TENOR: Database for Comprehensive mRNA-Seq Experiments in Rice

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What is TENOR?

TENOR (Transcriptome ENcyclopedia Of Rice)
A database that contains large-scale mRNA sequencing (mRNA-Seq) data obtained from rice under a wide variety of conditions.

[Image of TENOR logo]

URL
http://tenor.dna.affrc.go.jp

Publication

Funding
This work was supported by a grant from the Ministry of Agriculture, Forestry and Fisheries of Japan (Genomics for Agricultural Innovation, RTR1001).
TENOR provides rice transcriptome data under **10 abiotic stress** and **2 plant hormone** treatment conditions (+ no treatment)

*Shoot* and *Root* tissues of *Oryza sativa* L. ssp. japonica cv. *Nipponbare* (seedlings 10 days after germination)

at **Multiple timepoints**
(0h, 1h, 3h, 6h, 12h, 1d, 3d, 4d, 5d, 10d after treatments)

Total **140** conditions (250 billion bp from 3.5 billion reads)
10 abiotic stresses and 2 plant hormones

- Salinity
- Low Pi
- High Pi
- High Cd
- Low Cd
- Very-low Cd
- Drought
- Flood
- Cold
- Osmotic
- JA
- ABA
- No treatment

Previous studies published from our group
b. Oono Y, Kawahara Y et al. (2011) Rice

Hydroponic cultivation in growth chamber
(at 28°C temperatures, 16h-light/8h-dark cycle with the light period from 6:00 A.M. to 10:00 P.M., and 70-80% relative humidity)
All experiments were performed at a single laboratory under standardized conditions using a single analysis platform (mRNA-Seq)

- a highly reliable resource
- a standard data set

for comprehensive understanding of genome-wide gene expression under the various conditions
The TENOR development team

Sample & library preparation
- Youko Oono
- Jun Ogata
- Takashi Matsumoto

mRNA-Seq sequencing
- Harumi Sasaki
- Satomi Mori
- Hiroyuki Kanamori

DB & software development
- Yoshihiro Kawahara
- Hironobu Wakimoto
- Takeshi Itoh

National Institute of Agrobiological Sciences (NIAS)
Agrogenomics Research Center
Features of transcriptome data in TENOR

Use of **mRNA-Seq technique** provides
- transcriptional activity at single nucleotide resolution
- expression profile of unannotated transcripts

This transcript might be truncated

Distribution of mRNA-Seq reads on Genome browser
Features of transcriptome data in TENOR

Use of **mRNA-Seq technique** provides
- transcriptional activity at single nucleotide resolution
- expression profile of unannotated transcripts

No RAP-DB transcript

mRNA-Seq-based predicted transcripts

Distribution of mRNA-Seq reads

Low P, 5d, Root
Cold, 1d, Root
Drought, 1d, Root
**What is PARPNTE**

PARPNTE, which is our in-house gene prediction program, integrates alignments of mRNA-Seq reads (depth of coverage and splice junction) and a HMM-based algorithm for prediction of transcript structures and coding sequences.

<table>
<thead>
<tr>
<th>Program</th>
<th>Transcripts</th>
<th>Loci</th>
<th>Multi-exon transcripts</th>
<th>Base Sn</th>
<th>Sp</th>
<th>Exon Sn</th>
<th>Sp</th>
<th>Intron Sn</th>
<th>Sp</th>
</tr>
</thead>
<tbody>
<tr>
<td>PARPNTE</td>
<td>48,366</td>
<td>38,228</td>
<td>30,293</td>
<td>51.2</td>
<td>64.1</td>
<td>52.4</td>
<td>58.9</td>
<td>70.1</td>
<td>80.6</td>
</tr>
<tr>
<td>Cufflinks</td>
<td>45,415</td>
<td>30,617</td>
<td>30,249</td>
<td>59.0</td>
<td>50.8</td>
<td>49.1</td>
<td>54.2</td>
<td>69.3</td>
<td>79.5</td>
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</tbody>
</table>
## Statistics of annotated and unannotated genes

<table>
<thead>
<tr>
<th>Category</th>
<th>No. of loci</th>
<th>Mean transcript length (bp)</th>
<th>Mean CDS length (bp)</th>
<th>Mean no. of exons</th>
<th>Mean exp. level (RPK)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>RAP-DB representative genes</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>- with mRNA evidence</td>
<td>35,469</td>
<td>1,580.0</td>
<td>912.0</td>
<td>4.3</td>
<td>327.9</td>
</tr>
<tr>
<td>- ab initio pred. with EST</td>
<td>2,400</td>
<td>1,067.0</td>
<td>1,067.1</td>
<td>3.0</td>
<td>59.2</td>
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<tr>
<td><strong>RAP-DB predicted genes</strong></td>
<td>8,121</td>
<td>541.3</td>
<td>541.3</td>
<td>1.6</td>
<td>4.7</td>
</tr>
<tr>
<td><strong>Unannotated genes</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>- PARPNTE protein-coding</td>
<td>742</td>
<td>2,069.1</td>
<td>552.8</td>
<td>2.3</td>
<td>40.1</td>
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<tr>
<td>- PARPNTE non-coding</td>
<td>2,274</td>
<td>1,281.2</td>
<td>-</td>
<td>2.0</td>
<td>48.5</td>
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<tr>
<td>- Cufflinks genes</td>
<td>1,263</td>
<td>943.4</td>
<td>-</td>
<td>1.8</td>
<td>22.5</td>
</tr>
</tbody>
</table>
Functions in TENOR
Google search for TENOR

Google search results:

TENOR - Transcriptome ENcyclopedia Of Rice | Home
tenor.dna.affrc.go.jp/ このページを読む

TENOR: Database for Comprehensive mRNA-Seq ...
www.ncbi.nlm.nih.gov/pubmed/26578693 - このページを読む
Y Kawahara 著 - 2016 - 引用元 2 - 関連記事
TENOR: Database for Comprehensive mRNA-Seq Experiments in Rice. Kawahara Y(1), Oono Y(1), Wakimoto H(2), Ogata J(1), Kanamori H(1), Sasaki H(1), ...
Three entrances on the top page

by Keywords

by Genomic coordinates

by Responsive expression profiles

Genome Browser  Responsive Gene Search  Data Download  About TENOR
SPX genes play important roles in phosphorus signaling network regulating root growth and phosphorus homeostasis.
### Conditions

<table>
<thead>
<tr>
<th>Transcript ID</th>
<th>Description</th>
<th>High Salinity</th>
<th>Low Phosphate</th>
<th>High Phosphate</th>
<th>High Cadmium</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>1h</td>
<td>1d</td>
<td>5d</td>
<td>10d</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1h</td>
<td>1d</td>
<td>5d</td>
<td>10d</td>
</tr>
<tr>
<td>Os02t0202200-01</td>
<td>SPX, N-terminal domain containing protein.</td>
<td>-1.03 1.00</td>
<td>1.92 1.00</td>
<td>2.13 0.77</td>
<td>20.54 0.00</td>
</tr>
<tr>
<td>Os03t0827500-02</td>
<td>SPX, N-terminal domain containing protein.</td>
<td>1.01 1.00</td>
<td>1.14 1.00</td>
<td>-1.13 1.00</td>
<td>1.16 1.00</td>
</tr>
<tr>
<td>Os06t0603600-01</td>
<td>SPX domain-containing protein, Phosphate (Pi) homeostasis</td>
<td>-1.12 0.31</td>
<td>1.11 1.00</td>
<td>1.83 0.20</td>
<td>8.62 0.00</td>
</tr>
<tr>
<td>Os06t0603600-02</td>
<td>SPX domain-containing protein, Phosphate (Pi) homeostasis</td>
<td>-1.13 0.29</td>
<td>1.14 1.00</td>
<td>1.73 0.37</td>
<td>8.94 0.00</td>
</tr>
<tr>
<td>Os07t0614700-01</td>
<td>SPX, N-terminal domain containing protein.</td>
<td>-1.32 0.07</td>
<td>2.77 0.69</td>
<td>2.92 0.46</td>
<td>18.44 0.00</td>
</tr>
</tbody>
</table>

**FC**: fold-changes relative to the control samples

**FDR**: statistical significances of differential expressions
Three entrances on the top page

by Responsive expression profiles
Search by responsive expression profile

Thresholds: Fold change (FC) $\geq$ 10, FDR < 0.01
Search type: and

Set search parameters

Specify responsive expression patterns
### Phosphate starvation induced genes

#### Pi transporters

<table>
<thead>
<tr>
<th>Transcript ID</th>
<th>Description</th>
<th>FC</th>
<th>FDR</th>
<th>FC</th>
<th>FDR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Os06t0324601-00</td>
<td>Hypothetical gene.</td>
<td>19.0</td>
<td>0.000</td>
<td>54.3</td>
<td>0.000</td>
</tr>
<tr>
<td>Os06t0324800-01</td>
<td>Major facilitator superfamily protein. (PT9)</td>
<td>19.4</td>
<td>0.000</td>
<td>56.7</td>
<td>0.000</td>
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<tr>
<td>Os06t0325200-00</td>
<td>Major facilitator superfamily protein. (PT10)</td>
<td>19.9</td>
<td>0.000</td>
<td>36.5</td>
<td>0.000</td>
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<tr>
<td>Os06t0325350-00</td>
<td>Hypothetical gene.</td>
<td>21.2</td>
<td>0.000</td>
<td>42.2</td>
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</table>

#### SPX genes

<table>
<thead>
<tr>
<th>Transcript ID</th>
<th>Description</th>
<th>FC</th>
<th>FDR</th>
<th>FC</th>
<th>FDR</th>
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</thead>
<tbody>
<tr>
<td>Os07t0614700-01</td>
<td>SPX, N-terminal domain containing protein.</td>
<td>29.0</td>
<td>0.000</td>
<td>127.9</td>
<td>0.000</td>
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<tr>
<td>Os07t0614850-00</td>
<td>Hypothetical gene.</td>
<td>31.5</td>
<td>0.000</td>
<td>152.1</td>
<td>0.000</td>
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<td>Os08t0375400-01</td>
<td>Plant disease resistance response protein family protein.</td>
<td>23.7</td>
<td>0.002</td>
<td>54.4</td>
<td>0.002</td>
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<td>Os08t0383800-00</td>
<td>Taurine catabolism dioxygenase TauD/TfdA domain containing protein.</td>
<td>25.5</td>
<td>0.000</td>
<td>53.6</td>
<td>0.000</td>
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<tr>
<td>Os09t0381400-01</td>
<td>Similar to Ervatamin C (EC 3.4.22-.) (ERV-C).</td>
<td>20.2</td>
<td>0.000</td>
<td>17.4</td>
<td>0.000</td>
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<tr>
<td>Os09t0381400-02</td>
<td>Similar to cysteine protease.</td>
<td>20.9</td>
<td>0.000</td>
<td>26.2</td>
<td>0.000</td>
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</table>
**Links to other DB & viewer**

<table>
<thead>
<tr>
<th>Transcript ID</th>
<th>GB</th>
<th>EPV</th>
<th>RAPDB</th>
<th>XPro</th>
<th>CoExp</th>
</tr>
</thead>
<tbody>
<tr>
<td>Os07t0324601-00</td>
<td></td>
<td></td>
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<td></td>
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</tr>
<tr>
<td>Os07t0324800-01</td>
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<td>Os07t0325000-00</td>
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<tr>
<td>Os07t0325350-00</td>
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<tr>
<td>Os07t0614700-01</td>
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<tr>
<td>Os07t0614850-00</td>
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<td></td>
</tr>
</tbody>
</table>

**GB**: Genome Browser  
**EPV**: Expression Profile Viewer  
**RAPDB**: Rice Annotation Project DB (RAP-DB)  
**XPro**: RiceXPro  
**CoExp**: List of co-expressed genes
Expression Profile Viewer (EPV)

By hovering the mouse cursor over ,
You can quickly overview expression profiles
Expression Profile Viewer (EPV)

Output: PNG, Table View and CSV
Change scale: logarithmic/arithmetic
Genome Browser (GBrowse)

Transcripts
cis-regulatory elements
distribution of mRNA-Seq reads
Genome Browser (GBrowse)
Genome Browser (GBrowse)

Link to GBrowse: http://tenor.dna.affrc.go.jp/gb2/gbrowse/rnaseq_db/?chr06:12,679,000..12,713,999
cis-regulatory elements in 1kb upstream regions

New PLACE
A Database of Plant Cis-acting Regulatory DNA Elements

PLACE is a database of motifs found in plant cis-acting regulatory DNA elements, all from previously published reports. It covers vascular plants only (But since April 2006, we changed the policy. See the release note for PLACE 26.0). In addition to the motifs originally reported, their variations in other genes or in other plant species reported later are also compiled. The PLACE database also contains a brief description of each motif and relevant literature with PubMed ID numbers. DDBJ/EMBL/GenBank nucleotide sequence databases accession numbers will be also included. See 'sample record'. List of entries can be found in 'place.dat'.

Paste a FASTA format sequence, please.
Upper limit of multi FASTA is 20 sequences.

Data file of Plant Cis-acting Regulatory DNA Elements:
place.dat  place.seq (30.0, 469 entries, Jan.8, 2007, © Kenichi Higo)

If you use this data file in published research, please cite:
cis-regulatory elements in 1kb upstream regions
cis-regulatory elements in 1kb upstream regions
cis-regulatory elements in 1kb upstream regions

PHR1-binding sequence found in the upstream regions of phosphate starvation responsive genes from several plant species; phr1 (phosphate starvation response 1) gene codes for PHR1 protein related to PSR1 gene in C. reinhardtii;

phosphate; starvation; MYB;

Arabidopsis thaliana; Lycopersicon esculentum (tomato); Medicago truncatula; Hordeum vulgare (barley);

A conserved MYB transcription factor involved in phosphate starvation signaling both in vascular plants and in unicellular algae.
Genes Dev. 15: 2122-2133. (2001)
PubMed: 11511543

Schunmann PH, Richardson AE, Smith FW, Delhaize E.
Characterization of promoter expression patterns derived from the Pht1 phosphate transporter genes of barley (Hordeum vulgare L.).
PubMed: 15020637

Schunmann PH, Richardson AE, Vickers CE, Delhaize E.
Promoter analysis of the barley Pht1;1 phosphate transporter gene identifies regions controlling root expression and responsiveness to phosphate deprivation.
PubMed: 15542491

NAME:P1BS
Motif:GNATATNC

Link to PLACE data
co-expressed genes

By clicking CoExp, you can get the list of co-expressed transcripts.
Top 200 co-expressed transcripts

- **Os06t0324800-01 (PT9)**: Major facilitator superfamily protein.

### PCC

- **GB, EPV, RAPDB, XPro**

### Showing 1 to 10 of 200 entries

<table>
<thead>
<tr>
<th>Rank</th>
<th>Transcript ID</th>
<th>Description</th>
<th>PCC</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Os06t0324601-00</td>
<td>Hypothetical gene.</td>
<td>0.9594</td>
</tr>
<tr>
<td>2</td>
<td>Os03t0408600-00</td>
<td>Major facilitator superfamily protein.</td>
<td>0.9111</td>
</tr>
<tr>
<td>3</td>
<td>Os03t0265301-00</td>
<td>Major facilitator superfamily protein.</td>
<td>0.8527</td>
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<tr>
<td>4</td>
<td>Os03t0265301-00</td>
<td>Major facilitator superfamily protein.</td>
<td>0.8451</td>
</tr>
<tr>
<td>5</td>
<td>Os06t0325200-00</td>
<td>Major facilitator superfamily protein.</td>
<td>0.8006</td>
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<tr>
<td>6</td>
<td>Os07t0614700-01</td>
<td>SPX, N-terminal domain containing protein</td>
<td>0.8280</td>
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<tr>
<td>7</td>
<td>Os07t0614850-00</td>
<td>Hypothetical protein.</td>
<td>0.8237</td>
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<tr>
<td>8</td>
<td>Os07t0375400-01</td>
<td>Plant disease resistance protein</td>
<td>0.8234</td>
</tr>
<tr>
<td>9</td>
<td>Os08t0383800-00</td>
<td>Taurine catabolism dioxygenase</td>
<td>0.8192</td>
</tr>
<tr>
<td>10</td>
<td>Os09t0381400-01</td>
<td>Similar to Ervatamia</td>
<td>0.8170</td>
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</tbody>
</table>

**PCC**: Pearson’s correlation of coefficient
Links to external databases

- Links to databases for the gene Os07t0614700-01:
  - GB
  - EPV
  - RAPDB
  - XPro
  - CoExp

**Details**

**LOCUS**
Os07t0614700

**DESCRIPTION**
SPX, N-terminal domain containing protein.

**TRANSCRIPT EVIDENCE**
AK243609 (DDBJ, Best hit)

**PROTEIN EVIDENCE**
QBH398 (Uniprot)

**CGSNL GENE SYMBOL**

**CGSNL GENE NAME**

**CGSNL GENE SYMBOL SYNONYM(S)**
OsSPX6

**CGSNL GENE NAME SYNONYM(S)**
SPX (SYG/PH081/XPR1) domain gene 6

**RiceXPro**

**Field / Development**

<table>
<thead>
<tr>
<th>Locus ID</th>
<th>FeatureNum</th>
<th>Accession</th>
<th>Description</th>
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</thead>
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<td>3679</td>
<td>C181690</td>
<td>SPX, N-terminal domain containing protein.</td>
</tr>
</tbody>
</table>

Select All  Download selected graph
Link to TENOR in RAP-DB

Os07t0614700-01

Details  DB references  Sequences

INTERPRO
- SPX, N-terminal (IPR004331)

KEGG
- Os07t0614700-01

KOME
- J100005G1 (Online Clone Ordering)

ORYZABASE
- 11157

PLANT GENE FAMILY DATABASE (PGFD)

EXPRESSION DATABASES
- TENOR

SPX, N-terminal domain containing protein.
Downloadable data files

Data Downloads

TENOR Data

RNA-Seq transcripts

- Unannotated PARP-NTE protein-coding transcripts that do not overlap with any RAP-DB transcripts.
  - [GFF] [exonwise GTF] [FASTA (transcript)] [FASTA (CDS)] [FASTA (protein)]
- Unannotated PARP-NTE non protein-coding transcripts that do not overlap with any RAP-DB transcripts.
  - [GFF] [exonwise GTF] [FASTA (transcript)]
- Unannotated Cufflinks transcripts with strand information that do not overlap with any RAP-DB and PARP-NTE transcripts.
  - [GFF] [exonwise GTF] [FASTA (transcript)]

Other annotation

- cis-regulatory elements in the 1-kb promoter regions of all transcripts predicted by the PLACE database.
  - [GFF]

Expression profile data

- Gene expression levels (RPK) for each transcript
  - [normalized RPK]

mRNA-Seq-based predicted transcripts (GFF/GTF/FASTA)
cis-regulatory elements (GFF)
normalized expression profiles (tab-delimited txt)
Similarity of responsive transcriptome

enriched cis-elements

enriched GO
Summary

TENOR
Transcriptome ENcyclopedia Of Rice

Search by Keywords/responsive expression profiles

Expression profiles & co-expression information

Transcriptional activity at single nucleotide resolution under the 140 conditions

cis-regulatory element