


**PotTransDB:**  
**Potato Transcriptome Database**  
User Manual

Home Screen of the **PotTransDB** database will appear as shown in image below. In which you will get several options to search for DElncRNAs, eTM-DElncRNA, cis-DElncRNA, CircRNA, DEGs, Alternate splicing as well as contact information and user manual.

**PotTransDB**  
Potato Transcriptome Database

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#### About PotTransDB

Potato (*Solanum tuberosum* L.) ranks third among the world's most significant food crops, following rice and wheat, in terms of human consumption. It boasts high yields of dry matter and calories per unit area and time, making it a valuable source of energy, proteins, vitamins, and minerals. Over a billion people worldwide enjoy potatoes both in their fresh form and as processed products like chips and French fries. Potatoes are a crop that requires intensive fertilization, with **nitrogen (N)** being a vital nutrient for optimal plant growth, tuber yield, and quality. Unfortunately, the excessive application of nitrogen in potato farming is a prevalent practice aimed at achieving high tuber yields. Here, the transcriptome data of potato under **nitrogen stress** were studied.

This work was supported by the grant CABin Scheme Network project on Agricultural Bioinformatics and Computational Biology (F.No. Agril.Edn. 14/2/2017-A&P dated 02.08.2017), received from Indian Council of Agricultural Research (ICAR).

#### Results

Items	Shoot	Root	Stolen
Total no. of DEGs : 1233	249	209	775
Total no. DElncRNA : 269	57	53	159
Total no. eTM-DElncRNA : 31	04	08	19
Total no. of IRES-lncRNA:08	01	02	05
Total no. of circRNA: 47	24	06	17
Total no. of circRNA-miRNA :42	22	05	15
Total no. of IRES-circRNA: 02	0	01	01
Total no. of Alternative Splicing events:	17200	16599	16174

#### Source of data

SRA id	Control	Treatment
Shoot	<a href="#">SRR10135774</a>	<a href="#">SRR10135773</a>
Root	<a href="#">SRR10135772</a>	<a href="#">SRR10135771</a>
Stolen	<a href="#">SRR10135770</a>	<a href="#">SRR10135769</a>

## Search Options:

- **DElncRNAs Search:** Users can initiate searches specifically for Differentially Expressed lncRNAs.
- **eTM-DElncRNA Search:** This option enables users to search for lncRNAs that are endogenous target mimics (eTM) for miRNAs in specific tissues or cell types.
- **Cis-DElncRNA Search:** Users can explore lncRNAs with cis-regulatory effects on nearby genes.
- **CircRNA Search:** This option allows users to find information about Circular RNAs.
- **DEGs Search:** Users can search for Differentially Expressed Genes.
- **Alternate Splicing Search:** This feature facilitates the exploration of genes and lncRNAs involved in alternate splicing events.
- **Contact Information:** A direct link or section providing contact information, such as an email address or a contact form, for users to reach out for support or inquiries.
- **User Manual:** A link to a comprehensive user manual, guiding users on how to effectively use the database, interpret results, and troubleshoot any issues.

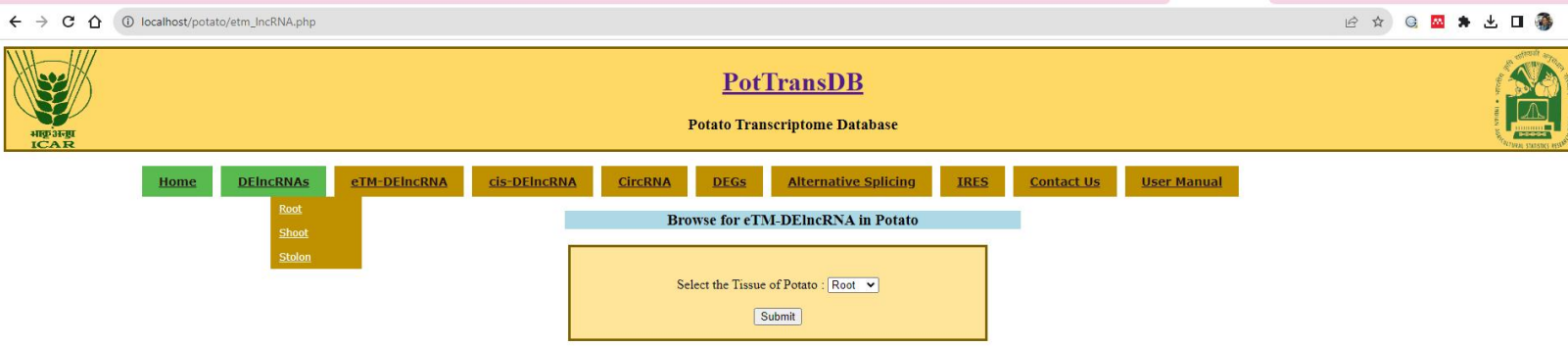
**Click on 'DElncRNAs' Icon:** Users will navigate to the 'DElncRNAs' section by clicking on the designated icon on the home screen.

**Dropdown Menu for Tissue Selection:** Upon selecting 'DElncRNAs,' a dropdown menu appears with three options: 'Root,' 'Shoot,' and 'Stolon'.

**Tissue Selection:** Users can choose the specific tissue of interest (Root, Shoot, or Stolon) from the dropdown menu. This selection is crucial for obtaining tissue-specific information.

**Retrieve Tissue-Specific Data:** After selecting the tissue, the system retrieves and displays data related to differentially expressed lncRNAs specifically in the chosen tissue.

This approach allows users to quickly and efficiently obtain tissue-specific information about differentially expressed lncRNAs in potatoes. It's a streamlined process that caters to users interested in specific aspects of gene expression in different potato tissues.



The screenshot displays the PotTransDB website interface. The browser address bar shows the URL `localhost/potato/etm_lncRNA.php`. The website header features the ICAR logo on the left, the title "PotTransDB" in the center, and the subtitle "Potato Transcriptome Database" below it. A navigation menu includes buttons for Home, DElncRNAs, eTM-DElncRNA, cis-DElncRNA, CircRNA, DEGs, Alternative Splicing, IRES, Contact Us, and User Manual. The DElncRNAs button is highlighted, and a dropdown menu is open, showing options for Root, Shoot, and Stolon. Below the navigation menu, a section titled "Browse for eTM-DElncRNA in Potato" contains a form with a dropdown menu labeled "Select the Tissue of Potato" set to "Root" and a "Submit" button. At the bottom of the page, the text reads: "ICAR-Indian Agricultural Statistics Research Institute Library Avenue, PUSA, New Delhi - 110 012" followed by the URL <https://iasri.icar.gov.in/>.

**Select Root Tissue:** After choosing 'Root' from the dropdown menu, users will access data specifically related to differentially expressed lncRNAs in the root tissue.

**Download Root-DElncRNA Sequences:** To empower users with the ability to utilize the data, there's an additional option to download the sequences of Root-DElncRNAs.

Clicking on this option initiates the download process.

**Similar Options for Shoot and Stolon:** Users can repeat the process for 'Shoot' and 'Stolon' tissues, selecting the tissue of interest and downloading the corresponding DElncRNA sequences.

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Root DElncRNA's Details

Click here for [Root DE-lncRNA sequence](#)

lncRNA id	Chr no.	Length	Start	End	FC value	pvalue	Exon	Class code	MFE	Targeted Gene	Targeted gene's Function
TCONS_00014685	2	885	40491307	40492192	-7.4687	0.0002	7	novel	-38.4	<a href="#">PGSC0003DMT400028259</a>	Bet1-like snare 1-1
TCONS_00032514	4	3249	36018222	36021471	-7.3988	0.0002	3	known	-36.2	<a href="#">PGSC0003DMT400006464</a>	DNA repair protein
TCONS_00045722	6	925	32068366	32069291	8.0278	0	3	novel	-36.7	<a href="#">PGSC0003DMT400090130</a>	Gene of unknown function
TCONS_00051873	7	938	633484	634422	8.2615	0	5	known	-39	<a href="#">PGSC0003DMT400053779</a>	Nuclease
TCONS_00047763	6	1039	59364445	59365484	-7.3988	0.0002	5	known	-43.4	<a href="#">PGSC0003DMT400061571</a>	Multiple myeloma tumor-associated protein
TCONS_00009259	1	859	83913382	83914241	-3.478	0.0002	3	known	-37.2	<a href="#">PGSC0003DMT400078534</a>	ER Phosphatidate Phosphatase
TCONS_00029813	4	3285	40841683	40844968	9.8789	0	5	known	NA	NA	NA
TCONS_00083997	12	4740	49376987	49381727	9.1468	0	2	known	NA	NA	NA
TCONS_00083999	12	4524	49379668	49384192	8.5825	0	5	known	NA	NA	NA
TCONS_00014688	2	882	40491307	40492189	7.6967	0.0001	7	known	NA	NA	NA
TCONS_00032490	4	2764	35615166	35617930	7.3361	0.0003	4	known	NA	NA	NA
TCONS_00063589	9	634	52779497	52780131	2.3039	0.0008	2	known	NA	NA	NA
TCONS_00034131	4	1228	71515022	71516250	3.0106	0.0002	2	novel	-35.6	<a href="#">PGSC0003DMT400012140</a>	Nucleic acid binding protein
TCONS_00032495	4	1327	35615166	35616493	-7.3988	0.0002	5	known	NA	NA	NA
TCONS_00083998	12	4030	49379668	49383698	-7.3988	0.0002	5	known	NA	NA	NA
TCONS_00032657	4	2019	46112710	46114729	-7.9809	0	6	known	NA	NA	NA
TCONS_00032789	4	1166	50885544	50886710	7.4028	0.0002	2	known	-38.3	<a href="#">PGSC0003DMT400000897</a>	Beta-galactosidase
TCONS_00008550	1	639	77371260	77371899	7.0334	0.001	5	known	-41.8	<a href="#">PGSC0003DMT400004017</a>	Anti-PCD protein
TCONS_00043556	6	2827	44374371	44377198	-8.3581	0	11	known	-36.1	<a href="#">PGSC0003DMT400007349</a>	Spliceosome associated protein
TCONS_00028793	4	1269	1798509	1799778	8.1494	0	4	novel	-28.8	<a href="#">PGSC0003DMT400073819</a>	NADH-ubiquinone oxidoreductase
TCONS_00024489	3	1756	35180961	35182717	8.5534	0	4	known	-40.3	<a href="#">PGSC0003DMT400014358</a>	AP2/ERF domain-containing transcription factor
TCONS_00053305	7	735	49654704	49655439	-2.8375	0.0003	3	known	-43.6	<a href="#">PGSC0003DMT400014748</a>	Phosphoethanolamine N-methyltransferase
TCONS_00064441	9	1994	1085861	1087855	7.6425	0.0001	4	known	-26.3	<a href="#">PGSC0003DMT400014965</a>	Gene of unknown function
TCONS_00051176	7	2007	5081311	5081818	8.028	0	7	known	-32.2	<a href="#">PGSC0003DMT400030148</a>	Aspartic proteinase

User can click on the target gene ID to get more information about the lncRNA targeted gene from Spud DB Genome browser

Target gene ID

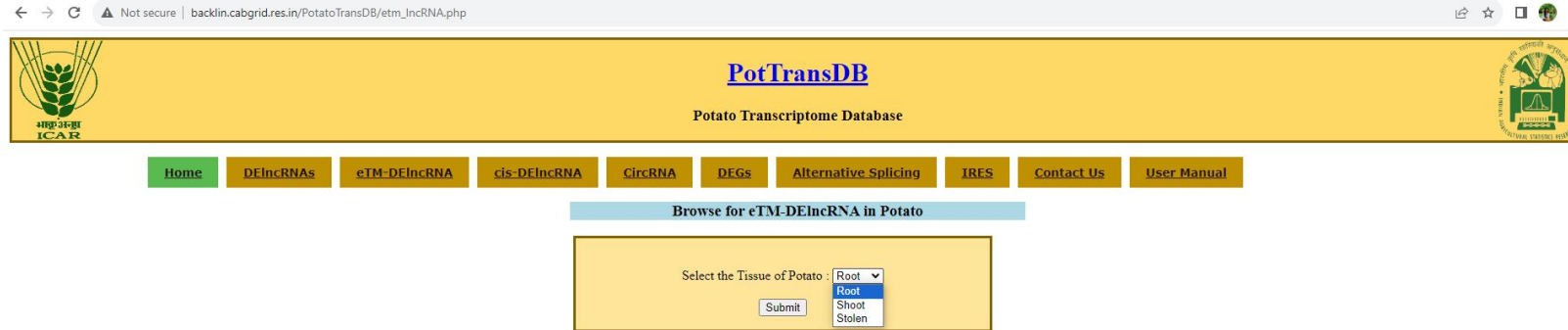
The screenshot displays the Spud DB Genome Browser interface for the potato genome. The browser title is "Spud DB Genome Browser Potato (Solanum tuberosum group Phureja DM1-3) PGSC v4.03 Pseudomolecules". The current view shows a genomic region on chromosome 6, with coordinates 1,461,421 to 1,464,702. The search bar contains the ID "PGSC0003DMT400028259", which is highlighted by a red callout box labeled "Target gene ID". The interface includes various navigation and search options, such as "Search", "Landmark or Region", and "Data Source". The main track displays several genomic features, including "Region - PGSC Loci", "PGSC Pseudomolecule Tiling Path (v4.03)", "PGSC Loci", "PGSC Representative Gene Models", and "PGSC Gene Models". The tracks show the location of the target gene and other related features, such as "Bet1-like snare 1-1". The interface also includes a "Tracks" section at the bottom with checkboxes for "Region - PGSC Loci", "BLASTP Top Hit", "Arabidopsis thaliana (TAIR 10) Top Hit - BLASTP", and "DM RNASeq Coverage".

**Click on 'eTM-DElncRNAs' Icon:** Users will access the 'eTM-DElncRNAs' section by clicking on the designated icon on the home screen.

**Dropdown Menu for Tissue Selection:** Upon selecting 'eTM-DElncRNAs,' a dropdown menu appears with three options: 'Root,' 'Shoot,' and 'Stolon'.

**Tissue Selection:** Users can choose the specific tissue of interest (Root, Shoot, or Stolon) from the dropdown menu. This selection is crucial for obtaining expression-tissue-matched data.

**Retrieve Tissue-Specific eTM-DElncRNA Data:** After selecting the tissue, the system retrieves and displays data related to eTM-DElncRNAs specifically in the chosen tissue.



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Users can easily access expression-tissue-matched differentially expressed lncRNA (eTM-DElncRNA) data for specific tissues by following a straightforward process.

Potato Transcriptome Database

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Browse for eTM-DElncRNA in Potato

Select the Tissue of Potato :

Total no. records of Stolon:15

eTM-DElncRNA id	Chr no.	Score	UPE(-)	miRNA
TCONS_00071423	10	2	12.433	<a href="#">stu-miR156e</a>
TCONS_00071424	10	2	12.433	<a href="#">stu-miR156e</a>
TCONS_00033377	4	2.5	11.116	<a href="#">stu-miR171c-3p</a>
TCONS_00033372	4	2.5	11.116	<a href="#">stu-miR171c-3p</a>
TCONS_00061660	8	2.5	14.011	<a href="#">stu-miR1886a</a>
TCONS_00061662	8	2.5	14.011	<a href="#">stu-miR1886a</a>
TCONS_00061661	8	2.5	14.011	<a href="#">stu-miR1886a</a>
TCONS_00013947	2	3	16.534	<a href="#">stu-miR477a-5p</a>
TCONS_00048264	6	2	17.711	<a href="#">stu-miR5303a</a>
TCONS_00038384	5	0.5	18.23	<a href="#">stu-miR5303e</a>
TCONS_00071067	10	2.5	22.414	<a href="#">stu-miR6025</a>
TCONS_00009378	1	3	13.918	<a href="#">stu-miR7992-5p</a>
TCONS_00055016	7	3	17.962	<a href="#">stu-miR8022</a>
TCONS_00064964	9	3	18.236	<a href="#">stu-miR8024a-3p</a>
TCONS_00008705	1	1.5	18.237	<a href="#">stu-miR8030-3p</a>
TCONS_00008703	1	1.5	18.237	<a href="#">stu-miR8030-3p</a>
TCONS_00083304	12	2	12.635	<a href="#">stu-miR8033-3p</a>
TCONS_00039528	5	1.5	23.522	<a href="#">stu-miR8039</a>
TCONS_00064718	9	2.5	12.335	<a href="#">stu-miR8039</a>

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<https://mirbase.org/results/?query=stu-miR156e>



User can click on miRNA ID to get the more information about the miRNA. The link will be directed to miRBase

The screenshot shows the miRBase website interface. The browser address bar displays the URL `mirbase.org/results/?query=stu-miR156e`. The page header includes the miRBase logo and navigation links: Home, Search, Browse, Help, Downloads. A search bar on the right contains the text "Search miRBase".

The main content area displays the message: "Your query 'stu-miR156e' returned 2 results". Below this, there is a "Download CSV File" button and a "Filter:" input field. A table shows the search results with columns: Name, Accession, Chromosome, Start, End, Strand, and Confidence. The table contains two entries:

Name	Accession	Chromosome	Start	End	Strand	Confidence
<a href="#">stu-MIR156e</a>	MI0025990	JH137825.1	159113	159199	+	-
<a href="#">stu-miR156e</a>	MIMAT0031346					

Below the table, it says "Showing 1 to 2 of 2 entries" and includes "Previous" and "Next" navigation buttons. At the bottom of the results section, there are three buttons: "Select all", "Reset", and "Fetch sequences".

The footer of the page features the University of Manchester logo on the left and the text "Comments or questions? Email [mirbase@manchester.ac.uk](mailto:mirbase@manchester.ac.uk)" on the right.

**Click on 'cis-DEIncRNAs' Icon:** Users will enter the 'cis-DEIncRNAs' section by clicking on the designated icon on the home screen.

**Dropdown Menu for Tissue Selection:** Upon selecting 'cis-DEIncRNAs,' a dropdown menu appears with three options: 'Root,' 'Shoot,' and 'Stolon'.

**Tissue Selection:** Users can then choose the specific tissue of interest (Root, Shoot, or Stolon) from the dropdown menu. This step is crucial for obtaining cis-regulatory effects data.

**Retrieve Tissue-Specific cis-DEIncRNA Data:** After selecting the tissue, the system retrieves and displays data related to cis-acting differentially expressed lncRNAs specifically in the chosen tissue.

The screenshot shows the PotTransDB website interface. The browser address bar displays 'localhost/potato/index.php'. The website header includes the ICAR logo, the title 'PotTransDB Potato Transcriptome Database', and a navigation menu with options: Home, DEIncRNAs, eTM-DEIncRNA, cis-DEIncRNA, CircRNA, DEGs, Alternative Splicing, IRES, Contact Us, and User Manual. A dropdown menu is open over the 'cis-DEIncRNA' option, showing 'Root', 'Shoot', and 'Stolon'. Below the menu is a photograph of a potato field. To the right, there is an 'About PotTransDB' section with text about potato and a 'Source of data' section with a table. A 'Summary' table is also present.

**About PotTransDB**

*Potato (Solanum tuberosum L.)* ranks third among the world's most significant food crops, following rice and wheat, in terms of human consumption. It boasts high yields of dry matter and calories per unit area and time, making it a valuable source of energy, proteins, vitamins, and minerals. Over a billion people worldwide enjoy potatoes both in their fresh form and as processed products like chips and French fries. Potatoes are a crop that requires intensive fertilization, with nitrogen (N) being a vital nutrient for optimal plant growth, tuber yield, and quality. Unfortunately, the excessive application of nitrogen in potato farming is a prevalent practice aimed at achieving high tuber yields. Here, the transcriptome data of potato under **nitrogen stress** were studied.

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**Source of data**

Tissue	Control	Treatment
Shoot	SRR10135774	SRR10135773
Root	SRR10135772	SRR10135771
Stolon	SRR10135770	SRR10135769

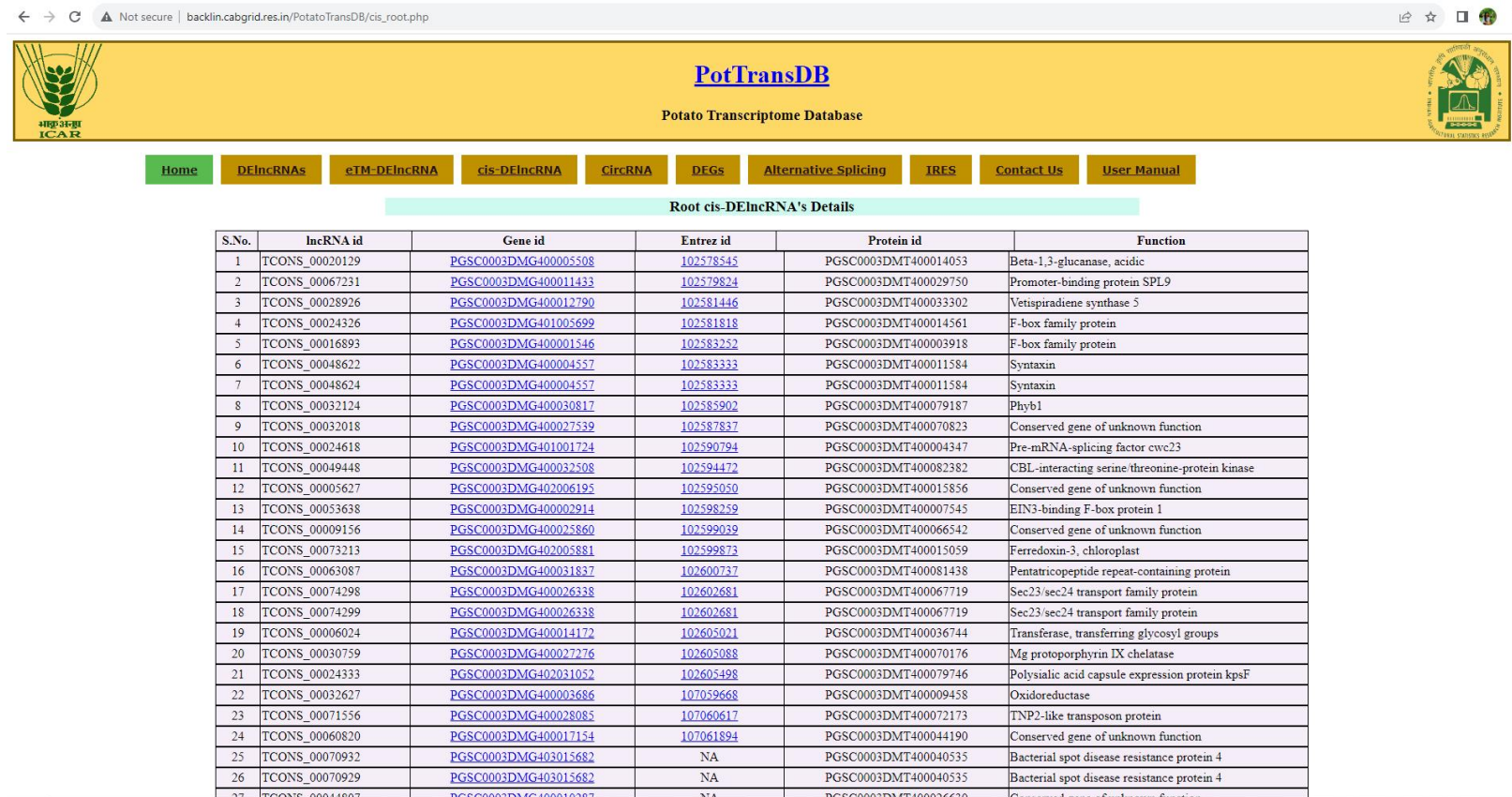
**Summary**

Items	Shoot	Root	Stolon
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No. of IRES-circRNAs: 02	0	01	01
No. of Alternative Splicing events:	17200	16599	16174

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localhost/potato/cis\_root.php

Users can easily access information on cis-regulatory effects of differentially expressed lncRNAs (cis-DELncRNAs) in specific tissues by following these steps.



The screenshot shows the PotTransDB website interface. The header includes the ICAR logo, the title 'PotTransDB Potato Transcriptome Database', and a navigation menu with buttons for Home, DElncRNAs, eTM-DElncRNA, cis-DElncRNA, CircRNA, DEGs, Alternative Splicing, IRES, Contact Us, and User Manual. The main content area displays a table titled 'Root cis-DELncRNA's Details' with the following columns: S.No., lncRNA id, Gene id, Entrez id, Protein id, and Function. The table lists 27 entries, each with a unique lncRNA ID, its corresponding gene and protein IDs, and a brief description of the protein's function.

S.No.	lncRNA id	Gene id	Entrez id	Protein id	Function
1	TCONS_00020129	<a href="#">PGSC0003DMG400005508</a>	<a href="#">102578545</a>	PGSC0003DMT400014053	Beta-1,3-glucanase, acidic
2	TCONS_00067231	<a href="#">PGSC0003DMG400011433</a>	<a href="#">102579824</a>	PGSC0003DMT400029750	Promoter-binding protein SPL9
3	TCONS_00028926	<a href="#">PGSC0003DMG400012790</a>	<a href="#">102581446</a>	PGSC0003DMT400033302	Vetispiradiene synthase 5
4	TCONS_00024326	<a href="#">PGSC0003DMG401005699</a>	<a href="#">102581818</a>	PGSC0003DMT400014561	F-box family protein
5	TCONS_00016893	<a href="#">PGSC0003DMG400001546</a>	<a href="#">102583252</a>	PGSC0003DMT400003918	F-box family protein
6	TCONS_00048622	<a href="#">PGSC0003DMG400004557</a>	<a href="#">102583333</a>	PGSC0003DMT400011584	Syntaxin
7	TCONS_00048624	<a href="#">PGSC0003DMG400004557</a>	<a href="#">102583333</a>	PGSC0003DMT400011584	Syntaxin
8	TCONS_00032124	<a href="#">PGSC0003DMG400030817</a>	<a href="#">102585902</a>	PGSC0003DMT400079187	Phybl
9	TCONS_00032018	<a href="#">PGSC0003DMG400027539</a>	<a href="#">102587837</a>	PGSC0003DMT400070823	Conserved gene of unknown function
10	TCONS_00024618	<a href="#">PGSC0003DMG401001724</a>	<a href="#">102590794</a>	PGSC0003DMT400004347	Pre-miRNA-splicing factor cwc23
11	TCONS_00049448	<a href="#">PGSC0003DMG400032508</a>	<a href="#">102594472</a>	PGSC0003DMT400082382	CBL-interacting serine threonine-protein kinase
12	TCONS_00005627	<a href="#">PGSC0003DMG402006195</a>	<a href="#">102595050</a>	PGSC0003DMT400015856	Conserved gene of unknown function
13	TCONS_00053638	<a href="#">PGSC0003DMG400002914</a>	<a href="#">102598259</a>	PGSC0003DMT400007545	EIN3-binding F-box protein 1
14	TCONS_00009156	<a href="#">PGSC0003DMG400025860</a>	<a href="#">102599039</a>	PGSC0003DMT400066542	Conserved gene of unknown function
15	TCONS_00073213	<a href="#">PGSC0003DMG402005881</a>	<a href="#">102599873</a>	PGSC0003DMT400015059	Ferredoxin-3, chloroplast
16	TCONS_00063087	<a href="#">PGSC0003DMG400031837</a>	<a href="#">102600737</a>	PGSC0003DMT400081438	Pentatricopeptide repeat-containing protein
17	TCONS_00074298	<a href="#">PGSC0003DMG400026338</a>	<a href="#">102602681</a>	PGSC0003DMT400067719	Sec23/sec24 transport family protein
18	TCONS_00074299	<a href="#">PGSC0003DMG400026338</a>	<a href="#">102602681</a>	PGSC0003DMT400067719	Sec23/sec24 transport family protein
19	TCONS_00006024	<a href="#">PGSC0003DMG400014172</a>	<a href="#">102605021</a>	PGSC0003DMT400036744	Transferase, transferring glycosyl groups
20	TCONS_00030759	<a href="#">PGSC0003DMG400027276</a>	<a href="#">102605088</a>	PGSC0003DMT400070176	Mg protoporphyrin IX chelatase
21	TCONS_00024333	<a href="#">PGSC0003DMG402031052</a>	<a href="#">102605498</a>	PGSC0003DMT400079746	Polysialic acid capsule expression protein kpsF
22	TCONS_00032627	<a href="#">PGSC0003DMG400003686</a>	<a href="#">107059668</a>	PGSC0003DMT400009458	Oxidoreductase
23	TCONS_00071556	<a href="#">PGSC0003DMG400028085</a>	<a href="#">107060617</a>	PGSC0003DMT400072173	TNP2-like transposon protein
24	TCONS_00060820	<a href="#">PGSC0003DMG400017154</a>	<a href="#">107061894</a>	PGSC0003DMT400044190	Conserved gene of unknown function
25	TCONS_00070932	<a href="#">PGSC0003DMG403015682</a>	NA	PGSC0003DMT400040535	Bacterial spot disease resistance protein 4
26	TCONS_00070929	<a href="#">PGSC0003DMG403015682</a>	NA	PGSC0003DMT400040535	Bacterial spot disease resistance protein 4
27	TCONS_00048607	<a href="#">PGSC0003DMG400010287</a>	NA	PGSC0003DMT400026630	Conserved gene of unknown function

User can click on Entrez gene ID of the target gene to view information on inflammation from NCBI

Entrez  
gene ID

Search NCBI  Search

Results found in 4 databases

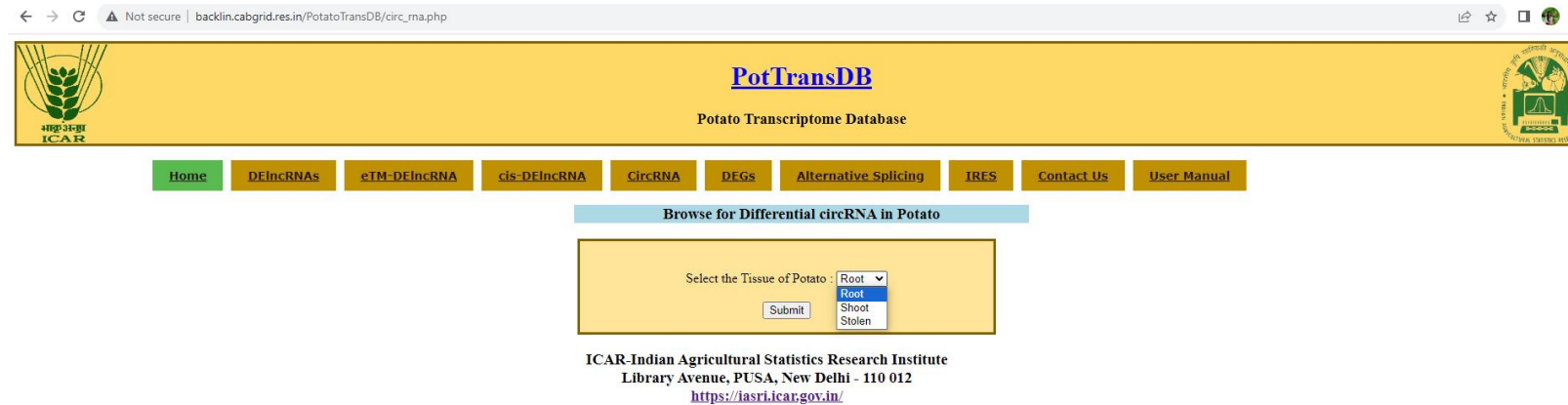
<b>Gene</b> <b>LOC102578545 - glucan endo-1,3-beta-glucosidase 8-like</b> Solanum tuberosum GeneID: 102578545	<b>GEO Profiles</b> <b>Latent gammaherpesvirus 68 infection of various organs</b> Mus musculus Slc30a2; solute carrier family 30 (zinc transporter), member 2 ID: 102578545	<b>Compounds</b> <b>DBPWSSGDRRHUNT-XPCIRFDXSA-N</b> C <sub>21</sub> H <sub>30</sub> O <sub>3</sub> (8R,9S,10R,13S,14S,17R)-17-acetyl-17-hydroxy-10,13-dimethyl-2,6,7,8,9,11,12,14,15,16-decahydro-1H-cyclopenta[a]phenanthren-3-one PubChem CID: 102578545
<b>Literature</b> Bookshelf (0) MeSH (0) NLM Catalog (0) PubMed (0) PubMed Central (0)	<b>Genes</b> Gene (1) GEO DataSets (0) GEO Profiles (1) HomoloGene (0) PopSet (0)	<b>Proteins</b> Conserved Domains (0) Identical Protein Groups (1) Protein (0) Protein Family Models (0) Structure (0)
<b>Genomes</b> Assembly (0)	<b>Clinical</b> ClinicalTrials.gov (0)	<b>PubChem</b> BioAssays (0)

**Click on 'circRNA' Icon:** Users will access the 'circRNA' section by clicking on the designated icon on the home screen.

**Dropdown Menu for Tissue Selection:** Upon selecting 'circRNA,' a dropdown menu appears with three options: 'Root,' 'Shoot,' and 'Stolon'.

**Tissue Selection:** Users can then choose the specific tissue of interest (Root, Shoot, or Stolon) from the dropdown menu.

**Retrieve Tissue-Specific circRNA Data:** After selecting the tissue, the system retrieves and displays data related to circular RNAs specifically in the chosen tissue.



The screenshot shows a web browser window with the URL `backlin.cabgrid.res.in/PotatoTransDB/circ_ma.php`. The page header features the **PotTransDB** logo and the text "Potato Transcriptome Database". Below the header is a navigation menu with buttons for Home, DEIncRNAs, eTM-DEIncRNA, cis-DEIncRNA, CircRNA, DEGs, Alternative Splicing, IRES, Contact Us, and User Manual. The main content area is titled "Browse for Differential circRNA in Potato" and contains a form with the label "Select the Tissue of Potato :". A dropdown menu is open, showing the options "Root", "Shoot", and "Stolon". A "Submit" button is located below the dropdown. At the bottom of the page, the text reads: "ICAR-Indian Agricultural Statistics Research Institute, Library Avenue, PUSA, New Delhi - 110 012, <https://iasri.icar.gov.in/>".

Users can follow a consistent and intuitive process to access circular RNA (circRNA) data specific to different tissues.

The screenshot shows the PotTransDB website interface. The browser address bar displays 'localhost/potato/circ\_rna.php?Tissue=Root&search=Submit'. The website header features the ICAR logo and the title 'PotTransDB Potato Transcriptome Database'. A navigation menu includes links for Home, DEIncRNAs, eTM-DEIncRNA, cis-DEIncRNA, CircRNA, DEGs, Alternative Splicing, IRES, Contact Us, and User Manual. A central search box prompts the user to 'Browse for Differentially expressed circRNA in Potato' and includes a dropdown menu for 'Select the Tissue of Potato' set to 'Root' and a 'Submit' button. Below the search box, it displays 'Total no. records of Root:22' and a link to 'Click here for Root circRNA sequence'. A table of results is shown below, listing circRNA IDs, chromosome numbers, lengths, start and end coordinates, Fc values, p-values, and associated sponge miRNAs.

circRNA id	Chr no.	Length	Start	End	Fc value	p-value	Sponge miRNA
ST_circR_Root-007	2	28260	20543784	20572044	-12.893	0	<a href="#">stu-miR8024a-3p</a>
ST_circR_Root-008	4	134385	4352380	4486765	-12.321	0	<a href="#">stu-miR7984d-5p</a>
ST_circR_Root-009	11	45579	44126704	44172283	-10.888	0	<a href="#">stu-miR6024-5p</a>
ST_circR_Root-010	8	16780	3168909	3185689	-6.962	0.00027	<a href="#">stu-miR8040-3p</a>
ST_circR_Root-012	8	45468	33300311	33345779	-2.478	4.0E-5	<a href="#">stu-miR8008a</a>
ST_circR_Root-013	11	24673	42861429	42886102	-2.252	2.0E-5	<a href="#">stu-miR8014-3p</a>
ST_circR_Root-015	3	8373	322727	331100	-1.883	9.0E-5	<a href="#">stu-miR8007a-5p</a>
ST_circR_Root-016	5	51622	42534785	42586407	-1.815	0.00015	<a href="#">stu-miR8001a</a>
ST_circR_Root-017	11	10402	5090921	5101323	-1.737	0.00032	<a href="#">stu-miR7983-5p</a>
ST_circR_Root-018	11	54777	43423886	43478663	-1.692	0.00053	<a href="#">stu-miR398a-5p</a>
ST_circR_Root-019	12	34549	60523902	60558451	-1.634	0.00054	<a href="#">stu-miR6026-5p</a>
ST_circR_Root-020	6	29174	58401472	58430646	-1.506	0.0019	<a href="#">stu-miR7984a</a>
ST_circR_Root-021	2	68087	22975854	23043941	1.513	0.0017	<a href="#">stu-miR8028-3p</a>
ST_circR_Root-022	11	83023	43908028	43991051	1.676	0.00042	<a href="#">stu-miR5303g</a>
ST_circR_Root-023	2	31832	31249653	31281485	1.799	0.00032	<a href="#">stu-miR7982a</a>
ST_circR_Root-024	6	18029	57961801	57979830	2.436	2.0E-5	<a href="#">stu-miR8007b-5p</a>

User can click on miRNA ID to get the more information about the miRNA. The link will be directed to miRBase

The screenshot shows the miRBase search results page. The browser address bar displays `mirbase.org/results/?query=stu-miR8024a-3p`. The page header includes the miRBase logo and navigation links: Home, Search, Browse, Help, Downloads. A search bar on the right contains the text "Search miRBase".

The main content area displays the message: "Your query **"stu-miR8024a-3p"** returned 1 results". Below this, there is a "Download CSV File" button and a "Filter:" input field. A table shows the search results with columns for "Name" and "Accession". The single result is `stu-miR8024a-3p` with accession number `MIMAT0030923`. The "Name" cell is circled in red, and a red arrow points from a box labeled "miRNA ID" to this cell. Below the table, it says "Showing 1 to 1 of 1 entries" and includes "Previous" and "Next" navigation buttons.

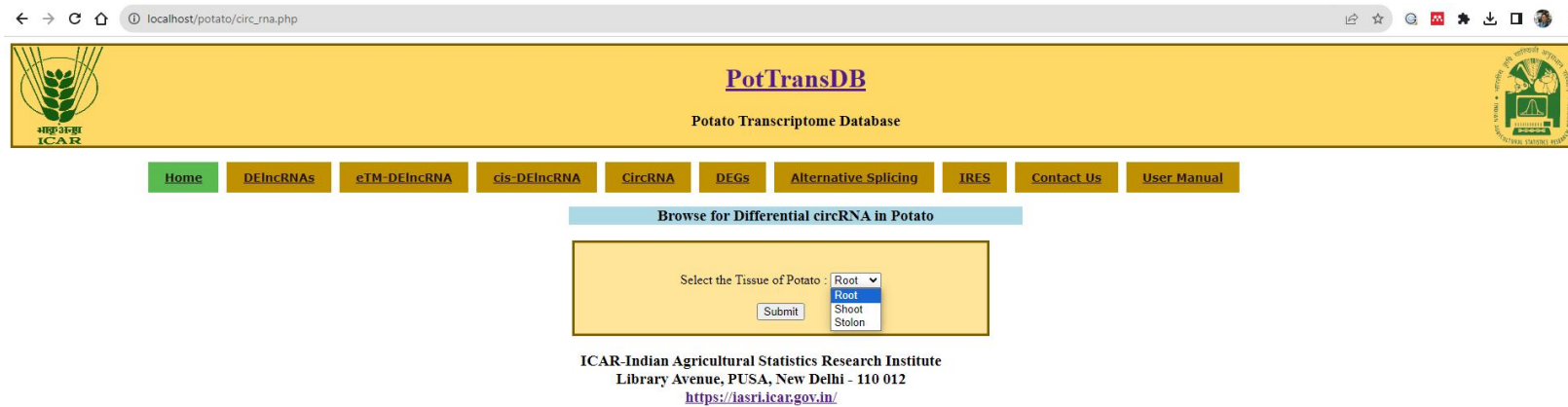
At the bottom of the page, there is a footer with the Manchester University logo and the text: "Comments or questions? Email [mirbase@manchester.ac.uk](mailto:mirbase@manchester.ac.uk)".

**Click on 'DEGs' Icon:** Users will enter the 'DEGs' section by clicking on the designated icon on the home screen.

**Dropdown Menu for Tissue Selection:** Upon selecting 'DEGs,' a dropdown menu appears with three options: 'Root,' 'Shoot,' and 'Stolon'.

**Tissue Selection:** Users can then choose the specific tissue of interest (Root, Shoot, or Stolon) from the dropdown menu.

**Retrieve Tissue-Specific DEG Data:** After selecting the tissue, the system retrieves and displays data related to differentially expressed genes specifically in the chosen tissue.




The screenshot shows a web browser window with the URL `localhost/potato/circ_rna.php`. The page features a yellow header with the **PotTransDB** logo and the text "Potato Transcriptome Database". Below the header is a navigation menu with buttons for Home, DEIncRNAs, eTM-DEIncRNA, cis-DEIncRNA, CircRNA, DEGs, Alternative Splicing, IRES, Contact Us, and User Manual. A light blue banner reads "Browse for Differential circRNA in Potato". Below this is a form with the label "Select the Tissue of Potato:" and a dropdown menu showing "Root", "Shoot", and "Stolon". A "Submit" button is located below the dropdown. At the bottom of the page, the text reads: "ICAR-Indian Agricultural Statistics Research Institute, Library Avenue, PUSA, New Delhi - 110 012, <https://iasri.icar.gov.in/>".




users can easily access information on differentially expressed genes (DEGs) specific to the tissue of interest.

← → ↻ Not secure | backlin.cabgrid.res.in/PotatoTransDB/deg\_root.php



## PotTransDB

Potato Transcriptome Database



Home
DEIncRNAs
eTM-DEIncRNA
cis-DEIncRNA
CircRNA
DEGs
Alternative Splicing
IRES
Contact Us
User Manual

**Differential Gene expression of Root Tissue**

Gene id	Locus	FC value	pvalue	Function	Pathway	KEGG id
<a href="#">PGSC0003DMT400051938</a>	NW_006239073.1:439743-440288	2.2028	3.0E-5	probable pectate lyase 8	NA	NA
<a href="#">PGSC0003DMT400021018</a>	NW_006239057.1:249460-251381	2.4409	0	zeatin O-glucosyltransferase-like	Zeatin biosynthesis	<a href="#">KEGG:00908</a>
<a href="#">PGSC0003DMT400033236</a>	NW_006238936.1:681872-682650	2.6934	0.0002	methylsterol monooxygenase 1-1-like	NA	<a href="#">KEGG:01100</a> <a href="#">KEGG:01110</a>
<a href="#">PGSC0003DMT400037714</a>	NW_006238978.1:294285-295173	2.7819	0	β-ketoacyl- synthase 6	Metabolic pathways	<a href="#">KEGG:01100</a>
<a href="#">PGSC0003DMT400037714</a>	NW_006238978.1:299017-299775	2.6576	0	β-ketoacyl- synthase 6	Metabolic pathways	<a href="#">KEGG:01100</a>
<a href="#">PGSC0003DMT400084224</a>	NW_006238995.1:1432329-1433040	2.2553	2.0E-5	acidic endochitinase	Metabolic pathways	<a href="#">KEGG:01100</a>
<a href="#">PGSC0003DMT400066961</a>	NW_006239021.1:657101-658140	2.056	0.00013	Malate cytoplasmic	Metabolic pathways	<a href="#">KEGG:01100</a>
<a href="#">PGSC0003DMT400035343</a>	NW_006239029.1:717399-718930	4.9301	0	NA	Metabolic pathways	<a href="#">KEGG:01100</a>
<a href="#">PGSC0003DMT400013351</a>	NW_006239030.1:481734-482197	2.2929	0.00014	probable pectinesterase 53	NA	<a href="#">KEGG:01100</a> <a href="#">KEGG:00040</a>
<a href="#">PGSC0003DMT400036565</a>	NW_006239062.1:387835-388279	2.1789	5.0E-5	flavonol synthase flavanone 3-hydroxylase	Metabolic pathways	<a href="#">KEGG:01100</a>
<a href="#">PGSC0003DMT400041565</a>	NW_006239078.1:20332-21100	3.3455	0	8-hydroxygeraniol dehydrogenase-like	Metabolic pathways	<a href="#">KEGG:01100</a>
<a href="#">PGSC0003DMT400034972</a>	NW_006239139.1:370294-371282	2.0366	2.0E-5	β-ketoacyl- synthase 11	NA	<a href="#">KEGG:01100</a> <a href="#">KEGG:01110</a> <a href="#">KEGG:00062</a>
<a href="#">PGSC0003DMT400056145</a>	NW_006239363.1:127074-127412	2.4748	0	chlorophyllase- chloroplasmic-like	Metabolic pathways	<a href="#">KEGG:01100</a>
<a href="#">PGSC0003DMT400016363</a>	NW_006239445.1:292676-293261	2.0345	0.0001	serine mitochondrial-like	NA	<a href="#">KEGG:01100</a> <a href="#">KEGG:01110</a> <a href="#">00670</a> <a href="#">00630</a>
<a href="#">PGSC0003DMT400065518</a>	NW_006239664.1:21106-22384	2.2257	0	peroxidase 3-like	Metabolic pathways	<a href="#">KEGG:01100</a>
<a href="#">PGSC0003DMT400030898</a>	NW_006238973.1:2194325-2194907	2.1848	2.0E-5	DNA replication licensing factor MCM5	DNA replication	<a href="#">KEGG:03030</a>
<a href="#">PGSC0003DMT400023333</a>	NW_006239030.1:859283-860098	2.0241	8.0E-5	DNA replication licensing factor MCM7	DNA replication	<a href="#">KEGG:03030</a>
<a href="#">PGSC0003DMT400023973</a>	NW_006238930.1:331251-332183	3.2415	0	L-ascorbate oxidase homolog	NA	NA
<a href="#">PGSC0003DMT400023973</a>	NW_006238930.1:332341-333507	3.1708	0	L-ascorbate oxidase homolog	NA	NA
<a href="#">PGSC0003DMT400003487</a>	NW_006238930.1:1184722-1186554	2.1831	0	vegetative cell wall gp1	NA	NA
<a href="#">PGSC0003DMT400003336</a>	NW_006238930.1:2148276-2149638	2.73	0	tubulin alpha chain	NA	NA
<a href="#">PGSC0003DMT400052053</a>	NW_006238930.1:3987923-3988723	2.1929	0	pollen allergen Che a 1	NA	NA
<a href="#">PGSC0003DMT400052053</a>	NW_006238930.1:3988900-39889613	2.8247	0	pollen allergen Che a 1	NA	NA
<a href="#">PGSC0003DMT400080097</a>	NW_006238935.1:922747-923763	4.1674	0	GDSL esterase lipase At1g33811	NA	NA
<a href="#">PGSC0003DMT400080096</a>	NW_006238935.1:924003-924496	3.0097	0	GDSL esterase lipase At1g33811	NA	NA
<a href="#">PGSC0003DMT400080082</a>	NW_006238935.1:1043683-1044976	2.1466	0.00014	glucuronoxylan 4-O-methyltransferase 3	NA	NA
<a href="#">PGSC0003DMT400080082</a>	NW_006238936.1:172858-175058	2.505	0	heavy metal associated isoprenylated plant 33	NA	NA

**Click on 'Alternative Splicing' Icon:** Users will enter the 'Alternative Splicing' section by clicking on the designated icon on the home screen.

**Dropdown Menu for Tissue Selection:** Upon selecting 'Alternative Splicing,' a dropdown menu appears with three options: 'Root,' 'Shoot,' and 'Stolon'.

**Tissue Selection:** Users can then choose the specific tissue of interest (Root, Shoot, or Stolon) from the dropdown menu.

**Retrieve Tissue-Specific Alternative Splicing Data:** After selecting the tissue, the system retrieves and displays data related to alternative splicing of transcripts specifically in the chosen tissue.

The screenshot shows the PotTransDB website interface. The browser address bar displays 'localhost/potato/index.php'. The website header includes the PotTransDB logo and the title 'Potato Transcriptome Database'. A navigation menu contains buttons for Home, DEIncRNAs, eTM-DEIncRNA, cis-DEIncRNA, CircRNA, DEGs, Alternative Splicing, IRES, Contact Us, and User Manual. The 'Alternative Splicing' button is highlighted, and a dropdown menu is open, showing options for Root, Shoot, and Stolon. The 'Stolon' option is selected. Below the navigation menu, there is a large image of a potato field. To the right of the image, the text 'About PotTransDB' is displayed, followed by a paragraph describing the significance of potatoes and the study's focus on nitrogen stress. Below this text, a yellow box contains information about the funding source: 'This work was supported by the grant CABin Scheme Network project on Agricultural Bioinformatics and Computational Biology (F.No. Agril.Edn. 14/2/2017-A&P dated 02.08.2017), received from Indian Council of Agricultural Research (ICAR)'. Below the image, the 'Summary' section is displayed, featuring a table with columns for Items, Shoot, Root, and Stolon. The 'Source of data' section is also visible, featuring a table with columns for Tissue, Control, and Treatment.

**Summary**

Items	Shoot	Root	Stolon
No. of DEGs : 1233	249	209	775
No. DEIncRNAs : 269	57	53	159
No. eTM-DEIncRNAs : 31	04	08	19
No. of IRES-IncRNAs:08	01	02	05
No. of circRNAs: 47	24	06	17
No. of circRNA-miRNAs :42	22	05	15
No. of IRES-circRNAs: 02	0	01	01
No. of Alternative Splicing events:	17200	16599	16174

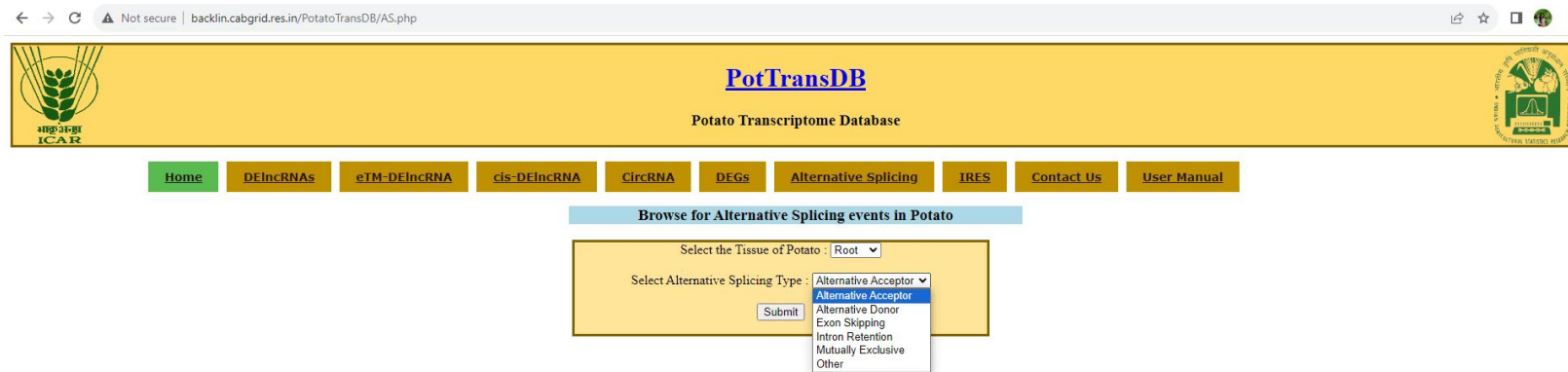
**Source of data**

Tissue	Control	Treatment
Shoot	SRR10135774	SRR10135773
Root	SRR10135772	SRR10135771
Stolon	SRR10135770	SRR10135769

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**Dropdown Menu for Alternative Splicing Type:** Another dropdown menu appears, allowing users to choose the type of alternative splicing they are interested in. This could include options like exon skipping, intron retention, alternative 5' or 3' splice sites, etc.

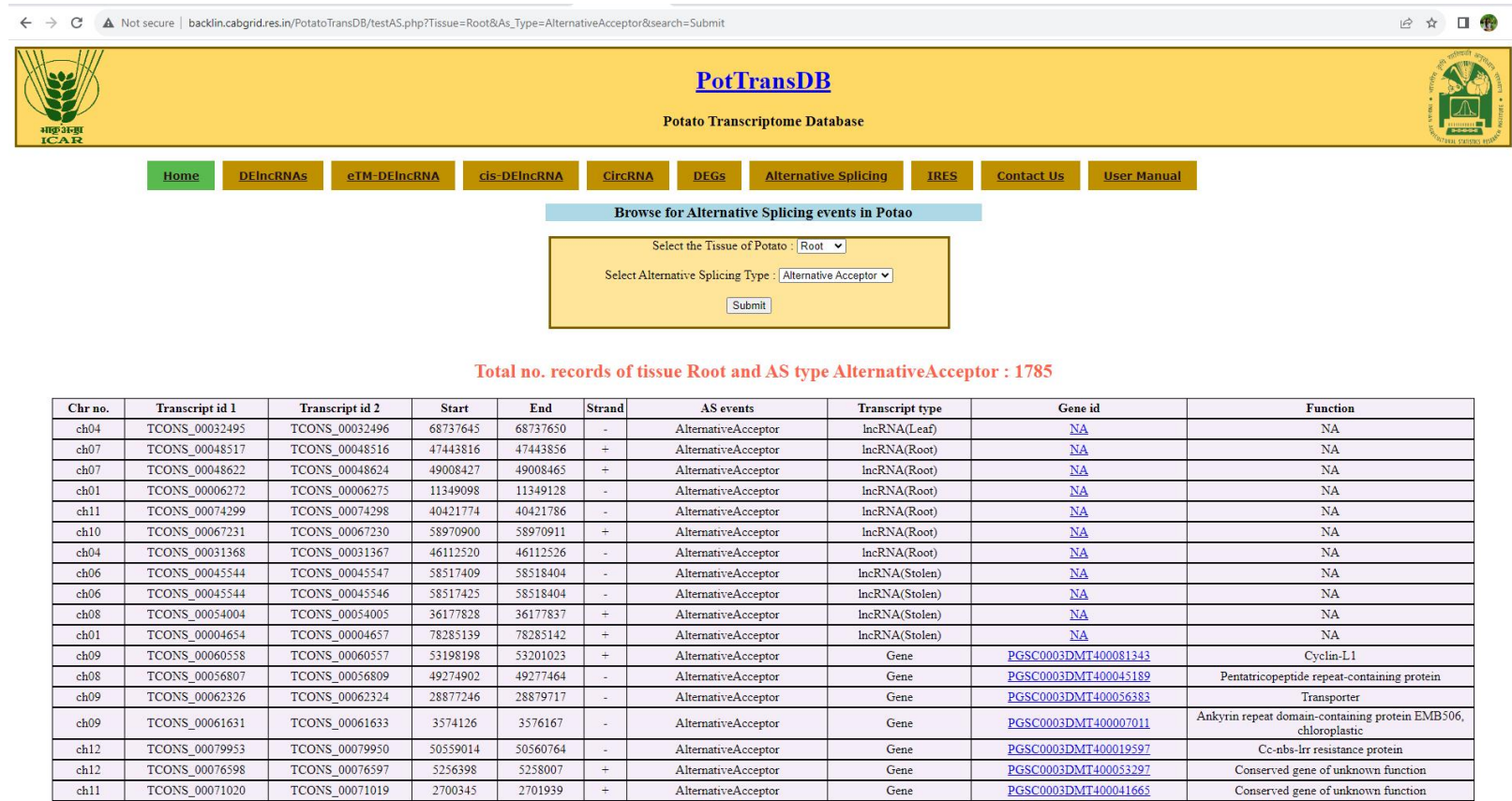
**Retrieve Tissue-Specific and Splicing Type-Specific Data:** After selecting both the tissue and alternative splicing type, the system retrieves and displays data related to alternative splicing of transcripts specifically in the chosen tissue and of the selected splicing type.



The screenshot shows a web browser window with the URL `backlin.cabgrid.res.in/PotatoTransDB/AS.php`. The page header is yellow and contains the **PotTransDB** logo and the text "Potato Transcriptome Database". Below the header is a navigation menu with buttons for Home, DEIncRNAs, eTM-DEIncRNA, cis-DEIncRNA, CircRNA, DEGs, Alternative Splicing, IRES, Contact Us, and User Manual. The main content area is titled "Browse for Alternative Splicing events in Potato" and contains a search form. The form has two dropdown menus: "Select the Tissue of Potato" (set to "Root") and "Select Alternative Splicing Type" (with a dropdown menu open showing options: Alternative Acceptor, Alternative Donor, Exon Skipping, Intron Retention, Mutually Exclusive, and Other). A "Submit" button is located below the second dropdown menu.

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Users can follow a consistent and straightforward process to obtain alternative splicing data based on their tissue and alternative splicing type preferences.



The screenshot shows the PotTransDB (Potato Transcriptome Database) website. The search interface is as follows:

- Search criteria: Tissue = Root, AS Type = Alternative Acceptor.
- Result: Total no. records of tissue Root and AS type AlternativeAcceptor : 1785.

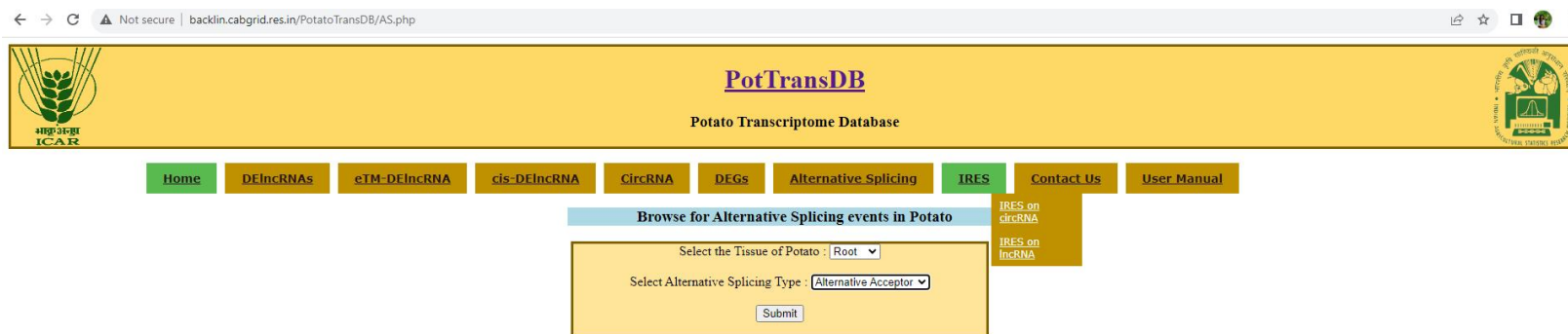
Chr no.	Transcript id 1	Transcript id 2	Start	End	Strand	AS events	Transcript type	Gene id	Function
ch04	TCONS_00032495	TCONS_00032496	68737645	68737650	-	AlternativeAcceptor	lncRNA(Leaf)	NA	NA
ch07	TCONS_00048517	TCONS_00048516	47443816	47443856	+	AlternativeAcceptor	lncRNA(Root)	NA	NA
ch07	TCONS_00048622	TCONS_00048624	49008427	49008465	+	AlternativeAcceptor	lncRNA(Root)	NA	NA
ch01	TCONS_00006272	TCONS_00006275	11349098	11349128	-	AlternativeAcceptor	lncRNA(Root)	NA	NA
ch11	TCONS_00074299	TCONS_00074298	40421774	40421786	-	AlternativeAcceptor	lncRNA(Root)	NA	NA
ch10	TCONS_00067231	TCONS_00067230	58970900	58970911	+	AlternativeAcceptor	lncRNA(Root)	NA	NA
ch04	TCONS_00031368	TCONS_00031367	46112520	46112526	-	AlternativeAcceptor	lncRNA(Root)	NA	NA
ch06	TCONS_00045544	TCONS_00045547	58517409	58518404	-	AlternativeAcceptor	lncRNA(Stolen)	NA	NA
ch06	TCONS_00045544	TCONS_00045546	58517425	58518404	-	AlternativeAcceptor	lncRNA(Stolen)	NA	NA
ch08	TCONS_00054004	TCONS_00054005	36177828	36177837	+	AlternativeAcceptor	lncRNA(Stolen)	NA	NA
ch01	TCONS_00004654	TCONS_00004657	78285139	78285142	+	AlternativeAcceptor	lncRNA(Stolen)	NA	NA
ch09	TCONS_00060558	TCONS_00060557	53198198	53201023	+	AlternativeAcceptor	Gene	<a href="#">PGSC0003DMT400081343</a>	Cyclin-L1
ch08	TCONS_00056807	TCONS_00056809	49274902	49277464	-	AlternativeAcceptor	Gene	<a href="#">PGSC0003DMT400045189</a>	Pentatricopeptide repeat-containing protein
ch09	TCONS_00062326	TCONS_00062324	28877246	28879717	-	AlternativeAcceptor	Gene	<a href="#">PGSC0003DMT400056383</a>	Transporter
ch09	TCONS_00061631	TCONS_00061633	3574126	3576167	-	AlternativeAcceptor	Gene	<a href="#">PGSC0003DMT400007011</a>	Ankyrin repeat domain-containing protein EMB506, chloroplastic
ch12	TCONS_00079953	TCONS_00079950	50559014	50560764	-	AlternativeAcceptor	Gene	<a href="#">PGSC0003DMT400019597</a>	Cc-ribs-Irr resistance protein
ch12	TCONS_00076598	TCONS_00076597	5256398	5258007	+	AlternativeAcceptor	Gene	<a href="#">PGSC0003DMT400053297</a>	Conserved gene of unknown function
ch11	TCONS_00071020	TCONS_00071019	2700345	2701939	+	AlternativeAcceptor	Gene	<a href="#">PGSC0003DMT400041665</a>	Conserved gene of unknown function

**Click on 'IRES' Icon:** Users enter the 'IRES' section by clicking on the designated icon.

**Dropdown Menu for IRES Selection:** Upon selecting 'IRES,' a dropdown menu appears with two options: 'IRES on CircRNA' and 'IRES on lncRNA.'

**IRES Selection:** Users can choose the specific IRES type they are interested in: either IRES associated with Circular RNAs or IRES associated with long non-coding RNAs.

**Retrieve IRES-Specific Data:** After selecting the IRES type, the system retrieves and displays data related to Internal Ribosome Entry Sites specifically for the chosen RNA type.

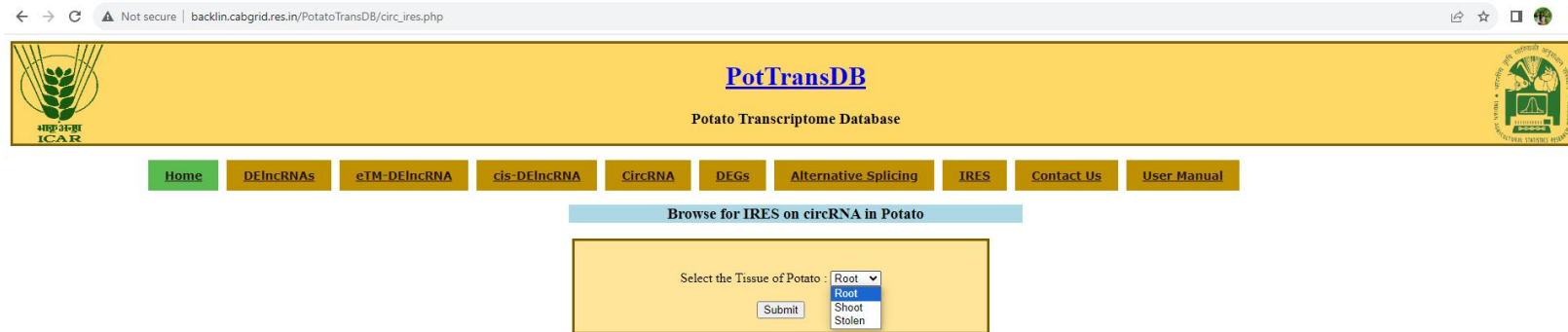


The screenshot shows a web browser window with the URL `backlin.cabgrid.res.in/PotatoTransDB/AS.php`. The page header features the ICAR logo on the left, the text "PotTransDB Potato Transcriptome Database" in the center, and another logo on the right. A navigation menu below the header includes buttons for Home, DElncRNAs, eTM-DElncRNA, cis-DElncRNA, CircRNA, DEGs, Alternative Splicing, IRES, Contact Us, and User Manual. The "IRES" button is highlighted, and a dropdown menu is open, showing two options: "IRES on circRNA" and "IRES on lncRNA". Below the navigation menu, a search box titled "Browse for Alternative Splicing events in Potato" contains two dropdown menus: "Select the Tissue of Potato" (set to "Root") and "Select Alternative Splicing Type" (set to "Alternative Acceptor"). A "Submit" button is located at the bottom of the search box.

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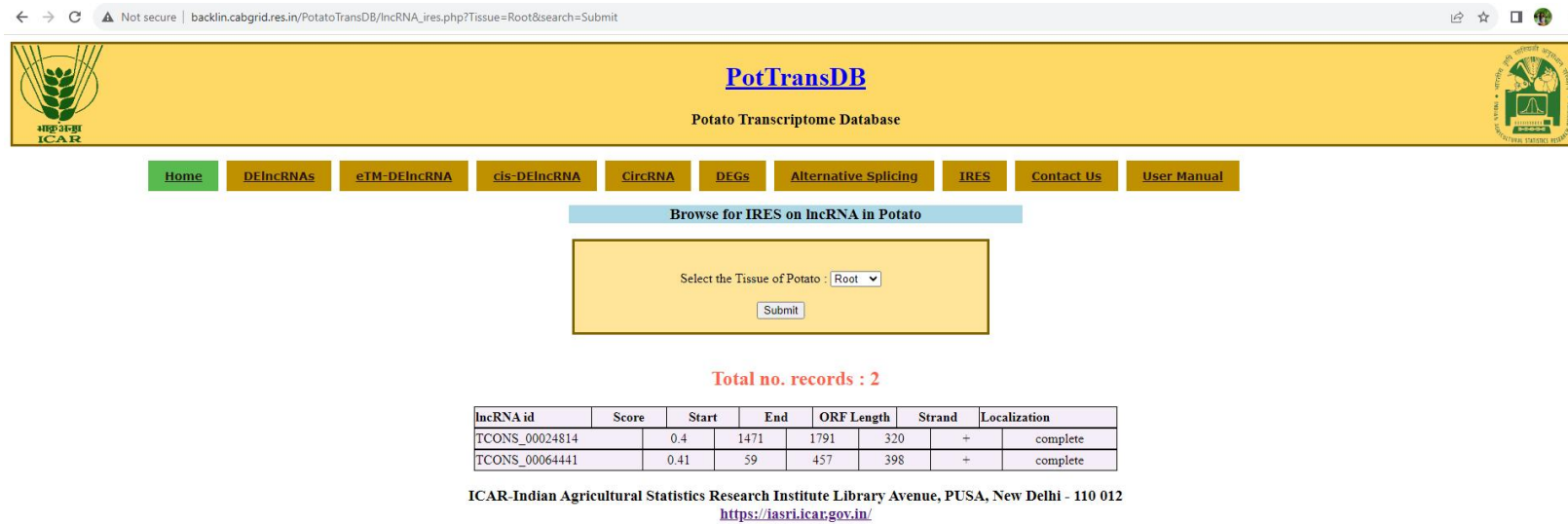
**Dropdown Menu for Tissue Selection:** Another dropdown menu appears, allowing users to choose the specific tissue of interest (Root, Shoot, or Stolon).

**Retrieve IRES-Specific and Tissue-Specific Data:** After selecting both the IRES type and tissue, the system retrieves and displays data related to Internal Ribosome Entry Sites specifically for the chosen RNA type and tissue.



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Users can easily navigate through the steps to access specific information on Internal Ribosome Entry Sites (IRES) associated with long non-coding RNAs (lncRNA) in potatoes.



The screenshot shows the PotTransDB website interface. The browser address bar displays the URL: `backlin.cabgrid.res.in/PotatoTransDB/lncRNA_ires.php?Tissue=Root&search=Submit`. The website header features the ICAR logo on the left, the title "PotTransDB" in the center, and the subtitle "Potato Transcriptome Database" below it. A navigation menu includes buttons for Home, DElncRNAs, eTM-DElncRNA, cis-DElncRNA, CircRNA, DEGs, Alternative Splicing, IRES, Contact Us, and User Manual. Below the menu, a search bar is titled "Browse for IRES on lncRNA in Potato" and contains a dropdown menu for "Select the Tissue of Potato" with "Root" selected, and a "Submit" button. Below the search bar, the text "Total no. records : 2" is displayed. A table with 7 columns (lncRNA id, Score, Start, End, ORF Length, Strand, Localization) shows two records. At the bottom, the website's address is listed as "ICAR-Indian Agricultural Statistics Research Institute Library Avenue, PUSA, New Delhi - 110 012" with the URL <https://iasri.icar.gov.in/>.

lncRNA id	Score	Start	End	ORF Length	Strand	Localization
TCONS_00024814	0.4	1471	1791	320	+	complete
TCONS_00064441	0.41	59	457	398	+	complete

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**Click on 'Contact Us' Icon:** Users can access the contact information section by clicking on the designated 'Contact Us' icon.

**Retrieve Developers' Contact Information:** Upon clicking, users are provided with contact details such as email addresses, phone numbers, or a contact form to reach out to the developers.

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<b>Mr. Sanjeev Kumar</b> Scientist Indian Agricultural Statistical Research Institute New Delhi-110012 Sanjeev.kumar@icar.gov.in <a href="#">details</a>	<b>Dr. Jagesh Kumar Tiwari</b> Senior Scientist ICAR-Indian Institute of Vegetable Research Varanasi, Uttar Pradesh jagesh.kumar@icar.gov.in <a href="#">details</a>	<b>Dr. A. R. Rao</b> ADG (PIM) Indian Council of Agricultural Research New Delhi-110001 rao.work.cshl@gmail.com <a href="#">details</a>

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backlin.cabgrid.res.in/PotatoTransDB/contact.php



**END**