Help manual of Cb-DElncRNAdb

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User can explore these options for extracting information which are available in the database.

For any information, please contact us in the email id provided in the contact us menu bar.

Cb-DElncRNA database

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Cb-DElncRNA Database

The Cluster bean is very hard, drought tolerant and cash crop. It is locally known as Guar. It is mainly cultivated for food as vegetables, feed and fodder. Transcriptome data of leaf, shoot and flower tissue of cluster bean were analyzed. This database contains information about **differentially expressed lncRNA, eTM-lncRNA, ceRNA, IRES-lncRNA and DE-lncRNA-SSR** . "This work was supported by the grants ICAR-Consortia Research Platform on Genomics (CRP-Genomics/IX/2017), received from Indian Council of Agricultural Research (ICAR)".

Results

Total no. DE-lncRNA : 3309

Total no. of eTM-lncRNA : 362

Total no. of ceRNA:139

Total no. of IRES-lncRNA:46

Total no. of DElncRNA-SSRs: 773

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Cb-DElncRNA database

Click on this menu for DE-lncRNA

Cb-DElncRNA Database

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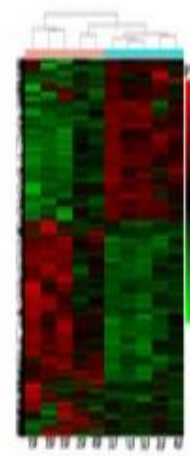Total no. of IRES-lncRNA:46

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Cb-DElncRNA database

DElncRNA-SSR details

DElncRNA

DElncRNA

The differentially expressed lncRNA help in the understanding of effect of environmental factors like biotic and abiotic on the expression of lncRNA. Also insight of function of lncRNA in various conditions.

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Cb-DElncRNA database

DElncRNA INFORMATION

lncRNA sequence

lncRNA id	Length	MFE	CPC index	Repetitive elements	SSR on lncRNA	sponge miRNA	Target of lncRNA
Cb_lnc_0001	6013	-23.23	-1.16	NA	Mono	Gor-miR_leaf-3111	EG990562.1
Cb_lnc_0002	4590	-22.83	-0.79	NA	NA	Gor-miR_root-3003	EG976249.1
Cb_lnc_0003	3959	-23.3	-1.32	NA	Mono	NA	EG991036.1
Cb_lnc_0004	3668	-21.74	-1.24	NA	NA	Gor-miR_leaf-3133	EG989380.1
Cb_lnc_0005	3635	-26.13	-0.9	NA	Mono	NA	EG985654.1
Cb_lnc_0006	3509	-21.69	-0.99	NA	NA	Gor-miR_seed-3092	EG987826.1
Cb_lnc_0007	3495	-24.04	-1.02	NA	Mono	Gor-miR_bud-3155	EG991154.1
Cb_lnc_0008	3495	-23.27	-1.13	LINE/L1	NA	NA	EG989077.1
Cb_lnc_0009	3360	-21.63	-1.21	NA	Mono	Gor-miR_stem-3080	EG990908.1
Cb_lnc_0010	3303	-22.02	-1.26	NA	NA	NA	EG987137.1
Cb_lnc_0011	3245	-24.27	-1.24	NA	c	Gor-miR_root-3052	EG986671.1
Cb_lnc_0012	3241	-25.64	-0.86	LTR/Gypsy	NA	Gor-miR_leaf-3034	EG990562.1
Cb_lnc_0013	3151	-24.86	-1	NA	NA	Gor-miR_bud-3088	EG990881.1
Cb_lnc_0014	3027	-22.19	-1.15	NA	NA	Gor-miR_bud-3022	EG989312.1
Cb_lnc_0015	3025	-20.92	-1.19	NA	Tetra	NA	EG991098.1
Cb_lnc_0016	2949	-25.07	-1.19	LTR/Copia	Mono	NA	EG991169.1
Cb_lnc_0017	2926	-25.42	-1.21	LTR/Gypsy	Mono	Gor-miR_seed-3124	EG988945.1
Cb_lnc_0018	2923	-22.96	-1.36	DNA/CMC-EnSpm	NA	NA	EG983991.1
Cb_lnc_0019	2917	-22.97	-1.27	NA	Mono	Gor-miR_root-3147	EG990221.1

Cb-DEIncRNA database

```
>Gor-miR_leaf-3157  Score: 3.0  TRINITY_DN26836_c1_g3_i2

Query:       1 TTGAGCCGCGTCAATATCT 19
               ||:|||||^:|*||||||
Sbjct:     744 AATTCGGCTTACTTATAGA 726
```

eTM-lncRNA

↓

Click here for eTM-lncRNA
details

eTM-lncRNA (endogenous Target mimic lncRNA)

The complimentary pairing between miRNAs and lncRNAs leads to the development of endogenous target mimics (eTMs) in the cells
As per Wu et al(2012) Rule for eTM lncRNA
i)No bulges allowed other than at 5'end 9th to12th position on miRNA sequence
ii) he bulge in eTMs should have onlythree nucleotides
iii) perfect nucleotide pairing essential at the 5'end 2ndto 8th position
iv) the total mismatches and G/U pairs within eTM andmiRNA pairing regions should be less than three except for the centralbulge
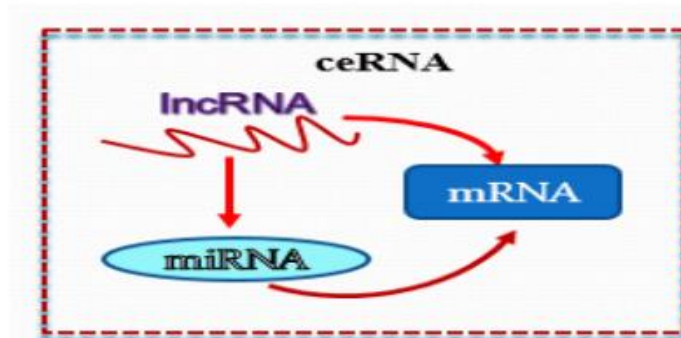
Cb-DElncRNA database

eTM-lncRNA INFORMATION

miRNA id	lncRNA id	Score	Alignment
Gor-miR_bud-3119	CB_lnc_0544	2.2	:||**||||||||||||
Gor-miR_leaf-3127	CB_lnc_0398	2.2	:|*|||*||||||||
Gor-miR_leaf-3165	CB_lnc_0326	2.2	:||||||*|||*||||
Gor-miR_root-3127	CB_lnc_0398	2.2	:|*|||*||||||||
Gor-miR_root-3147	CB_lnc_0625	2.2	:|*|||||||||||*
Gor-miR_seed-3096	CB_lnc_0064	1.8	:||||*||||||||||*

ceRNA (competetive endogenous RNA)

The presence of microRNAresponse elements (MREs) on the ncRNA sequence is responsible for the regulation of various ncRNA like long non-coding RNA, circular RNA via competition for binding of miRNA.

Click here for ceRNA complete information ← ceRNA

Cb-DElncRNA database

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Competing endogenous RNA INFORMATION

miRNA id	lncRNA id	miNA id
Gor-miR_seed-3124	CB_lnc_0760	EG975082.1
Gor-miR_stem-3058	CB_lnc_0174	EG975130.1
Gor-miR_leaf-3149	CB_lnc_0259	EG976044.1
Gor-miR_leaf-3054	CB_lnc_0937	EG976044.1
Gor-miR_stem-3054	CB_lnc_0937	EG976044.1
Gor-miR_root-3052	CB_lnc_1955	EG976107.1
Gor-miR_stem-3046	CB_lnc_1955	EG976107.1
Gor-miR_leaf-3018	CB_lnc_2200	EG976134.1
Gor-miR_leaf-3018	CB_lnc_2200	EG976134.1
Gor-miR_stem-3018	CB_lnc_2200	EG976134.1
Gor-miR_stem-3018	CB_lnc_2200	EG976134.1
Gor-miR_leaf-3170	CB_lnc_2269	EG976246.1
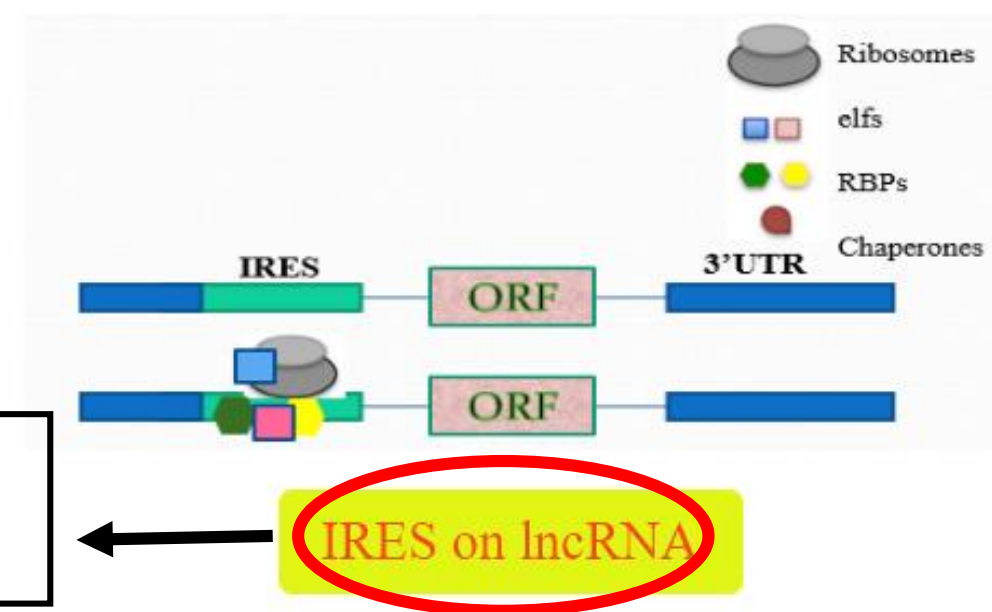
Internal ribosomal entry site

Translation can initiate internally in a cap-independent manner because of the presence of internal ribosome entry site (IRES) sequences. These IRES present in the 5'UTR of both coding and non-coding region of the genome.

Click here for IRES on lncRNA details

IRES on lncRNA

Cb-DElncRNA database

IRES-DElncRNA INFORMATION

lncRNA id	Probability	ORF length	start pos	end pos	Strand	Localization
CB_lnc_2110	0.56	102	2	307	+	5prime_partial
CB_lnc_0739	0.6	104	185	496	+	complete
CB_lnc_2249	0.58	106	656	339	-	complete
CB_lnc_1582	0.53	106	119	436	+	complete
CB_lnc_0152	0.59	111	1	333	+	5prime_partial
CB_lnc_0871	0.5	115	342	1	-	internal
CB_lnc_1567	0.67	88	262	2	-	3prime_partial
CB_lnc_2897	0.64	49	1	147	+	5prime_partial
CB_lnc_0672	0.62	61	293	111	-	5prime_partial
CB_lnc_1309	0.6	70	117	323	+	3prime_partial
CB_lnc_2847	0.59	45	428	294	-	5prime_partial
CB_lnc_1176	0.59	57	186	356	+	complete
CB_lnc_1455	0.58	34	212	313	+	complete

Cb-DElncRNA database

SSR → lncRNA

Clickn here for SSR on lncRNA complete information

SSR on lncRNA

SSR-derived lncRNA

Molecular markers including SSR (simple sequence repeat) do not affected by the change in environment and are important tool for plant breeder and geneticist. They occur throughout the genome (both coding and non-coding).lncRNA-derived SSRs were moderately polymorphic and showed higher transferability in related species.

Cb-DElncRNA database

DElncRNA derived SSR

lncRNA id	Standard	Motif	Type of SSR	Start Pos of SSR	End Pos of SSR	Length of SSR	Sequence
CB_lnc_0567	A	T	Mono	801	812	12	TTTTTTTTTTTT
CB_lnc_1394	AAAT	ATAA	Tetra	67	82	16	ATAAATAAATAAATAA
CB_lnc_1396	A	A	Mono	12	24	13	AAAAAAAAAAAAA
CB_lnc_1160	A	A	Mono	322	337	16	AAAAAAAAAAAAAAAA
CB_lnc_2166	A	A	Mono	399	445	47	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
CB_lnc_0002	AAG	TCT	Tri	572	592	21	TCTTCTTCTTCTTCTTCTTCT
CB_lnc_0003	A	T	Mono	185	201	17	TTTTTTTTTTTTTTTTT
CB_lnc_2168	AAAT	AATA	Tetra	386	401	16	AATAAATAAATAAATA
CB_lnc_2172	AATTC	GAATT	Penta	527	546	20	GAATTGAATTGAATTGAATT
CB_lnc_2172	AATT	AATT	Tetra	698	713	16	AATTAATTAATTAATT
CB_lnc_1403	A	A	Mono	1167	1181	15	AAAAAAAAAAAAAAA
CB_lnc_0581	A	A	Mono	429	446	18	AAAAAAAAAAAAAAAAAA
CB_lnc_2175	AAT	TAA	Tri	1588	1602	15	TAATAATAATAATAA
CB_lnc_1406	A	T	Mono	721	736	16	TTTTTTTTTTTTTTTT
CB_lnc_1406	AAAT	TTAT	Tetra	1395	1410	16	TTATTTATTTATTTAT
CB_lnc_2524	A	T	Mono	14	29	16	TTTTTTTTTTTTTTTT
CB_lnc_1409	A	A	Mono	470	481	12	AAAAAAAAAAAA
CB_lnc_0013	C	G	Mono	424	436	13	GGGGGGGGGGGGG
CB_lnc_0015	AACCAG	CCAGAA	Hexa	538	561	24	CCAGAACCAGAACCAGAACCAGAA
CB_lnc_0016	A	A	Mono	1	33	33	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
CB_lnc_0017	AT	AT	Di	208	227	20	ATATATATATATATATATAT

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Click here for details of conserved lncRNA ←

conserved lncRNA

Conserved lncRNA

The rate of evolution in the lncRNA is very high. lncRNAs are less conserved than other non-coding RNAs. They moderately conserved within species.

Cb-DElncRNA database

Conserved lncRNA INFORMATION

cluster bean lncRNA	Other plant's lncRNA	Identity	Coverage	e-value	Bits score
Cb_lnc_1225	Gmax_Glyma.10G146200.1	79.213	635	0	414
Cb_lnc_0123	Gmax_Glyma.02G106000.7	71.589	535	2.29e-21	106
Cb_lnc_2164	Gmax_Glyma.12G181700.3	79.962	529	0	357
Cb_lnc_0978	Gmax_Glyma.07G139400.1	78.805	519	0	324
Cb_lnc_1457	Gmax_Glyma.17G234900.2	79.482	502	0	335
Cb_lnc_1120	Pvulgaris_Phvul.007G111000.1	80.8	500	0	375
Cb_lnc_0013	Gmax_Glyma.15G063700.1	83.871	496	0	459
Cb_lnc_0551	Gmax_Glyma.08G147100.1	77.89	493	0	267
Cb_lnc_1201	Gmax_Glyma.09G202700.1	79.752	484	0	309
Cb_lnc_1268	Pvulgaris_Phvul.002G257800.1	80.38	474	0	324
Cb_lnc_1596	Gmax_Glyma.16G049700.1	73.987	469	1.32e-34	148
Cb_lnc_0548	Gmax_Glyma.10G235700.1	84.368	467	0	448
Cb_lnc_0144	Pvulgaris_Phvul.006G195900.1	86.183	427	0	448
Cb_lnc_1482	Gmax_Glyma.06G051300.1	77.99	418	0	248
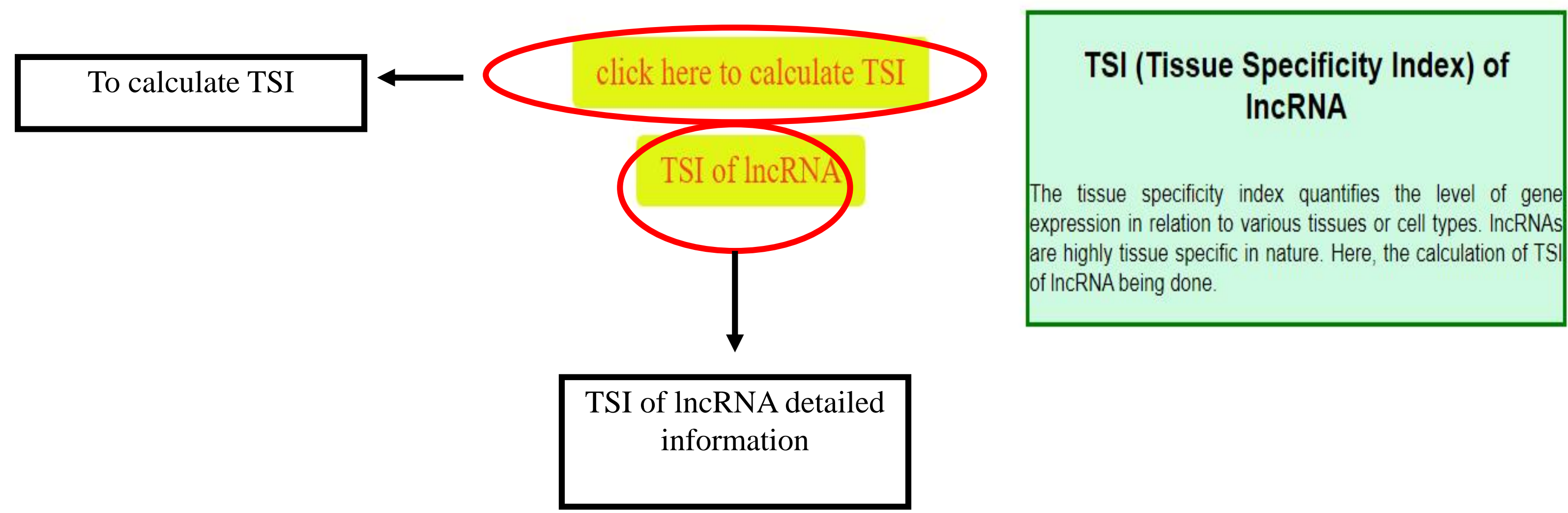
To calculate TSI

click here to calculate TSI

TSI of lncRNA

TSI of lncRNA detailed information

TSI (Tissue Specificity Index) of lncRNA

The tissue specificity index quantifies the level of gene expression in relation to various tissues or cell types. lncRNAs are highly tissue specific in nature. Here, the calculation of TSI of lncRNA being done.

Cb-DElncRNA database

TSI of lncRNA

S.No.	lncRNA id	TSI	Function of targeted genes
1	Cb_lnc_0061	0.961303	Tubby-like F-box protein 6 (AtTLP6)
2	Cb_lnc_1139	0.928773	Soyasaponin III rhamnosyltransferase (EC 2.4.1.273) (Soyasaponin glycosyltransferase 3) (UDP-rhamnose:soyasaponin III-rhamnosyltransferase)
3	Cb_lnc_0183	0.915481	RAN GTPase-activating protein 1 (AtRanGAP1) (RanGAP1)
4	Cb_lnc_0109	0.915155	Protein translation factor SUI1 homolog 1
5	Cb_lnc_0530	0.980492	Probable isoaspartyl peptidase/L-asparaginase 2 (EC 3.4.19.5) (L-asparagine amidohydrolase 2) [Cleaved into: Isoaspartyl peptidase/L-asparaginase 2 subunit alpha; Isoaspartyl peptidase/L-asparaginase 2 subunit beta]
6	Cb_lnc_0075	0.968085	Phosphoglycolate phosphatase 2 (EC 3.1.3.18)

TSI: Tissue Specificity Index

The tissue specificity index is a measure of the relative expression of a gene across different tissues or cell types. It is commonly used to identify genes that are highly expressed in a specific tissue, which can provide insights into the function of that tissue and the roles of the genes involved. The tissue specificity index is calculated by comparing the expression of a gene in a specific tissue to its expression in all other tissues in a given dataset. Genes with a high tissue specificity index are considered to be highly tissue-specific and may be involved in tissue-specific functions, while genes with a low tissue specificity index are considered to have a more universal role. The tissue specificity index is a useful tool for studying gene expression patterns and tissue-specific functions.

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Dr. Sarika Sahu
Scientist(Bioinformatiics)
Indian Agricultural Statistical
Research Institute
New Delhi-110012
sahusarikaiiita@gmail.com

Dr. A. R. Rao
ADG (PIM)
Indian Council of Agricultural
Research
New Delhi-110001
rao.work.cshl@gmail.com

Dr. Kishor Gaikwad
Principal Scientist
National Institute of
Plant Biotechnology
New Delhi-110012
kish2012@gmail.com