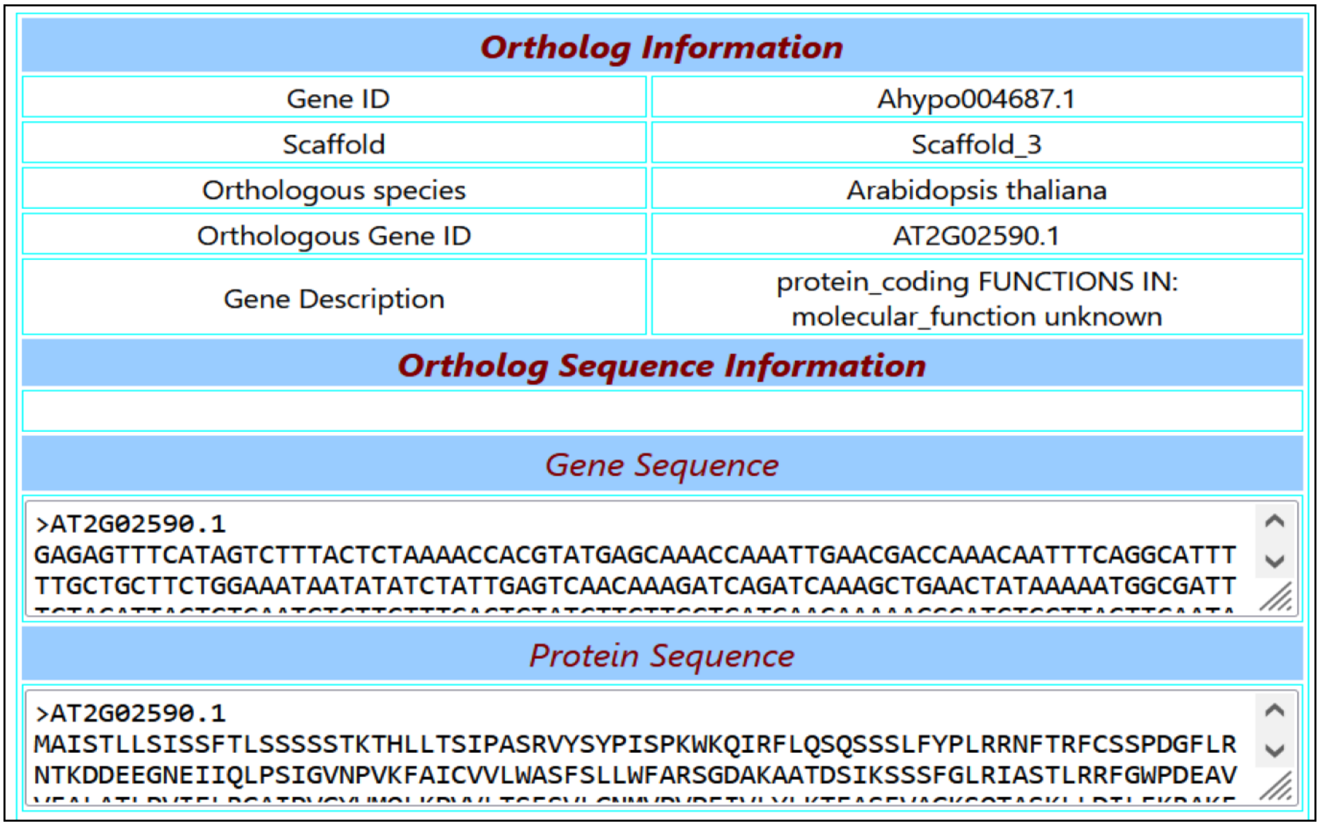
Protein Sequence

```
>Ahypo004687.1
MASTGVSIPTSNLLSLCLLNKKPHLFIIHCKYNIIPPSKGASQLNIRPLYYFSSPAPIKASADRNSDNQVNLVTN
FNFGERPVKTNKTVLWVLFWTSVSLVVFAFSKDAKAVGGSSSSSIKASSFGLKVASFLRGSGWTDEAIVFALATL
```

5' Upstream Sequence (2kb)

```
>Ahypo004687.1
GTTAAAACATAGTCATGTAAGATCTTGTTTGATTCGTCTCAATGCCAGGATTATTCATATCAACTTTTCATAATT
TTTATTTACCATAATTAAAGATATTATTACCTCGACATGTGTGAAAAAGCAAATGAAACAGCTGAAATGAATTAG
```

Ortholog Details: (It gives Ortholog information with *Arabidopsis thaliana* as well as sequence information)



Ortholog Information

Gene ID	Ahypo004687.1
Scaffold	Scaffold_3
Orthologous species	Arabidopsis thaliana
Orthologous Gene ID	AT2G02590.1
Gene Description	protein_coding FUNCTIONS IN: molecular_function unknown

Ortholog Sequence Information

Gene Sequence

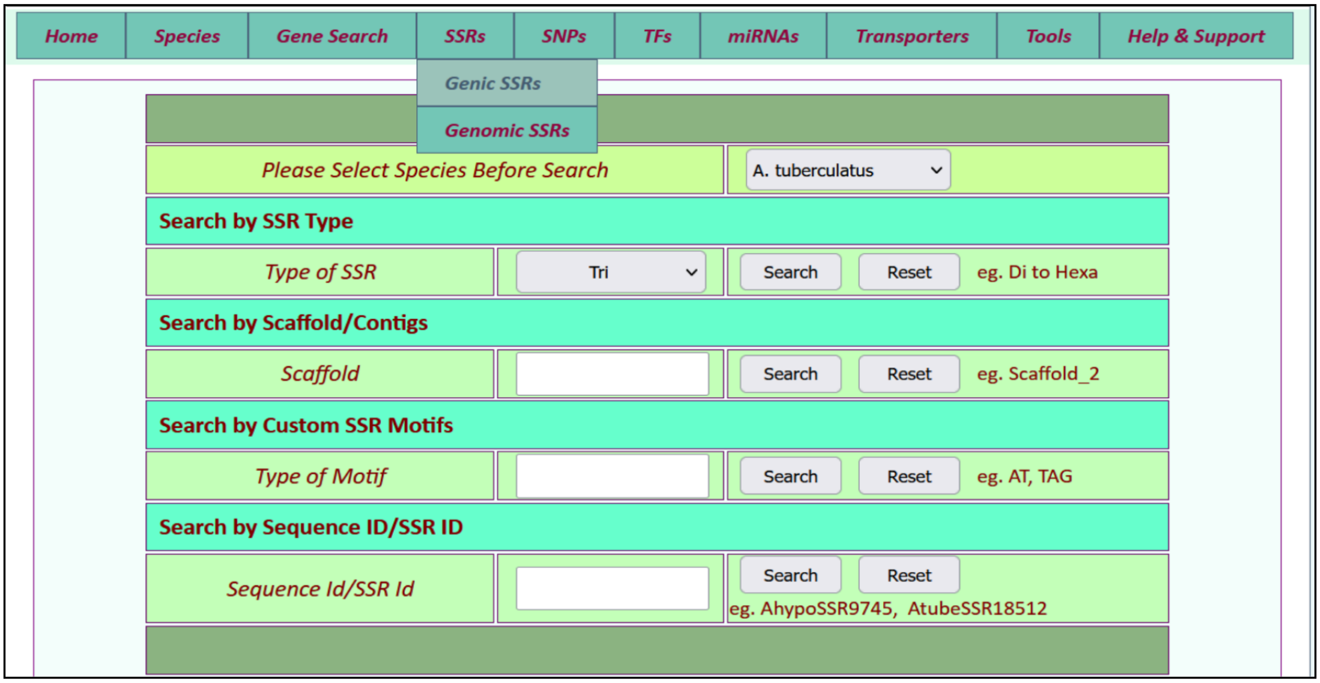
```
>AT2G02590.1
GAGAGTTTCATAGTCTTTACTCTAAAACCACGTATGAGCAAACCAAATTGAACGACCAAACAATTTCAGGCATTT
TTGCTGCTTCTGGAAATAATATATCTATTGAGTCAACAAAGATCAGATCAAAGCTGAACTATAAAAATGGCGATT
```

Protein Sequence

```
>AT2G02590.1
MAISTLLSISSFTLSSSSSTKTHLLTSIPASRVYSYPISPKWKQIRFLQSQSSSLFYPLRRNFTRFCSSPDGFLR
NTKDDEEGNEIIQLPSIGVNPVKFAICVVLWASFSLLWFARSGDAKAATDSIKSSSFGLRIASTLRRFGWPDEAV
```

4: SSRs (Genic and Genomic SSR Search)

Genic SSRs (First select the species from dropdown then select any of the four different criteria of SSR search)



Please Select Species Before Search: A. tuberculatus

Search by SSR Type

Type of SSR: Tri

eg. Di to Hexa

Search by Scaffold/Contigs

Scaffold

eg. Scaffold_2

Search by Custom SSR Motifs

Type of Motif

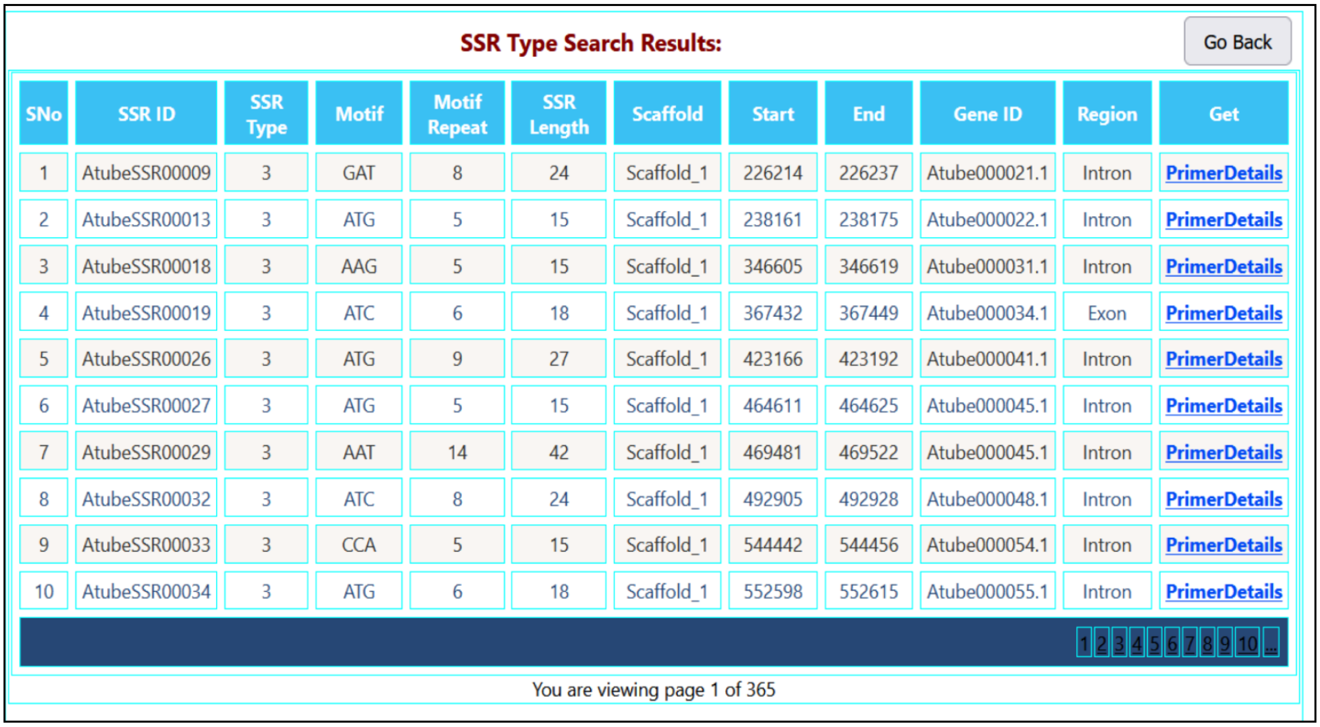
eg. AT, TAG

Search by Sequence ID/SSR ID

Sequence Id/SSR Id

eg. AhypoSSR9745, AtubeSSR18512

Search by SSR Type: (Select type of SSR from dropdown list then search)

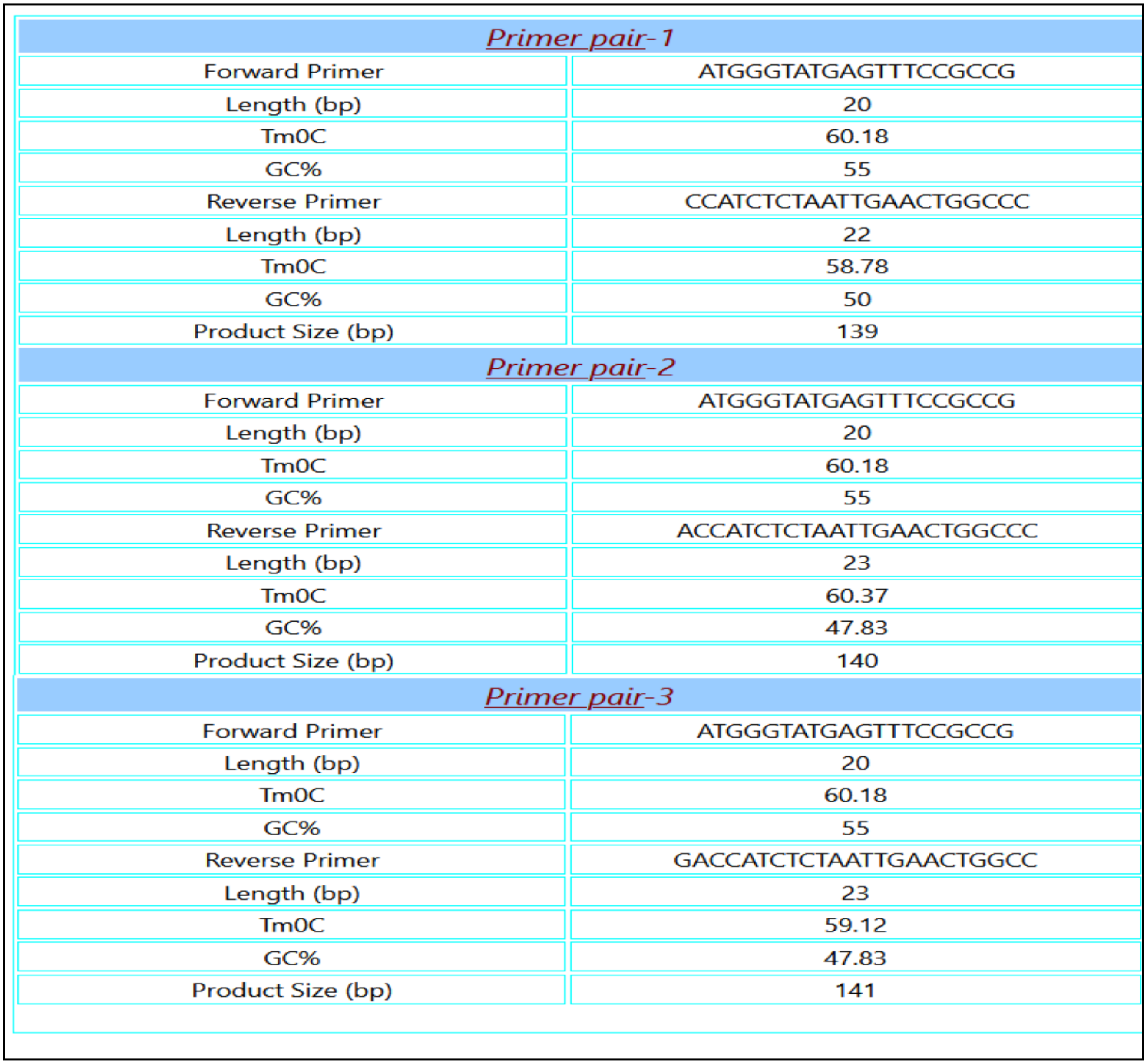


SSR Type Search Results:

SNo	SSR ID	SSR Type	Motif	Motif Repeat	SSR Length	Scaffold	Start	End	Gene ID	Region	Get
1	AtubeSSR00009	3	GAT	8	24	Scaffold_1	226214	226237	Atube000021.1	Intron	PrimerDetails
2	AtubeSSR00013	3	ATG	5	15	Scaffold_1	238161	238175	Atube000022.1	Intron	PrimerDetails
3	AtubeSSR00018	3	AAG	5	15	Scaffold_1	346605	346619	Atube000031.1	Intron	PrimerDetails
4	AtubeSSR00019	3	ATC	6	18	Scaffold_1	367432	367449	Atube000034.1	Exon	PrimerDetails
5	AtubeSSR00026	3	ATG	9	27	Scaffold_1	423166	423192	Atube000041.1	Intron	PrimerDetails
6	AtubeSSR00027	3	ATG	5	15	Scaffold_1	464611	464625	Atube000045.1	Intron	PrimerDetails
7	AtubeSSR00029	3	AAT	14	42	Scaffold_1	469481	469522	Atube000045.1	Intron	PrimerDetails
8	AtubeSSR00032	3	ATC	8	24	Scaffold_1	492905	492928	Atube000048.1	Intron	PrimerDetails
9	AtubeSSR00033	3	CCA	5	15	Scaffold_1	544442	544456	Atube000054.1	Intron	PrimerDetails
10	AtubeSSR00034	3	ATG	6	18	Scaffold_1	552598	552615	Atube000055.1	Intron	PrimerDetails

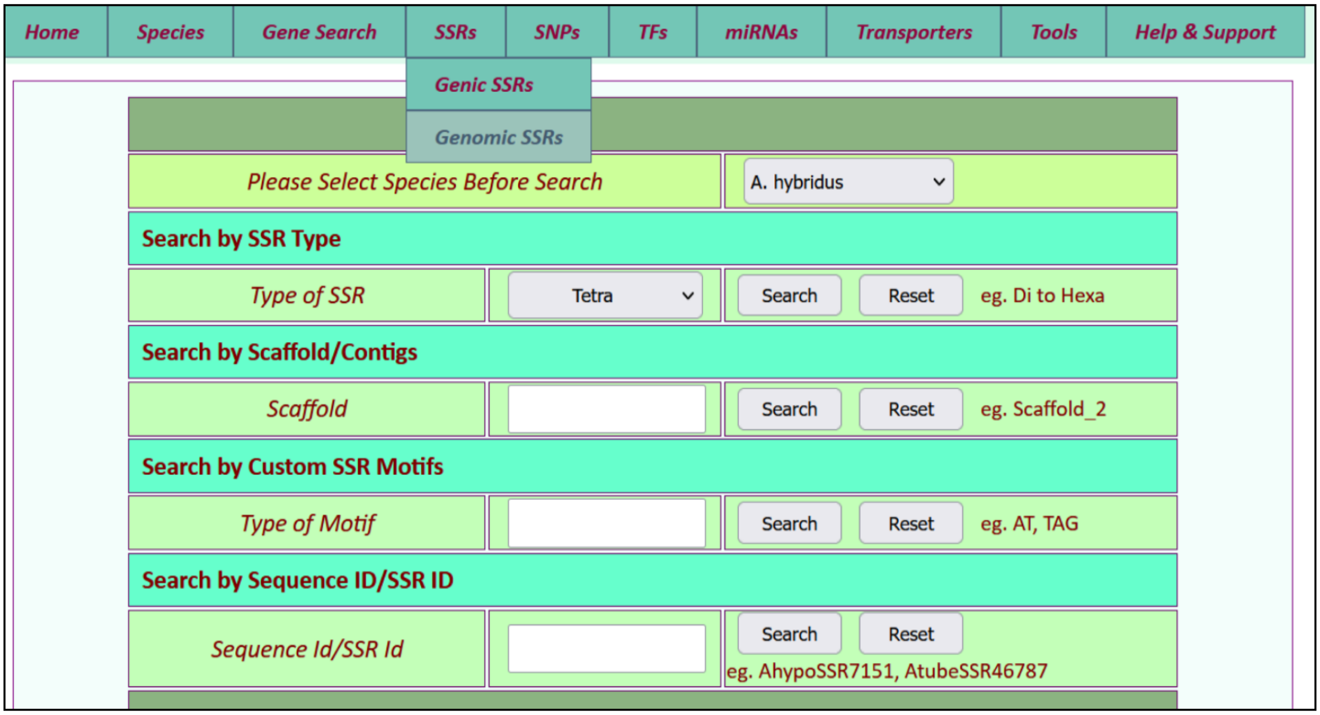
You are viewing page 1 of 365

Primer Details: (It gives three pair of primers details)



Primer pair-1	
Forward Primer	ATGGGTATGAGTTTCCGCCG
Length (bp)	20
Tm0C	60.18
GC%	55
Reverse Primer	CCATCTCTAATTGAACTGGCCC
Length (bp)	22
Tm0C	58.78
GC%	50
Product Size (bp)	139
Primer pair-2	
Forward Primer	ATGGGTATGAGTTTCCGCCG
Length (bp)	20
Tm0C	60.18
GC%	55
Reverse Primer	ACCATCTCTAATTGAACTGGCCC
Length (bp)	23
Tm0C	60.37
GC%	47.83
Product Size (bp)	140
Primer pair-3	
Forward Primer	ATGGGTATGAGTTTCCGCCG
Length (bp)	20
Tm0C	60.18
GC%	55
Reverse Primer	GACCATCTCTAATTGAACTGGCC
Length (bp)	23
Tm0C	59.12
GC%	47.83
Product Size (bp)	141

Genomic SSRs (First select the species from dropdown then select any of the four different criteria of SSR search)



Please Select Species Before Search
A. hybridus

Search by SSR Type

Type of SSR
Tetra
eg. Di to Hexa

Search by Scaffold/Contigs

Scaffold
eg. Scaffold_2

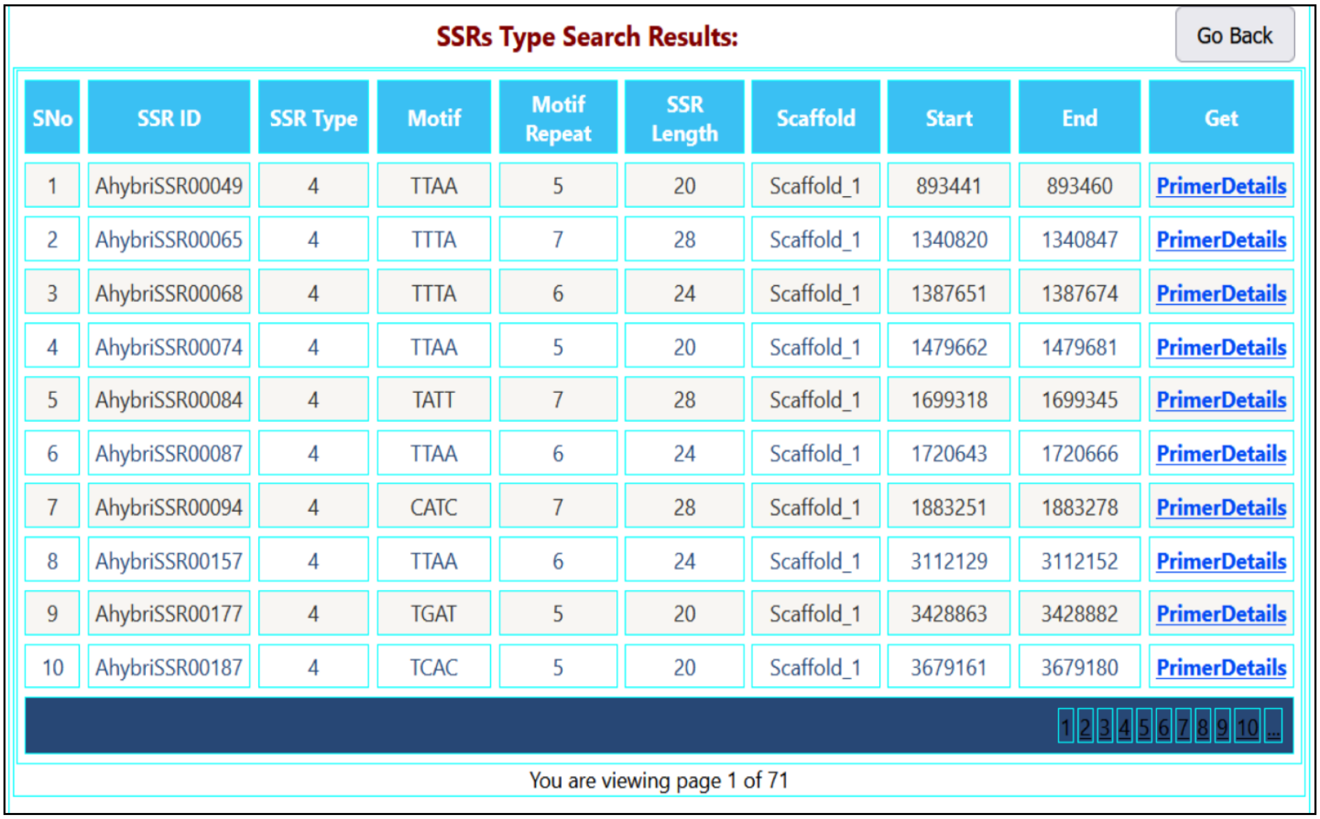
Search by Custom SSR Motifs

Type of Motif
eg. AT, TAG

Search by Sequence ID/SSR ID

Sequence Id/SSR Id
eg. AhypoSSR7151, AtubeSSR46787

Search by SSR Type: (Select type of SSR from dropdown list then search)

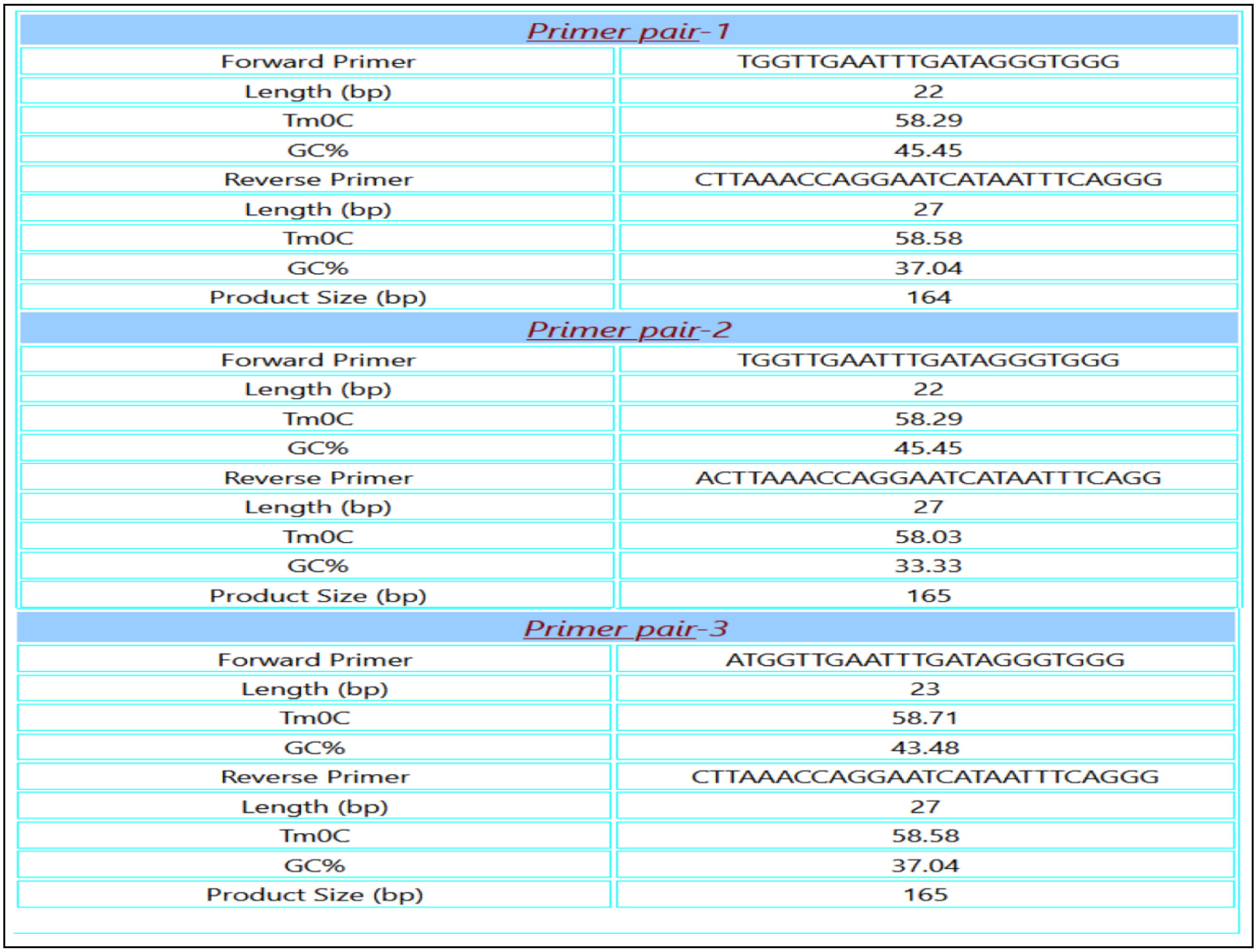


SSRs Type Search Results:

SNo	SSR ID	SSR Type	Motif	Motif Repeat	SSR Length	Scaffold	Start	End	Get
1	AhybriSSR00049	4	TTAA	5	20	Scaffold_1	893441	893460	PrimerDetails
2	AhybriSSR00065	4	TTTA	7	28	Scaffold_1	1340820	1340847	PrimerDetails
3	AhybriSSR00068	4	TTTA	6	24	Scaffold_1	1387651	1387674	PrimerDetails
4	AhybriSSR00074	4	TTAA	5	20	Scaffold_1	1479662	1479681	PrimerDetails
5	AhybriSSR00084	4	TATT	7	28	Scaffold_1	1699318	1699345	PrimerDetails
6	AhybriSSR00087	4	TTAA	6	24	Scaffold_1	1720643	1720666	PrimerDetails
7	AhybriSSR00094	4	CATC	7	28	Scaffold_1	1883251	1883278	PrimerDetails
8	AhybriSSR00157	4	TTAA	6	24	Scaffold_1	3112129	3112152	PrimerDetails
9	AhybriSSR00177	4	TGAT	5	20	Scaffold_1	3428863	3428882	PrimerDetails
10	AhybriSSR00187	4	TCAC	5	20	Scaffold_1	3679161	3679180	PrimerDetails

You are viewing page 1 of 71

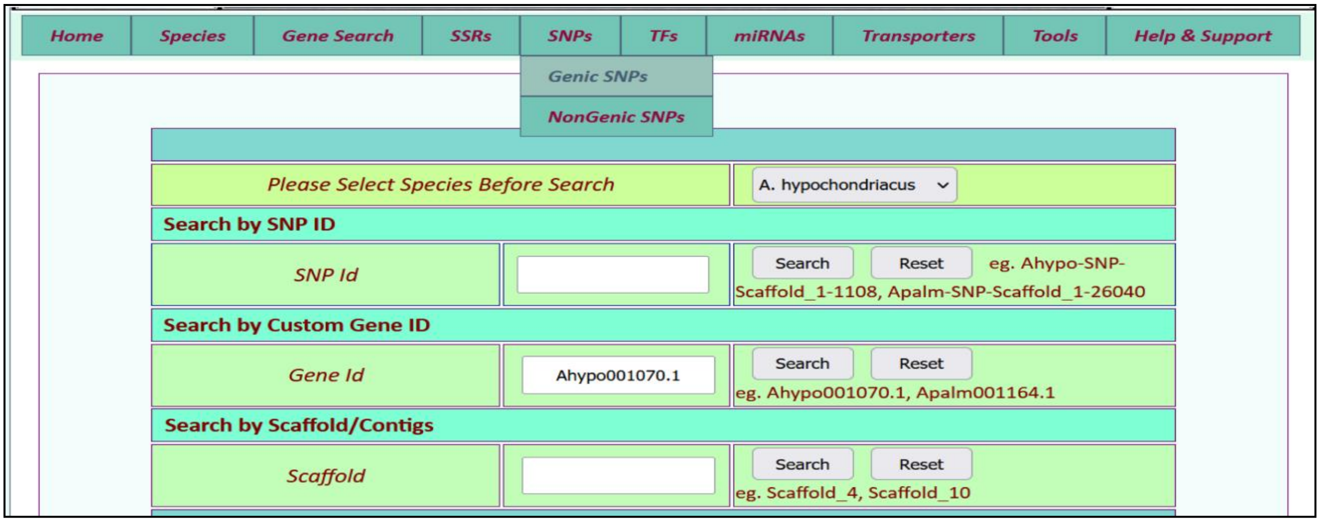
Primer Details: (It gives three pair of primers details)



Primer pair-1	
Forward Primer	TGGTTGAATTTGATAGGGTGGG
Length (bp)	22
Tm0C	58.29
GC%	45.45
Reverse Primer	CTTAAACCAGGAATCATAATTTCAGGG
Length (bp)	27
Tm0C	58.58
GC%	37.04
Product Size (bp)	164
Primer pair-2	
Forward Primer	TGGTTGAATTTGATAGGGTGGG
Length (bp)	22
Tm0C	58.29
GC%	45.45
Reverse Primer	ACTTAAACCAGGAATCATAATTTCAGG
Length (bp)	27
Tm0C	58.03
GC%	33.33
Product Size (bp)	165
Primer pair-3	
Forward Primer	ATGGTTGAATTTGATAGGGTGGG
Length (bp)	23
Tm0C	58.71
GC%	43.48
Reverse Primer	CTTAAACCAGGAATCATAATTTCAGGG
Length (bp)	27
Tm0C	58.58
GC%	37.04
Product Size (bp)	165

5: SNPs

(Genic SNPs-Search SNPs present in Gene region; first select the species from dropdown then any of the search criteria for genic SNPs search)



Please Select Species Before Search: A. hypochondriacus

Search by SNP ID

SNP Id: Search Reset eg. Ahypo-SNP-Scaffold_1-1108, Apalm-SNP-Scaffold_1-26040

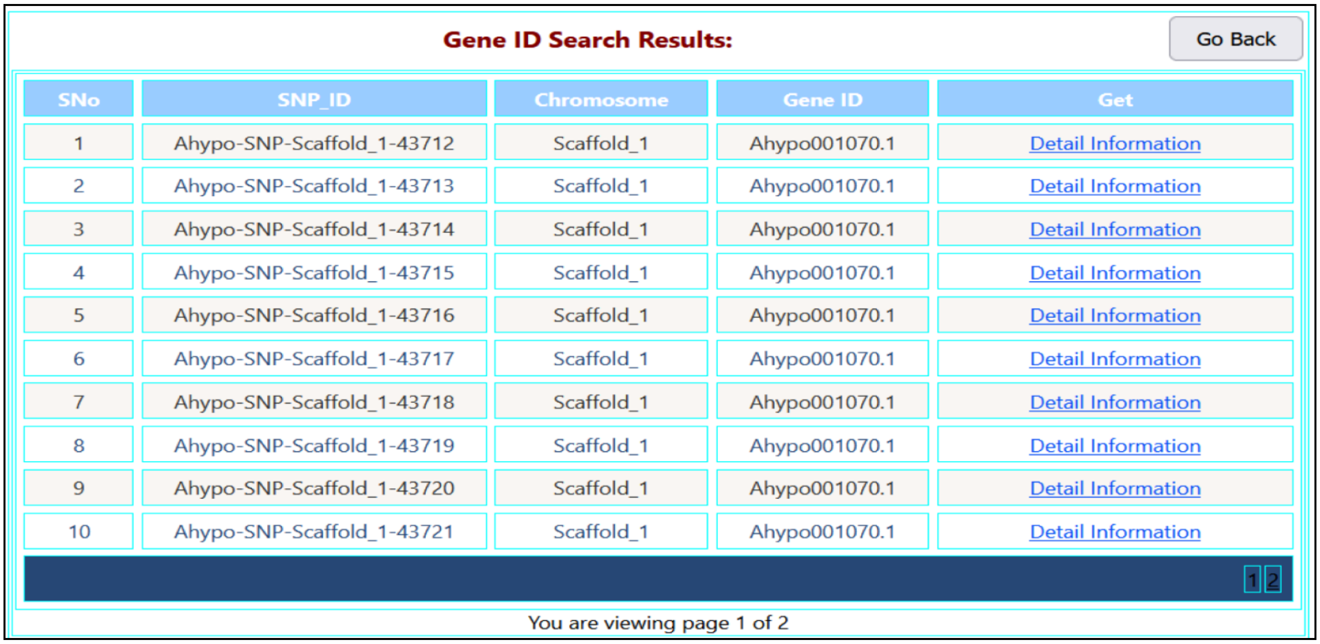
Search by Custom Gene ID

Gene Id: Ahypo001070.1 Search Reset eg. Ahypo001070.1, Apalm001164.1

Search by Scaffold/Contigs

Scaffold: Search Reset eg. Scaffold_4, Scaffold_10

Search by gene id: (It gives gene wise list of SNPs with gene details)

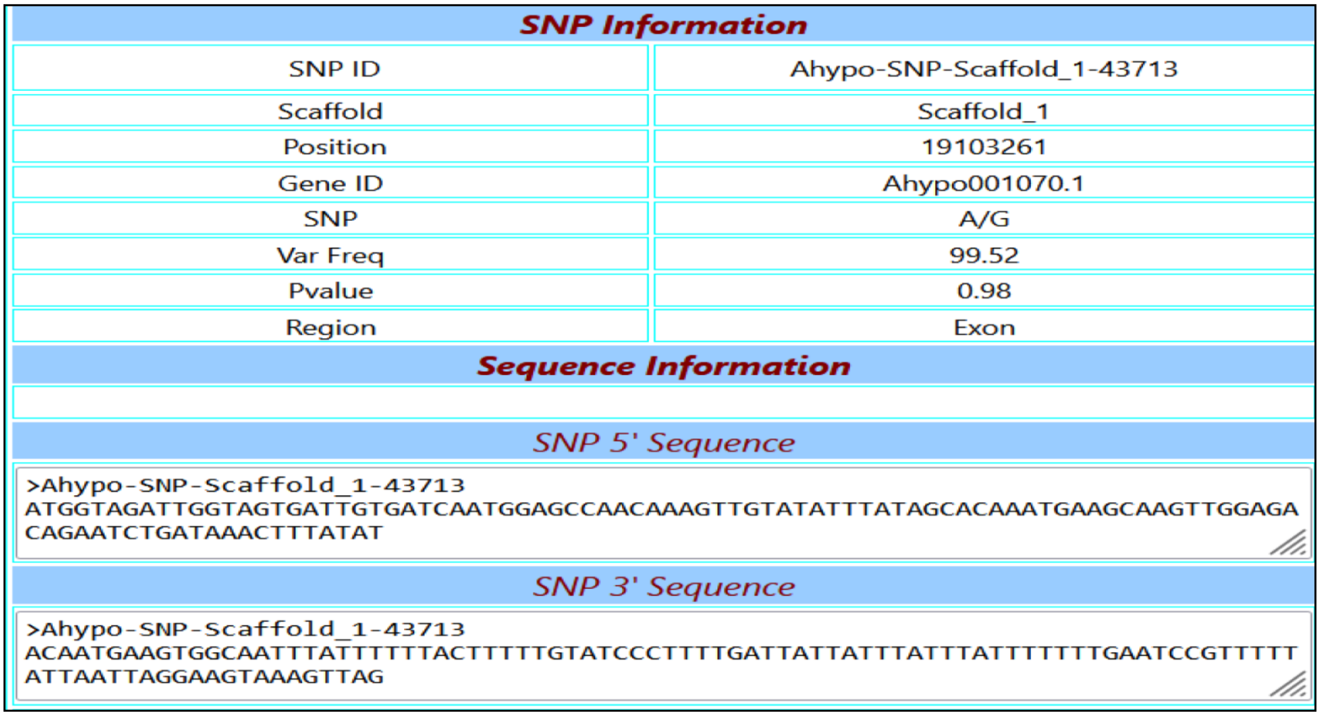


Gene ID Search Results:

SNo	SNP_ID	Chromosome	Gene ID	Get
1	Ahypo-SNP-Scaffold_1-43712	Scaffold_1	Ahypo001070.1	Detail Information
2	Ahypo-SNP-Scaffold_1-43713	Scaffold_1	Ahypo001070.1	Detail Information
3	Ahypo-SNP-Scaffold_1-43714	Scaffold_1	Ahypo001070.1	Detail Information
4	Ahypo-SNP-Scaffold_1-43715	Scaffold_1	Ahypo001070.1	Detail Information
5	Ahypo-SNP-Scaffold_1-43716	Scaffold_1	Ahypo001070.1	Detail Information
6	Ahypo-SNP-Scaffold_1-43717	Scaffold_1	Ahypo001070.1	Detail Information
7	Ahypo-SNP-Scaffold_1-43718	Scaffold_1	Ahypo001070.1	Detail Information
8	Ahypo-SNP-Scaffold_1-43719	Scaffold_1	Ahypo001070.1	Detail Information
9	Ahypo-SNP-Scaffold_1-43720	Scaffold_1	Ahypo001070.1	Detail Information
10	Ahypo-SNP-Scaffold_1-43721	Scaffold_1	Ahypo001070.1	Detail Information

You are viewing page 1 of 2

Detail Information: (It gives SNPs information as well as sequence information)



SNP Information

SNP ID	Ahypo-SNP-Scaffold_1-43713
Scaffold	Scaffold_1
Position	19103261
Gene ID	Ahypo001070.1
SNP	A/G
Var Freq	99.52
Pvalue	0.98
Region	Exon

Sequence Information

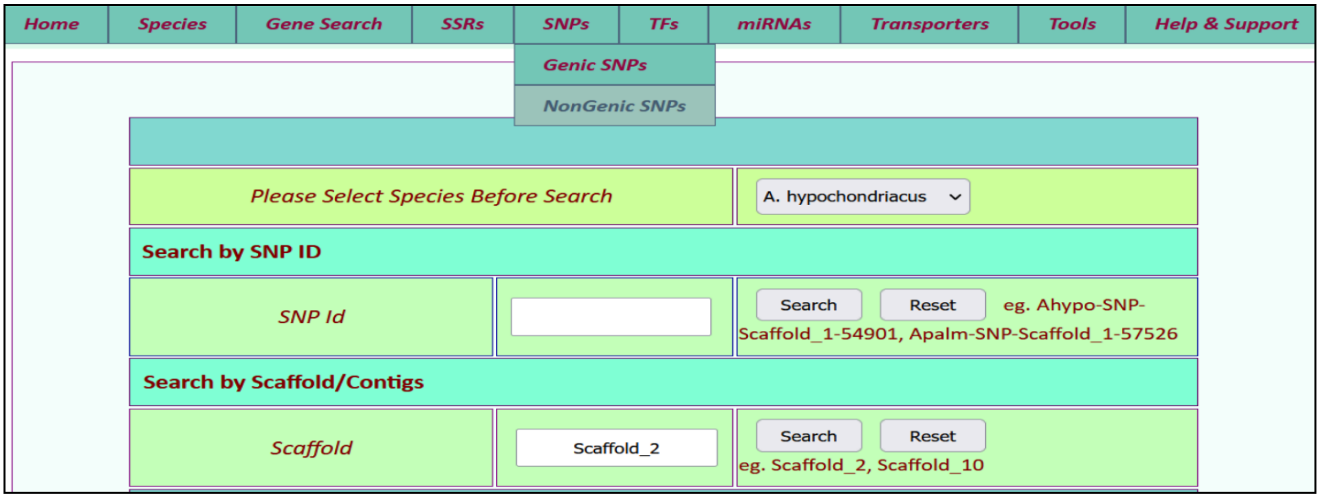
SNP 5' Sequence

```
>Ahypo-SNP-Scaffold_1-43713
ATGGTAGATTGGTAGTGATTGTGATCAATGGAGCCAACAAAGTTGTATATTTATAGCACAAATGAAGCAAGTTGGAGA
CAGAATCTGATAAACTTTATAT
```

SNP 3' Sequence

```
>Ahypo-SNP-Scaffold_1-43713
ACAATGAAGTGGCAATTTATTTTTTACTTTTTGTATCCCTTTTGATTATTATTTATTTATTTTTTTGAATCCGTTTTT
ATTAATTAGGAAGTAAAGTTAG
```

(**Non Genic SNPs-**Search SNPs present in non-genic region; first select the species from dropdown then any of the search criteria for non-genic SNPs search)



Please Select Species Before Search: A. hypochondriacus

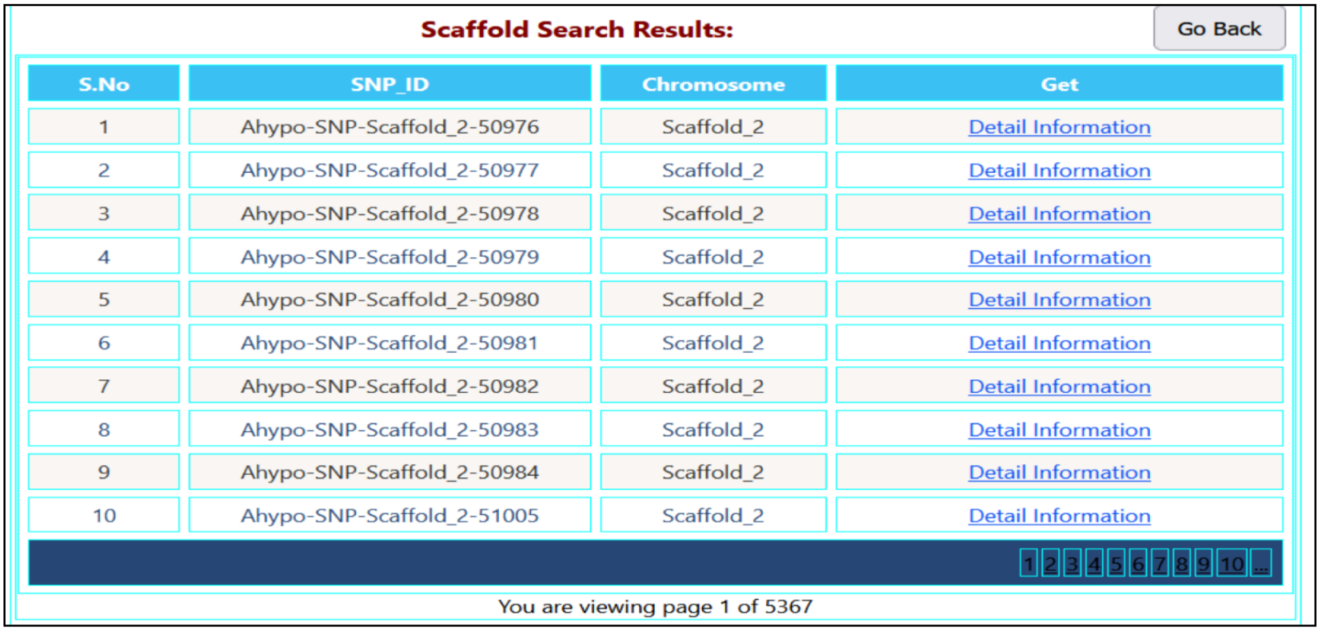
Search by SNP ID

SNP Id: eg. Ahypo-SNP-Scaffold_1-54901, Apalm-SNP-Scaffold_1-57526

Search by Scaffold/Contigs

Scaffold: Scaffold_2 — eg. Scaffold_2, Scaffold_10

Search by scaffold: (It gives list of non genic SNPs present in scaffold 2 of species *A. hypochondriacus*)

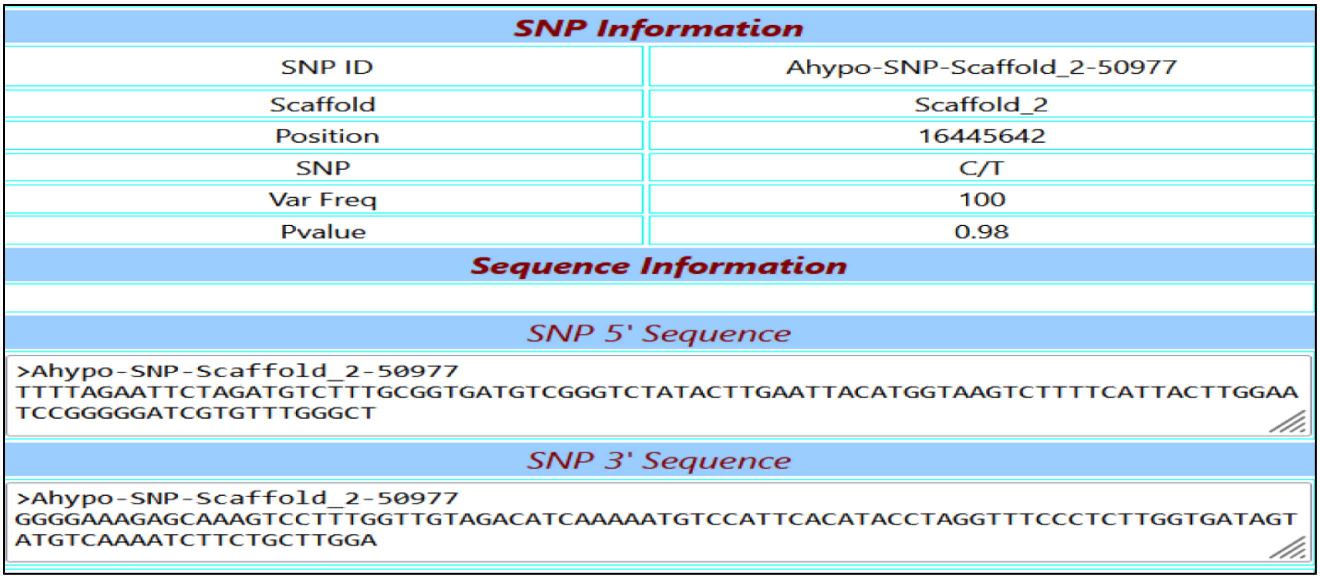


Scaffold Search Results:

S.No	SNP_ID	Chromosome	Get
1	Ahypo-SNP-Scaffold_2-50976	Scaffold_2	Detail Information
2	Ahypo-SNP-Scaffold_2-50977	Scaffold_2	Detail Information
3	Ahypo-SNP-Scaffold_2-50978	Scaffold_2	Detail Information
4	Ahypo-SNP-Scaffold_2-50979	Scaffold_2	Detail Information
5	Ahypo-SNP-Scaffold_2-50980	Scaffold_2	Detail Information
6	Ahypo-SNP-Scaffold_2-50981	Scaffold_2	Detail Information
7	Ahypo-SNP-Scaffold_2-50982	Scaffold_2	Detail Information
8	Ahypo-SNP-Scaffold_2-50983	Scaffold_2	Detail Information
9	Ahypo-SNP-Scaffold_2-50984	Scaffold_2	Detail Information
10	Ahypo-SNP-Scaffold_2-51005	Scaffold_2	Detail Information

You are viewing page 1 of 5367

Detail Information: (It gives SNPs information as well as sequence information)



SNP Information

SNP ID	Ahypo-SNP-Scaffold_2-50977
Scaffold	Scaffold_2
Position	16445642
SNP	C/T
Var Freq	100
Pvalue	0.98

Sequence Information

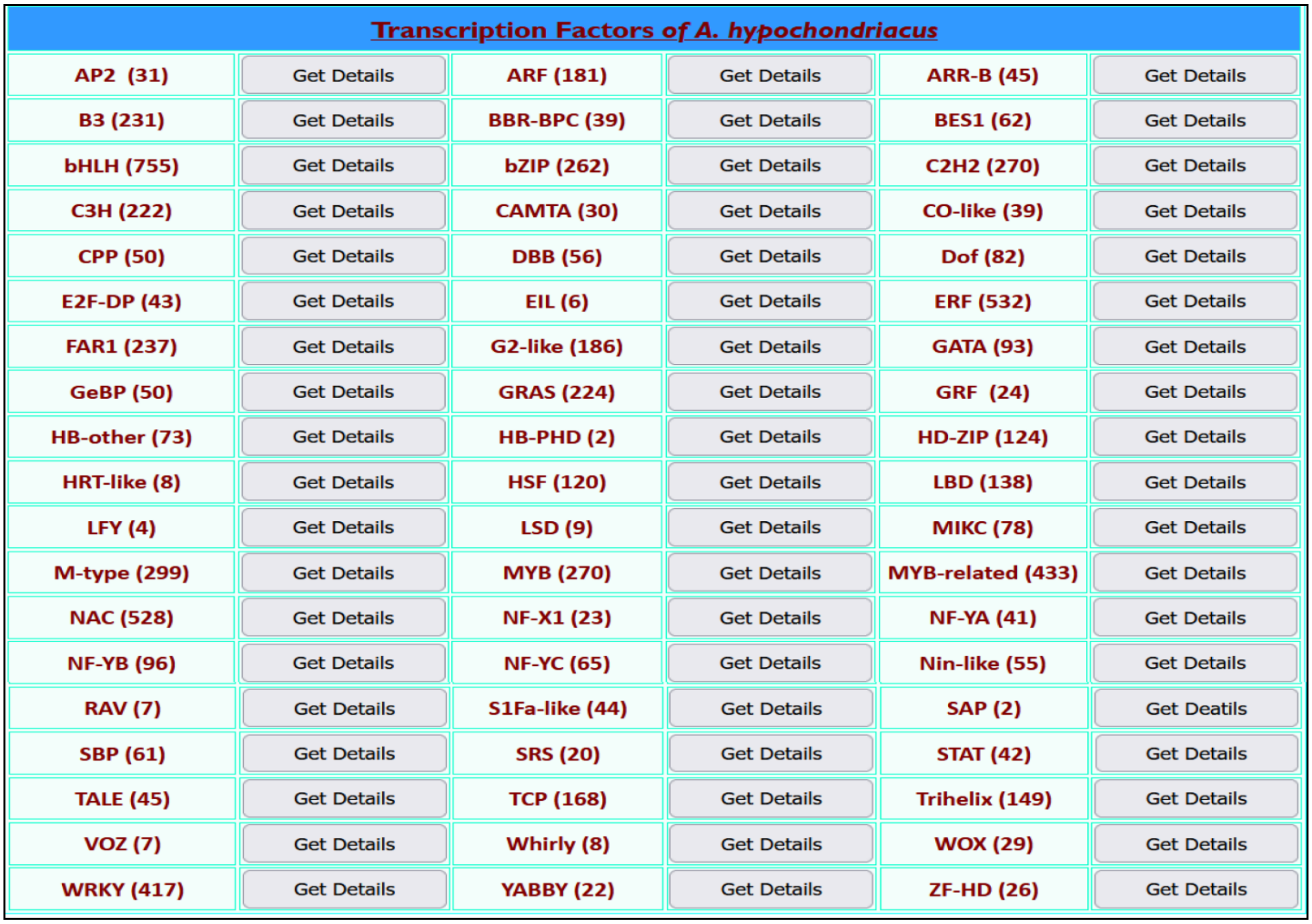
SNP 5' Sequence

```
>Ahypo-SNP-Scaffold_2-50977
TTTTAGAATTCTAGATGTCTTTGCGGTGATGTCGGGTCTATACTTGAATTACATGGTAAGTCTTTTCATTACTTGGAA
TCCGGGGGATCGTGTTTGGGCT
```

SNP 3' Sequence

```
>Ahypo-SNP-Scaffold_2-50977
GGGGAAAGAGCAAAGTCCTTTGGTTGTAGACATCAAAAATGTCCATTCACATACCTAGGTTTCCCTCTTGGTGATAGT
ATGTCAAAATCTTCTGCTTGGA
```

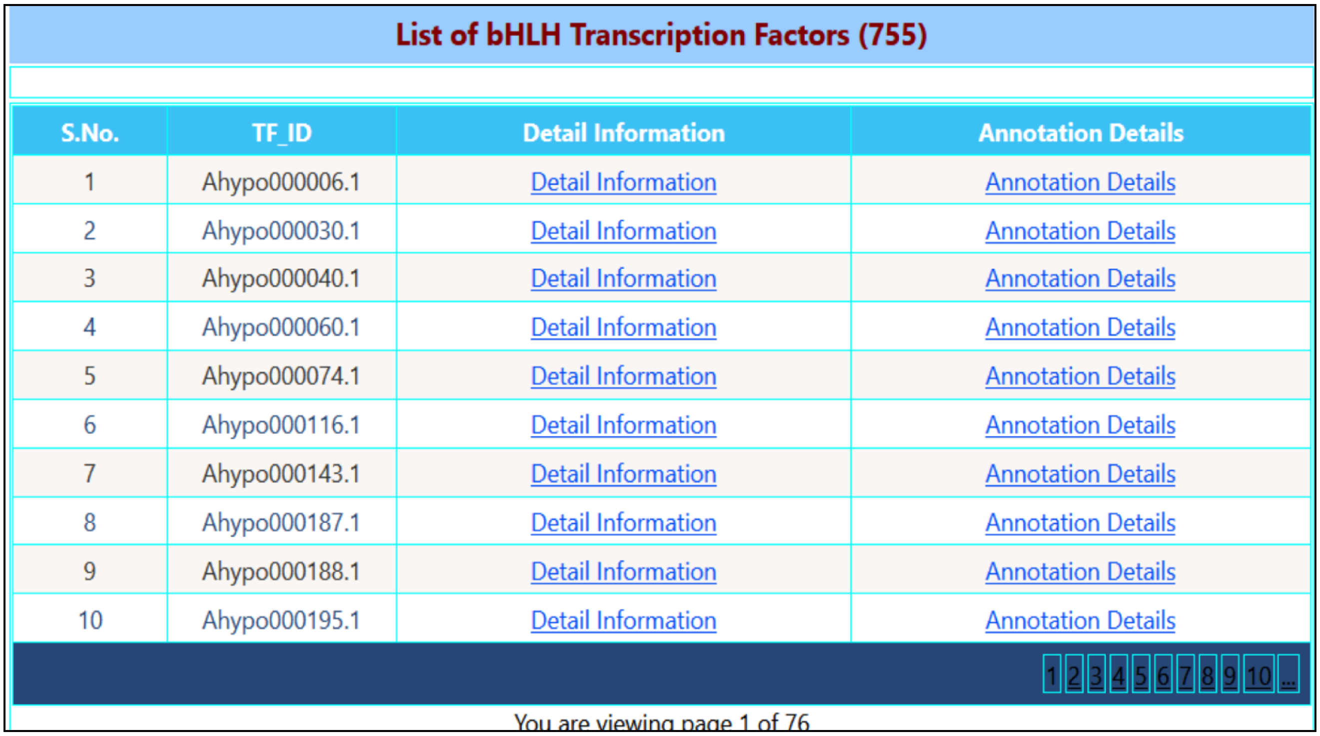
6: TFs (It gives list of different types of transcription factors predicted in Amaranth species)



Transcription Factors of *A. hypochondriacus*

AP2 (31)	Get Details	**ARF (181)**	Get Details	**ARR-B (45)**	Get Details
B3 (231)	Get Details	**BBR-BPC (39)**	Get Details	**BES1 (62)**	Get Details
bHLH (755)	Get Details	**bZIP (262)**	Get Details	**C2H2 (270)**	Get Details
C3H (222)	Get Details	**CAMTA (30)**	Get Details	**CO-like (39)**	Get Details
CPP (50)	Get Details	**DBB (56)**	Get Details	**Dof (82)**	Get Details
E2F-DP (43)	Get Details	**EIL (6)**	Get Details	**ERF (532)**	Get Details
FAR1 (237)	Get Details	**G2-like (186)**	Get Details	**GATA (93)**	Get Details
GeBP (50)	Get Details	**GRAS (224)**	Get Details	**GRF (24)**	Get Details
HB-other (73)	Get Details	**HB-PHD (2)**	Get Details	**HD-ZIP (124)**	Get Details
HRT-like (8)	Get Details	**HSF (120)**	Get Details	**LBD (138)**	Get Details
LFY (4)	Get Details	**LSD (9)**	Get Details	**MIKC (78)**	Get Details
M-type (299)	Get Details	**MYB (270)**	Get Details	**MYB-related (433)**	Get Details
NAC (528)	Get Details	**NF-X1 (23)**	Get Details	**NF-YA (41)**	Get Details
NF-YB (96)	Get Details	**NF-YC (65)**	Get Details	**Nin-like (55)**	Get Details
RAV (7)	Get Details	**S1Fa-like (44)**	Get Details	**SAP (2)**	Get Deatils
SBP (61)	Get Details	**SRS (20)**	Get Details	**STAT (42)**	Get Details
TALE (45)	Get Details	**TCP (168)**	Get Details	**Trihelix (149)**	Get Details
VOZ (7)	Get Details	**Whirly (8)**	Get Details	**WOX (29)**	Get Details
WRKY (417)	Get Details	**YABBY (22)**	Get Details	**ZF-HD (26)**	Get Details

Click on bHLH Get Details button: (It gives list of TFs present in bHLH family)

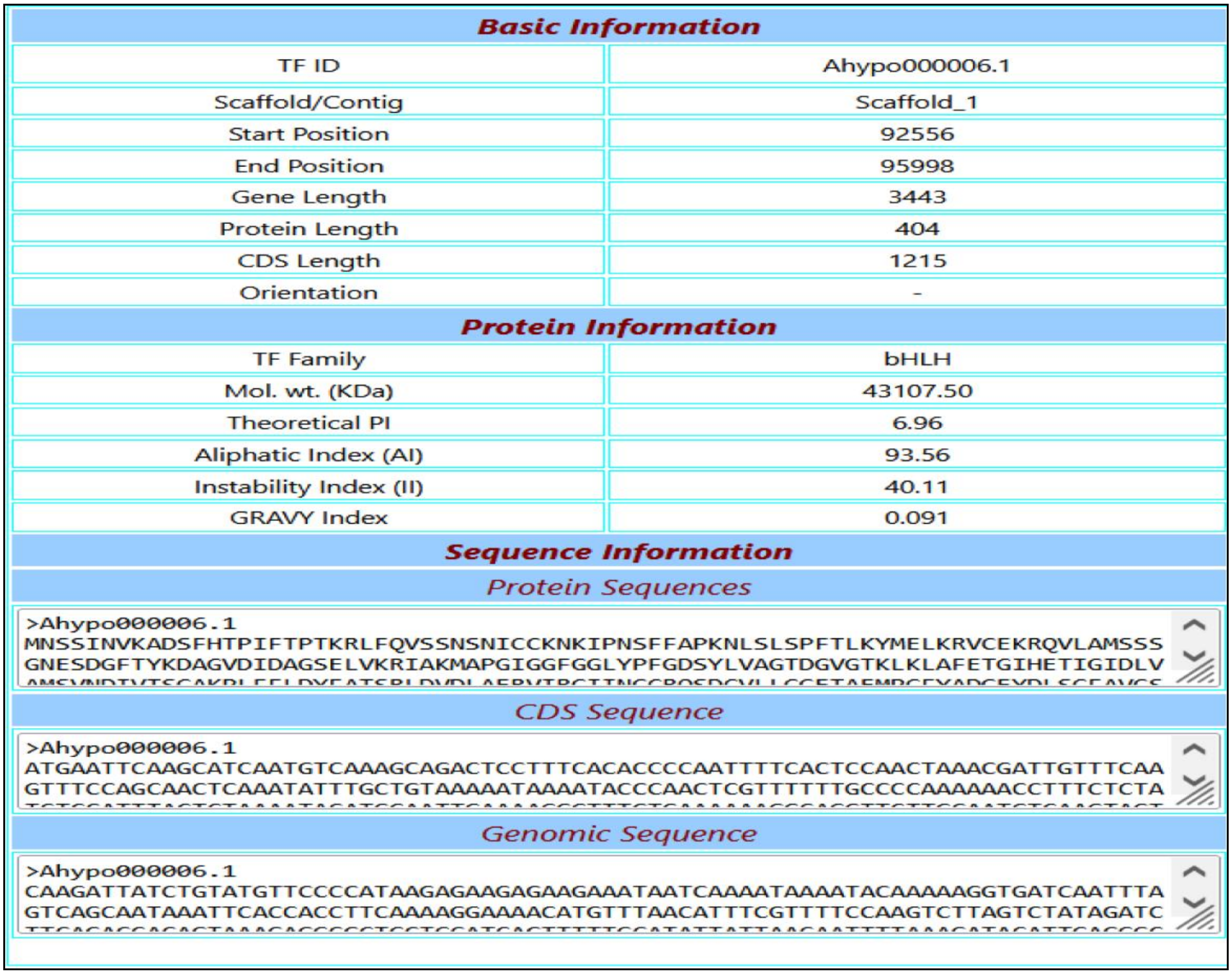


List of bHLH Transcription Factors (755)

S.No.	TF_ID	Detail Information	Annotation Details
1	Ahypo000006.1	Detail Information	Annotation Details
2	Ahypo000030.1	Detail Information	Annotation Details
3	Ahypo000040.1	Detail Information	Annotation Details
4	Ahypo000060.1	Detail Information	Annotation Details
5	Ahypo000074.1	Detail Information	Annotation Details
6	Ahypo000116.1	Detail Information	Annotation Details
7	Ahypo000143.1	Detail Information	Annotation Details
8	Ahypo000187.1	Detail Information	Annotation Details
9	Ahypo000188.1	Detail Information	Annotation Details
10	Ahypo000195.1	Detail Information	Annotation Details

You are viewing page 1 of 76

Detail Information: (It gives TFs basic, protein level as well as sequence information)



Basic Information

TF ID	Ahypo000006.1
Scaffold/Contig	Scaffold_1
Start Position	92556
End Position	95998
Gene Length	3443
Protein Length	404
CDS Length	1215
Orientation	-

Protein Information

TF Family	bHLH
Mol. wt. (KDa)	43107.50
Theoretical PI	6.96
Aliphatic Index (AI)	93.56
Instability Index (II)	40.11
GRAVY Index	0.091

Sequence Information

Protein Sequences

```
>Ahypo000006.1
MNSSINVKADSFHTPIFTPTKRLFQVSSNSNICCKNKIPNSFFAPKNLSLSPFTLKYMELKRVCEKRQVLAMSSS
GNESDGFTYKDAGVDIDAGSELVKRIAKMAPGIGGFGGLYPFGDSYLVAGTDGVGTKLKLAFETGIHETIGIDLV
```

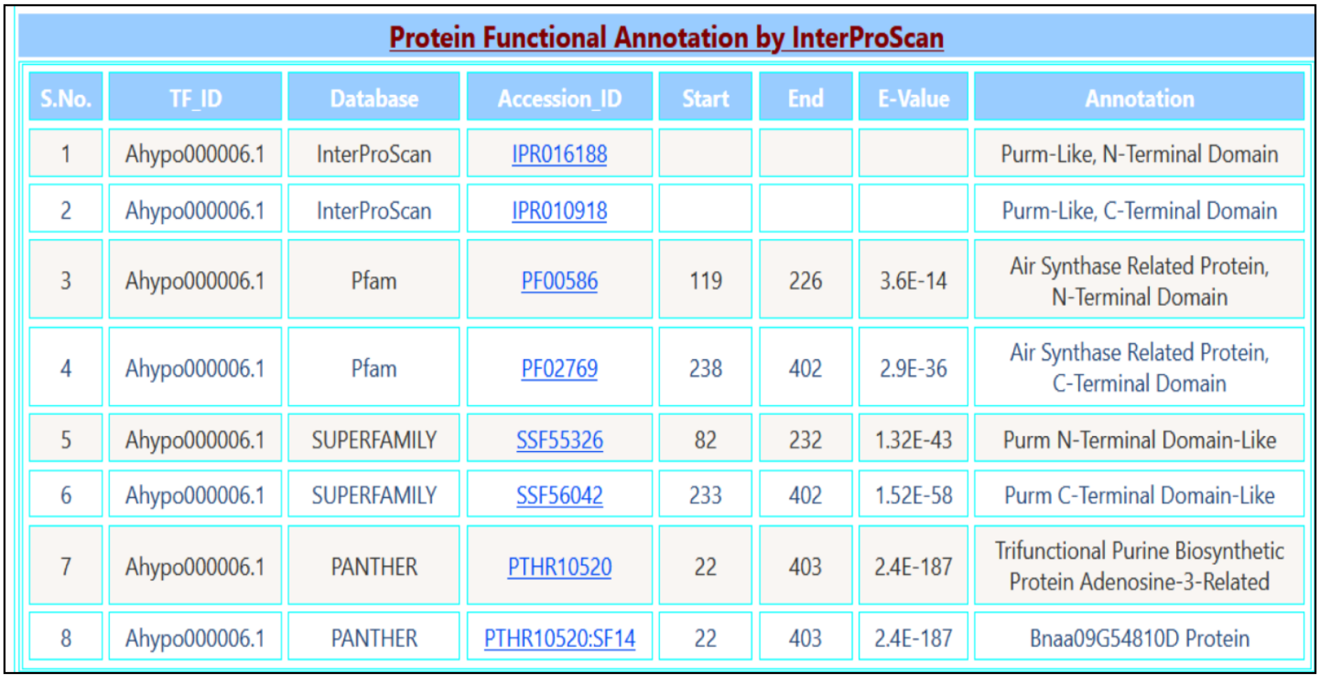
CDS Sequence

```
>Ahypo000006.1
ATGAATTCAAGCATCAATGTCAAAGCAGACTCCTTTCACACCCCAATTTTCACTCCAACTAAACGATTGTTTCAA
GTTTCCAGCAACTCAAATATTTGCTGTAAAAATAAAATACCCAACTCGTTTTTTGCCCCAAAAAACCTTTCTCTA
```

Genomic Sequence

```
>Ahypo000006.1
CAAGATTATCTGTATGTTCCCCATAAGAGAAGAGAAGAAATAATCAAAATAAAATACAAAAAGGTGATCAATTTA
GTCAGCAATAAATTCACCACCTTCAAAAGGAAAACATGTTTAACATTTCGTTTTCCAAGTCTTAGTCTATAGATC
```

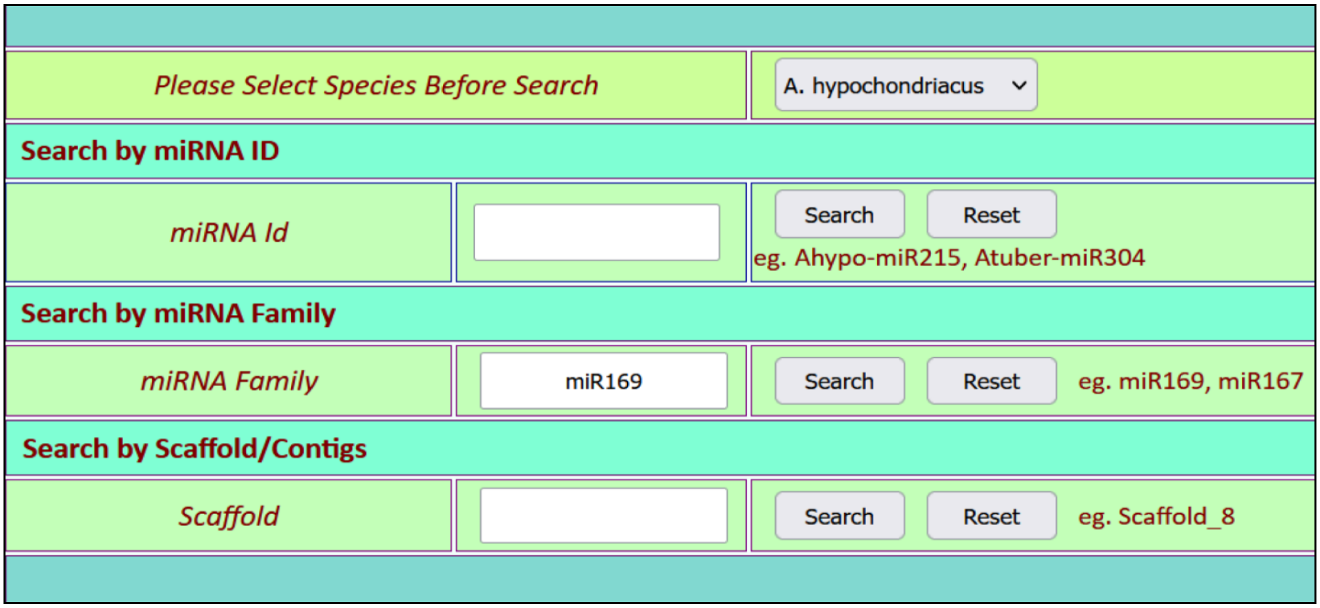
Annotation Details: (It gives annotation details predicted from Interproscan)



Protein Functional Annotation by InterProScan

S.No.	TF_ID	Database	Accession_ID	Start	End	E-Value	Annotation
1	Ahypo000006.1	InterProScan	IPR016188				Purm-Like, N-Terminal Domain
2	Ahypo000006.1	InterProScan	IPR010918				Purm-Like, C-Terminal Domain
3	Ahypo000006.1	Pfam	PF00586	119	226	3.6E-14	Air Synthase Related Protein, N-Terminal Domain
4	Ahypo000006.1	Pfam	PF02769	238	402	2.9E-36	Air Synthase Related Protein, C-Terminal Domain
5	Ahypo000006.1	SUPERFAMILY	SSF55326	82	232	1.32E-43	Purm N-Terminal Domain-Like
6	Ahypo000006.1	SUPERFAMILY	SSF56042	233	402	1.52E-58	Purm C-Terminal Domain-Like
7	Ahypo000006.1	PANTHER	PTHR10520	22	403	2.4E-187	Trifunctional Purine Biosynthetic Protein Adenosine-3-Related
8	Ahypo000006.1	PANTHER	PTHR10520:SF14	22	403	2.4E-187	Bnaa09G54810D Protein

7: miRNAs (First select the species from dropdown the choose any search criteria of miRNA search)



Please Select Species Before Search — A. hypochondriacus

Search by miRNA ID

miRNA Id

eg. Ahypo-miR215, Atuber-miR304

Search by miRNA Family

miRNA Family: miR169

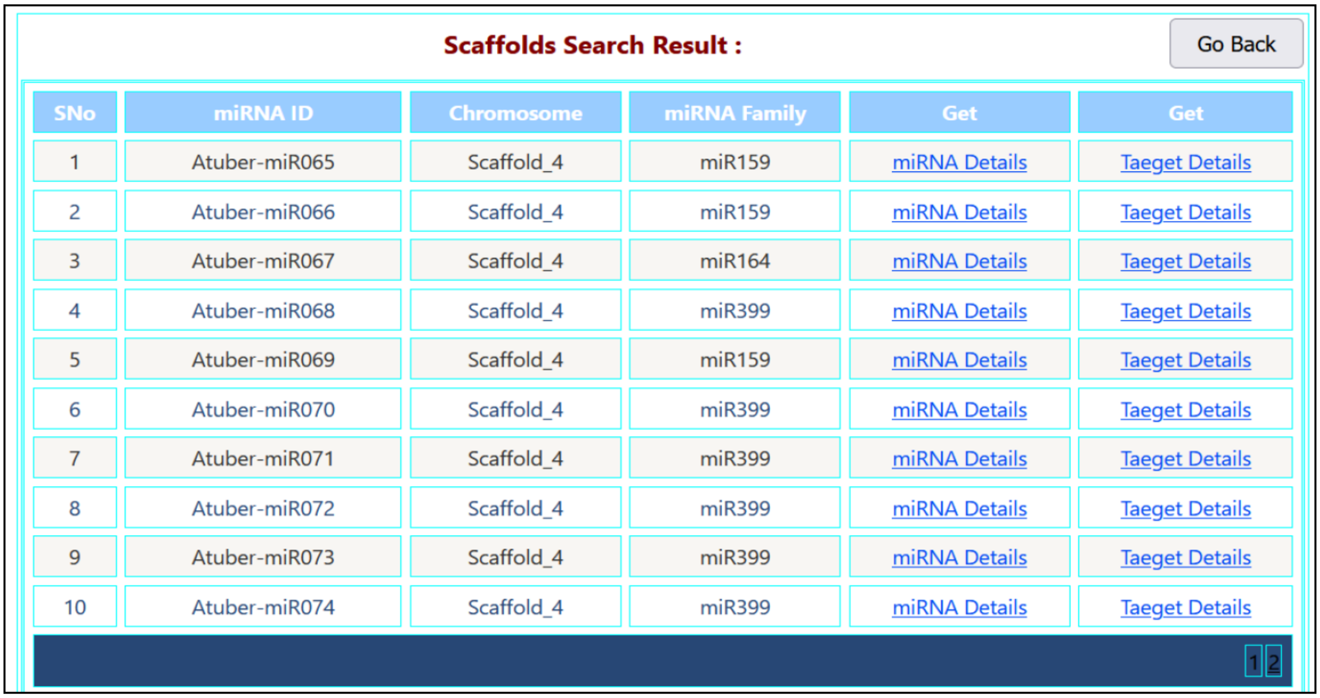
eg. miR169, miR167

Search by Scaffold/Contigs

Scaffold

eg. Scaffold_8

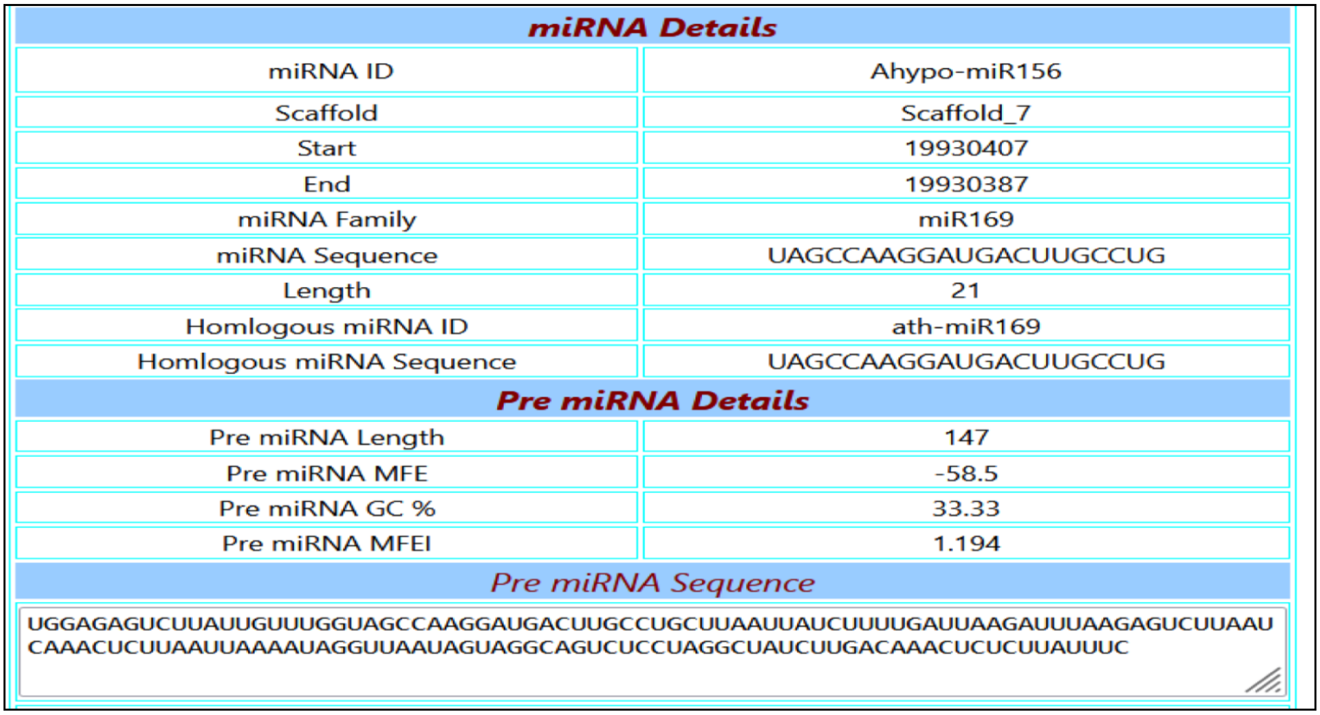
Search by Scaffold (It gives list of miRNAs belongs to scaffold4 in species *A. tuberculatus*)



Scaffolds Search Result :

SNo	miRNA ID	Chromosome	miRNA Family	Get	Get
1	Atuber-miR065	Scaffold_4	miR159	miRNA Details	Taeget Details
2	Atuber-miR066	Scaffold_4	miR159	miRNA Details	Taeget Details
3	Atuber-miR067	Scaffold_4	miR164	miRNA Details	Taeget Details
4	Atuber-miR068	Scaffold_4	miR399	miRNA Details	Taeget Details
5	Atuber-miR069	Scaffold_4	miR159	miRNA Details	Taeget Details
6	Atuber-miR070	Scaffold_4	miR399	miRNA Details	Taeget Details
7	Atuber-miR071	Scaffold_4	miR399	miRNA Details	Taeget Details
8	Atuber-miR072	Scaffold_4	miR399	miRNA Details	Taeget Details
9	Atuber-miR073	Scaffold_4	miR399	miRNA Details	Taeget Details
10	Atuber-miR074	Scaffold_4	miR399	miRNA Details	Taeget Details

Click on miRNA Details: (It gives detail of particular miRNA)

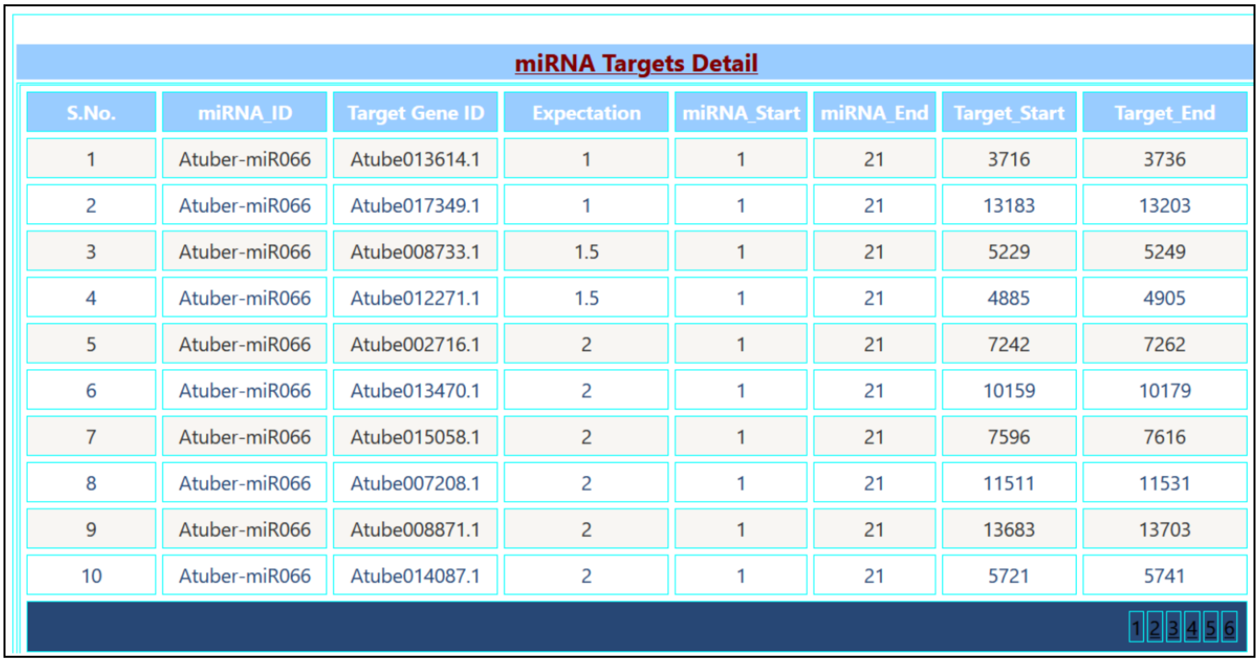


miRNA Details	
miRNA ID	Ahypo-miR156
Scaffold	Scaffold_7
Start	19930407
End	19930387
miRNA Family	miR169
miRNA Sequence	UAGCCAAGGAUGACUUGCCUG
Length	21
Homlogous miRNA ID	ath-miR169
Homlogous miRNA Sequence	UAGCCAAGGAUGACUUGCCUG
Pre miRNA Details	
Pre miRNA Length	147
Pre miRNA MFE	-58.5
Pre miRNA GC %	33.33
Pre miRNA MFEI	1.194

Pre miRNA Sequence

UGGAGAGUCUUAUUGUUUGGUAGCCAAGGAUGACUUGCCUGCUUAAUUAUCUUUUGAUUAAGAUUUAAGAGUCUUAAUCAAACUCUUAAUUAAAAUAGGUUAAUAGUAGGCAGUCUCCUAGGCUAUCUUGACAAACUCUCUUAUUUC

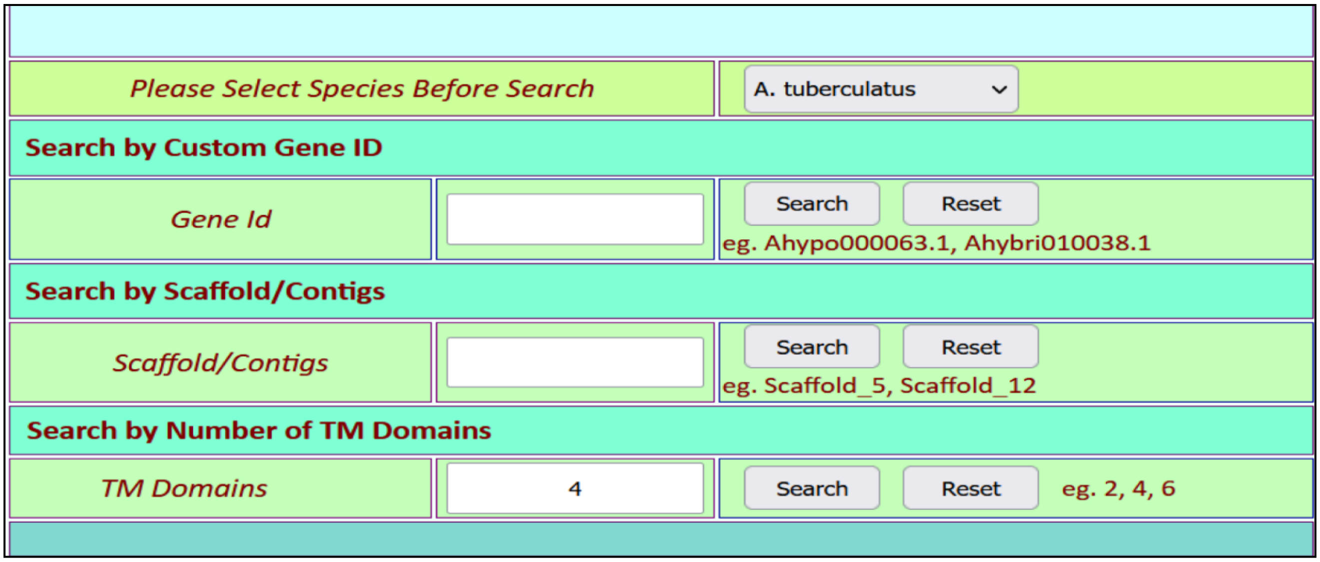
Click on Target Details: **(It gives detail of Targeted genes information of particular miRNA)**



miRNA Targets Detail

S.No.	miRNA_ID	Target Gene ID	Expectation	miRNA_Start	miRNA_End	Target_Start	Target_End
1	Atuber-miR066	Atube013614.1	1	1	21	3716	3736
2	Atuber-miR066	Atube017349.1	1	1	21	13183	13203
3	Atuber-miR066	Atube008733.1	1.5	1	21	5229	5249
4	Atuber-miR066	Atube012271.1	1.5	1	21	4885	4905
5	Atuber-miR066	Atube002716.1	2	1	21	7242	7262
6	Atuber-miR066	Atube013470.1	2	1	21	10159	10179
7	Atuber-miR066	Atube015058.1	2	1	21	7596	7616
8	Atuber-miR066	Atube007208.1	2	1	21	11511	11531
9	Atuber-miR066	Atube008871.1	2	1	21	13683	13703
10	Atuber-miR066	Atube014087.1	2	1	21	5721	5741

8: Transporters **(First select the species from dropdown then choose any of the search criteria for Transportes search)**



Please Select Species Before Search: A. tuberculatus

Search by Custom Gene ID

Gene Id: eg. Ahypo000063.1, Ahybri010038.1

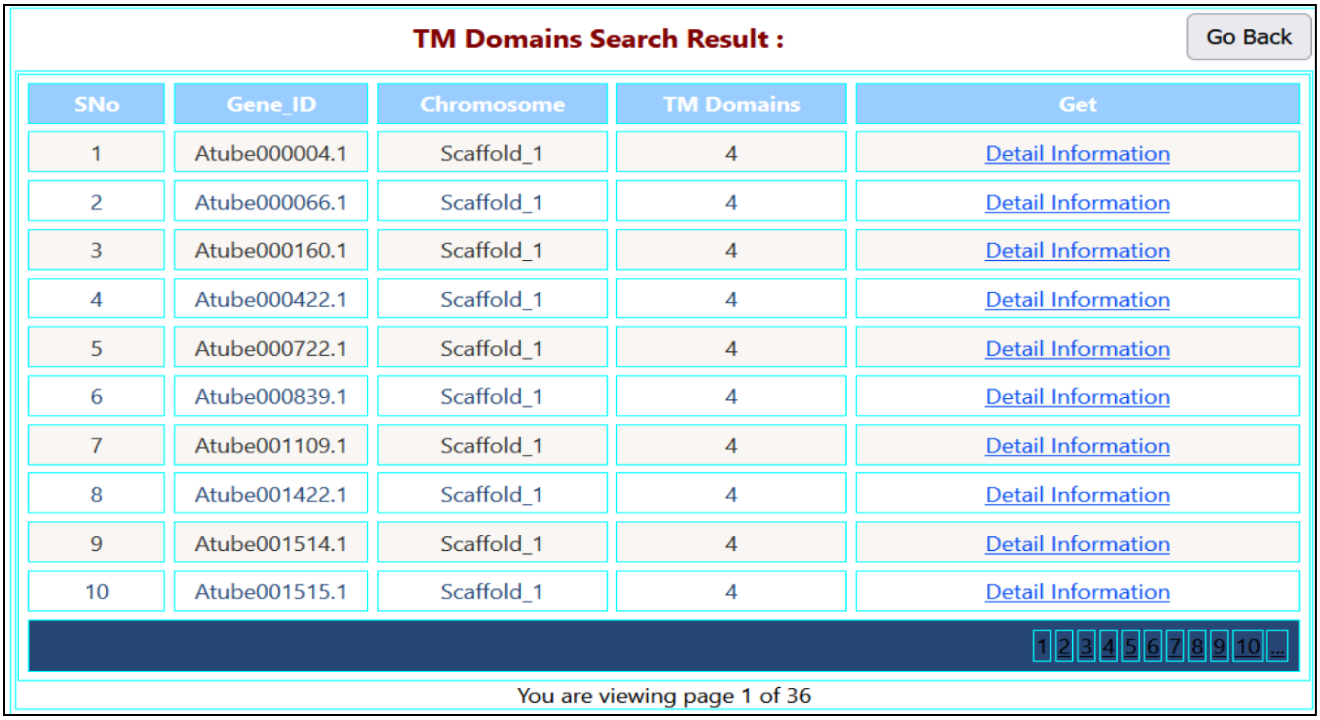
Search by Scaffold/Contigs

Scaffold/Contigs: eg. Scaffold_5, Scaffold_12

Search by Number of TM Domains

TM Domains: 4 eg. 2, 4, 6

Search by TM Domains: (It gives result based on TM Domain search)

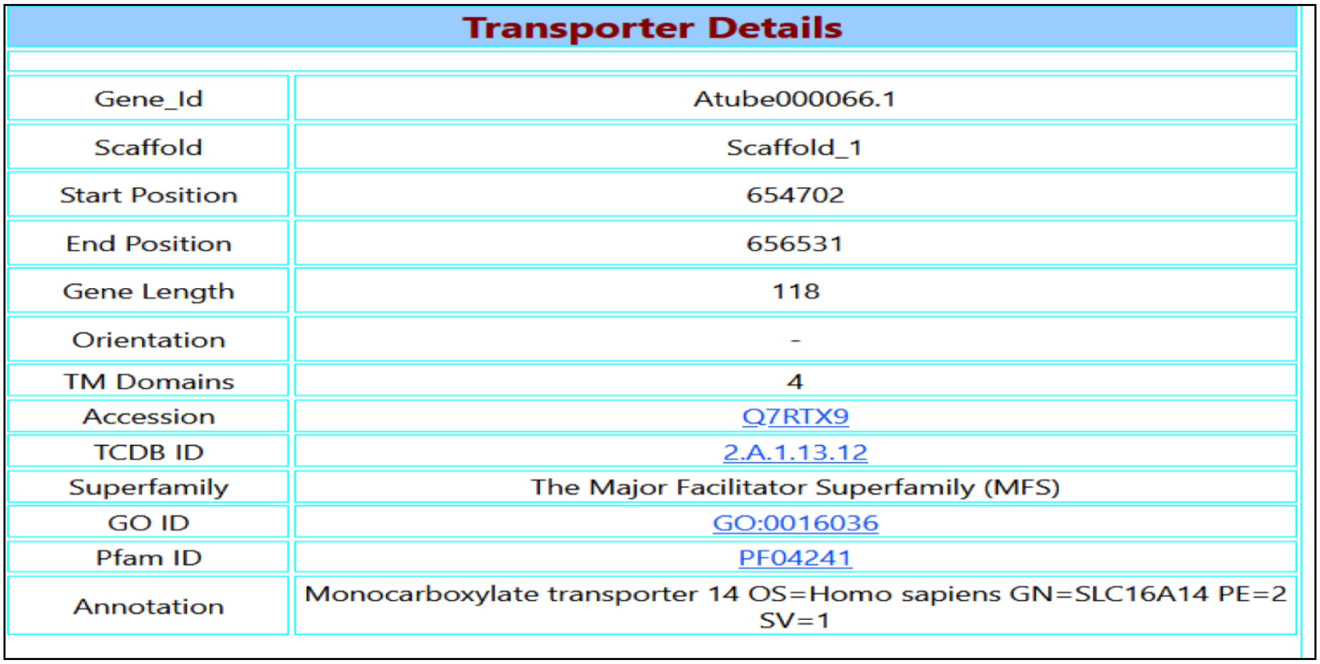


TM Domains Search Result :

SNo	Gene_ID	Chromosome	TM Domains	Get
1	Atube000004.1	Scaffold_1	4	Detail Information
2	Atube000066.1	Scaffold_1	4	Detail Information
3	Atube000160.1	Scaffold_1	4	Detail Information
4	Atube000422.1	Scaffold_1	4	Detail Information
5	Atube000722.1	Scaffold_1	4	Detail Information
6	Atube000839.1	Scaffold_1	4	Detail Information
7	Atube001109.1	Scaffold_1	4	Detail Information
8	Atube001422.1	Scaffold_1	4	Detail Information
9	Atube001514.1	Scaffold_1	4	Detail Information
10	Atube001515.1	Scaffold_1	4	Detail Information

You are viewing page 1 of 36

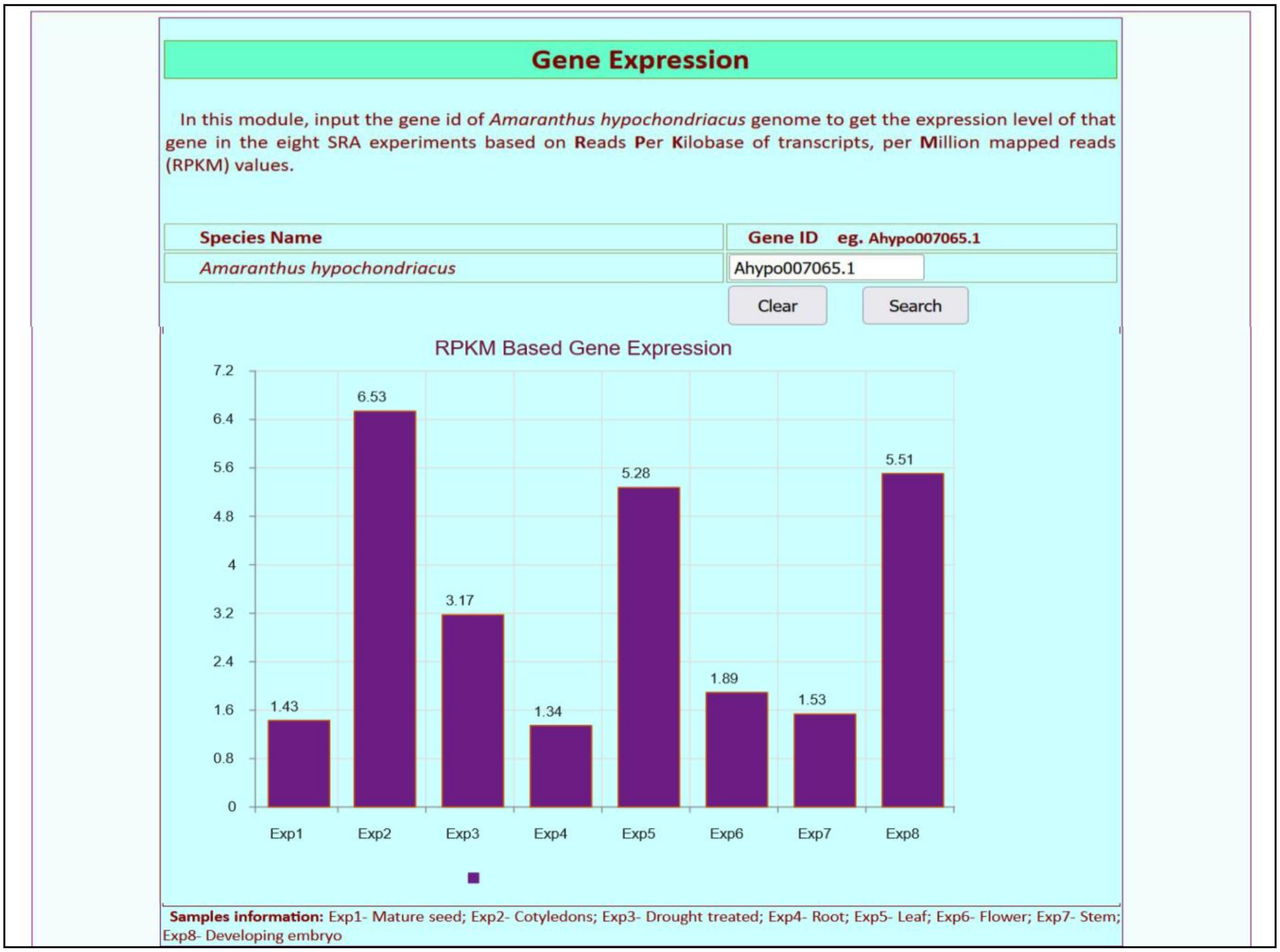
Detail Information: (It gives transporter details predicted from TCDB database)



Transporter Details

Gene_Id	Atube000066.1
Scaffold	Scaffold_1
Start Position	654702
End Position	656531
Gene Length	118
Orientation	-
TM Domains	4
Accession	Q7RTX9
TCDB ID	2.A.1.13.12
Superfamily	The Major Facilitator Superfamily (MFS)
GO ID	GO:0016036
Pfam ID	PF04241
Annotation	Monocarboxylate transporter 14 OS=Homo sapiens GN=SLC16A14 PE=2 SV=1

9: Tools (Gene Expression) (It provides the gene expression search module with the output bar chart for queried gene based on RPKM values)



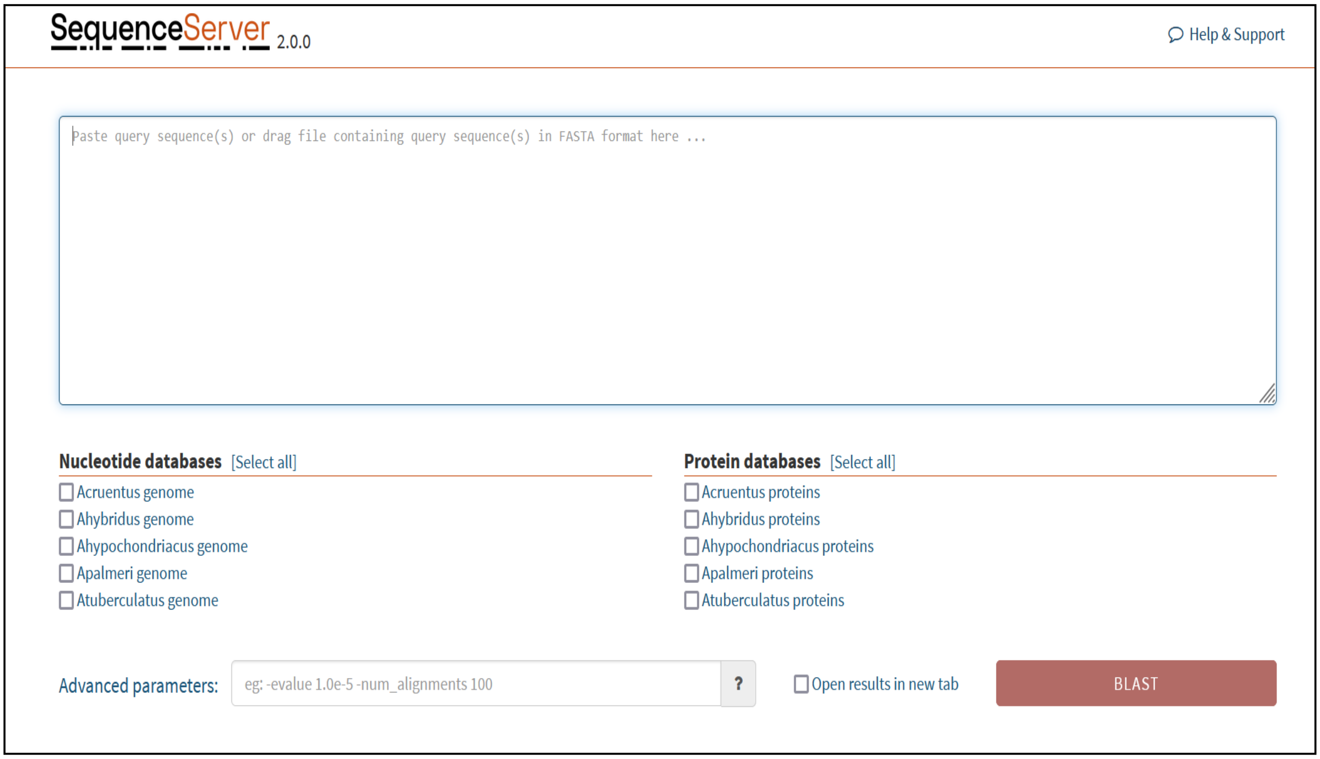
Gene Expression

In this module, input the gene id of *Amaranthus hypochondriacus* genome to get the expression level of that gene in the eight SRA experiments based on **R**eads **P**er **K**ilobase of transcripts, per **M**illion mapped reads (RPKM) values.

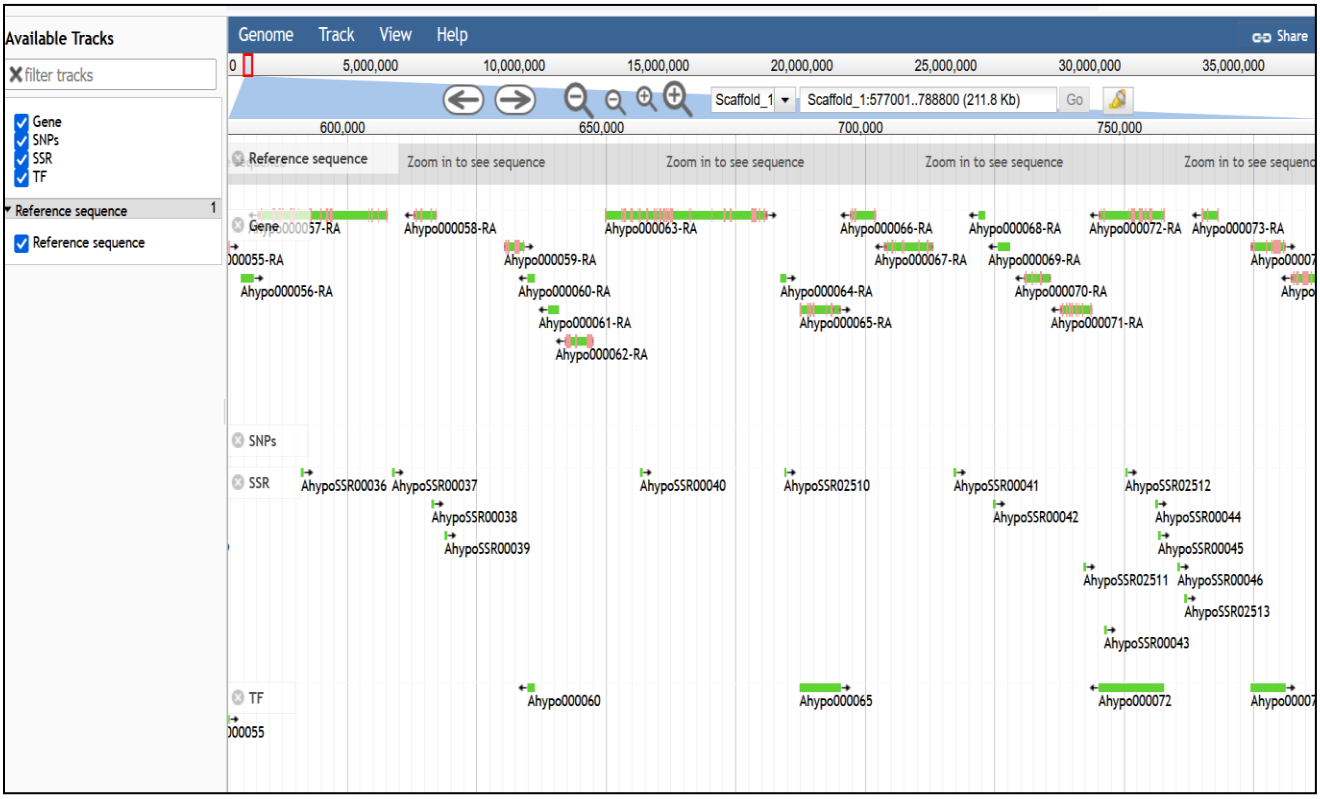
Species Name	**Gene ID** eg. **Ahypo007065.1**
Amaranthus hypochondriacus	Ahypo007065.1

Samples information: Exp1- Mature seed; Exp2- Cotyledons; Exp3- Drought treated; Exp4- Root; Exp5- Leaf; Exp6- Flower; Exp7- Stem; Exp8- Developing embryo

(Blast Search) (It provides the blast search facility against the genome as well as protein sequences of five amaranth species)

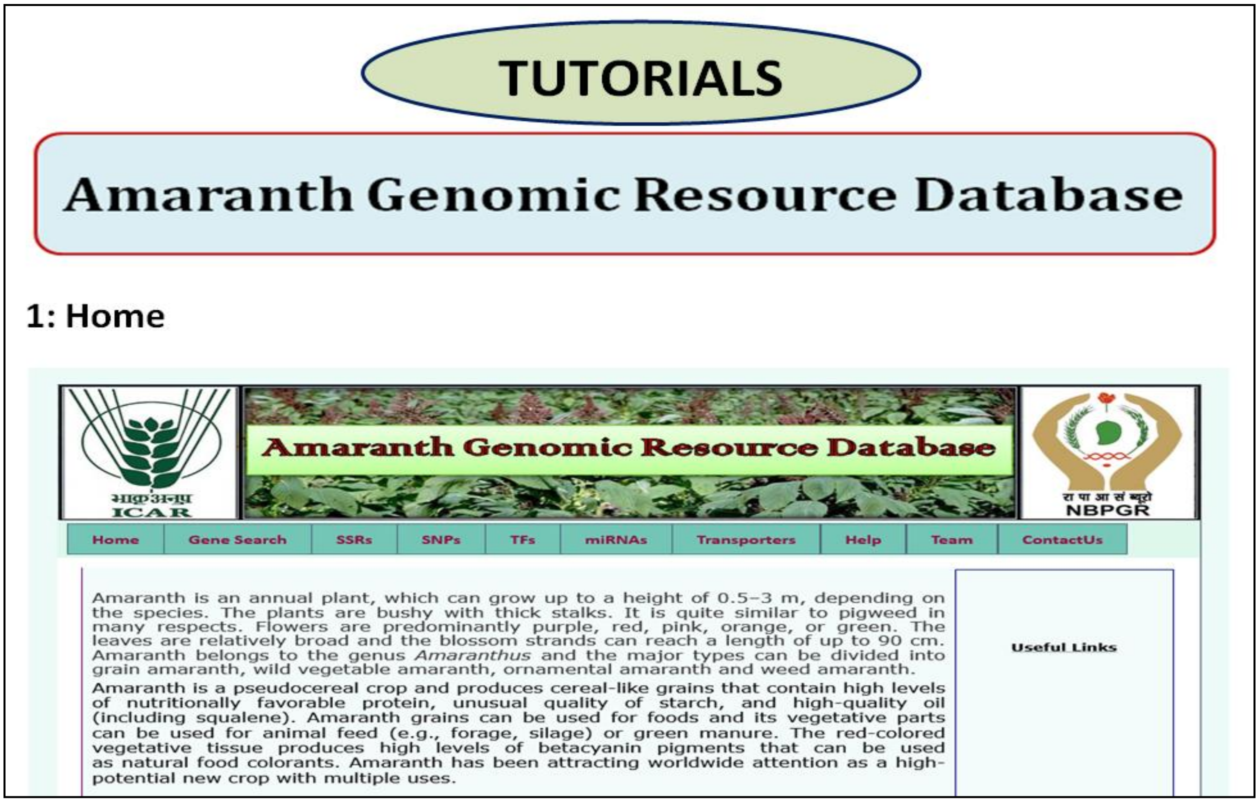


JBrowse (It visualizes the gene coordinates, SSRs, SNPs and TFs against the reference genomes of respective amaranth species)



10. Help & Support

Tutorials (It helps the users to easy usage of the database)



TUTORIALS

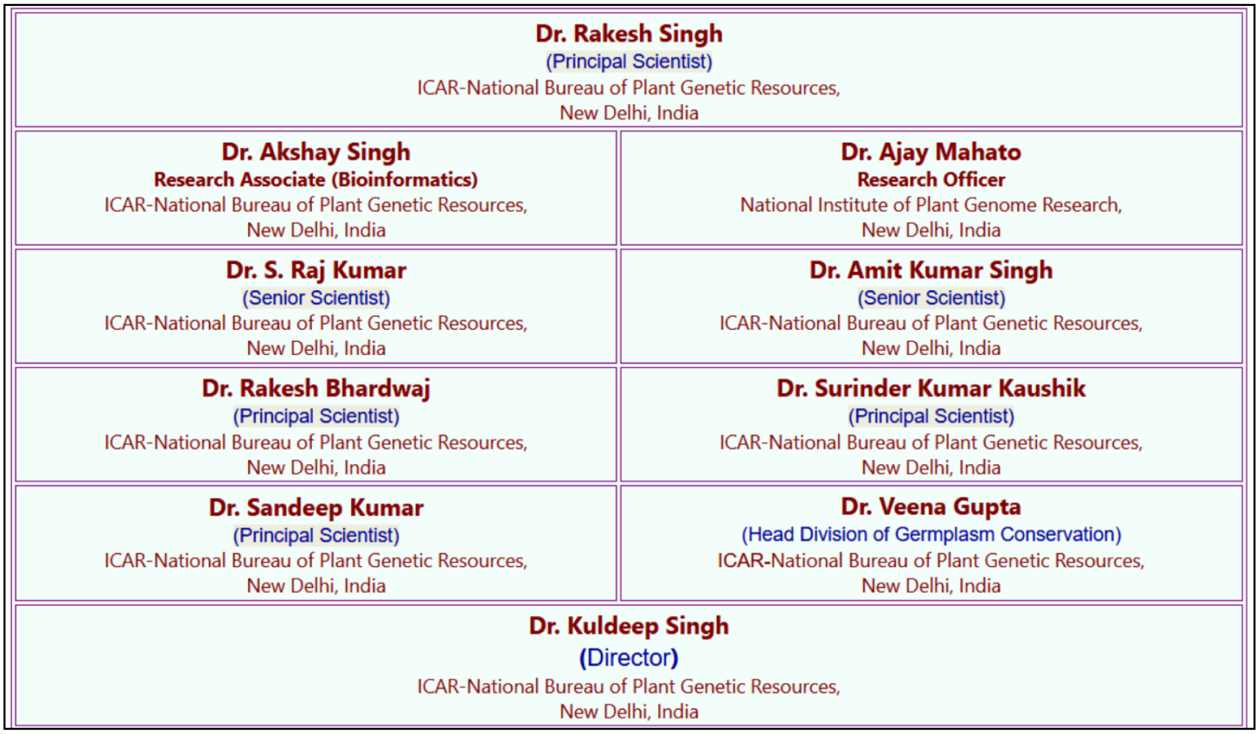
Amaranth Genomic Resource Database

1: Home

Amaranth is an annual plant, which can grow up to a height of 0.5–3 m, depending on the species. The plants are bushy with thick stalks. It is quite similar to pigweed in many respects. Flowers are predominantly purple, red, pink, orange, or green. The leaves are relatively broad and the blossom strands can reach a length of up to 90 cm. Amaranth belongs to the genus *Amaranthus* and the major types can be divided into grain amaranth, wild vegetable amaranth, ornamental amaranth and weed amaranth.

Amaranth is a pseudocereal crop and produces cereal-like grains that contain high levels of nutritionally favorable protein, unusual quality of starch, and high-quality oil (including squalene). Amaranth grains can be used for foods and its vegetative parts can be used for animal feed (e.g., forage, silage) or green manure. The red-colored vegetative tissue produces high levels of betacyanin pigments that can be used as natural food colorants. Amaranth has been attracting worldwide attention as a high-potential new crop with multiple uses.

Team (Team involved in this project)



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