Supplementary Material

**Supplementary Table 1. Plant spaceflight datasets and ground-based datasets related to spaceflight factors.** A small selection of meta-data associated with these studies is also included to indicate the breadth of the data available. GeneLab, GeneLab data repository (https://genelab-data.ndc.nasa.gov/); GEO, Gene Expression Omnibus (https://www.ncbi.nlm.nih.gov/geo/); Col-0, Columbia ecotype of *Arabidopsis thaliana*; Ws, Wassilewskija ecotype; Ler, Landsberg ecotype; Cvi, Cape Verdi islands ecotype; mutants of Arabidopsis: *phyD*, Phytochrome D; *arg*, Altered Response to Gravity; *act2*, Actin 2; *ATM,* Ataxia-telangiectasia mutated*; atr,* ATM and Rad 3-related*; xpf,* xeroderma pigementosa F endonuclease; RPM, random positioning machine; HZE, High atomic weight and high energy; ROS Meta, meta analysis of experiments related to reactive oxygen species response; BRIC, Biological Research in Canister.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Identifier** | **Reference** | **Genotype or ecotype** (*Arabidopsis* *thaliana* unless noted) |  **Notes** |  **Assay Method** |
| **Spaceflight** |
| GLDS-7 | (Paul et al., 2013) | WS & Col | Flight vs Ground | Microarray |
| GLDS-16 | (Ferl et al., 2015) | WS  | “ | Proteomics |
| GLDS-17 | (Paul et al., 2012) | Col | “ | Microarray |
| GLDS-37 | (Choi et al., 2019) | Col, WS, Ler, Cvi | “ | RNAseq |
| GLDS-38 | NA | Col | “ | RNAseq |
| GLDS-44 | (Kwon et al., 2015) | Col, *act2-3* | “ | Microarray |
| GLDS-57 | (Salmi and Roux, 2008) | *Ceratopteris reinhardii* | “ | Microarray |
| GLDS-59 | (Sugimoto et al., 2014) | *Brassica napa* | “ | RNAseq |
| GLDS-120 | (Paul et al., 2017) | *phyD*, WS, Col  | “ | RNAseq  |
| GLDS-121 | (Johnson et al., 2017) | Ler | “ | Microarray |
| GLDS-147 | (Zupanska et al., 2017) | Col, *arg1*  | “ | Microarray |
| GLDS-205 | (Zupanska et al., 2019) | Col, *hsfa2* | “ | Microarray |
| GLDS-213 | (Fengler et al., 2015) | Col  | “ | Microarray |
| GLDS-217 | (Zhou et al., 2019) | Col & WS | “ | RNAseq |
| GLDS-218 | (Beisel et al., 2019) | Col | “ | RNAseq |
| GLDS-251  | (Vandenbrink et al., 2019; Herranz et al., 2019) | Col | “ | RNAseq |
| NA | (Correll et al., 2013) | Ler  | “ | Microarray |
| NA | (Jin et al., 2015) | *Oryza sativa* | “ | Microarray |
| **Spaceflight-related, ground-based studies** |
| GLDS-38 | (Kruse et al., 2017) | Col | RNA later treatment | RNAseq & Proteomics |
| GEO: GSE29787 | (Manzano et al., 2012) | Col | RPM, magnetic levitation | Microarray |
| NA | (Culligan et al., 2006) | WS, *atm, atr, xpf‐2* | 10Gy radiation | Microarray |
| GLDS-46 / GEO: GSE61484 | (Missirian et al., 2014) | Col and *atm1-1* | HZE & Gamma radiation | Microarray |
|  GLDS-22 | (Visscher et al., 2010) | Col & *cax1-1* | MgCl2 salts  | Microarray |
| NA | (Willems et al., 2016) | Col, Ler, WS | ROS Meta analysis | Microarray |
| GEO: GSE5749 | (Birnbaum et al., 2003) | Col | Root tissue map | Microarray |
| NA | (Basu et al., 2017) | Col | BRIC hardware effect | RNAseq, proteomics |
| GLDS-208 | (Krishnamurthy et al., 2018) | Col | Root tip transcriptome | Microarray & RNAseq |
| GLDS-144 | (Kamal et al., 2019) | Col | RPM, cell cycle analysis | Microarray |
| GLDS-45 | NA | Col | Clinostat responses | Microarray |
| GLDS-8 | (Manzano et al., 2012) | Ler | Magnetic levitation | Microarray |

**Supplementary Table 2:** Tools included in the TOAST database graphical user interface.

|  |  |  |
| --- | --- | --- |
| **Database / tool linked** | **Use** | **Reference** |
| SUBA4 | Subcellular consensus  | (Hooper et al., 2017) |
| ATTED | Symbol & ortholog network | (Obayashi et al., 2018) |
| ePlant | Gene viewer | (Waese et al., 2017) |
| GeneSlider | Gene promoter viewer | (Waese et al., 2017) |
| Thalemine | Gene & network viewer | (Krishnakumar et al., 2016) |
| Expression Angler | Co-expressed genes | (Austin et al., 2016) |
| eFP-Seq Browser | Aggregated RNAseq search | (Sullivan et al., 2019) |
| Promomer | Network Promoter Viewer | (Toufighi et al., 2005) |
| STRING | Network viewer | (Szklarczyk et al., 2019) |
| Genemania | Network viewer | (Franz et al., 2018) |
| Arabidopsis interaction viewer | Arabidopsis Network Viewer | (Geisler-Lee et al., 2007) |
| Rice interaction viewer | Rice Network Viewer | (Ho et al., 2012) |
| Genevisble | RNAseq visualization | (Hruz et al., 2008) |
| CATdb | Access processed microarrays | (Gagnot et al., 2008) |
| AGRIS TF database | Transcription factor filter | (Palaniswamy et al., 2006) |
| microRNA annotation TAIR10 | Gene set filter | (Lamesch et al., 2012) |
| Gene Families TAIR10 selection | Gene set filter | (Lamesch et al., 2012) |
| EBI Expression atlas | Access processed microarrays | (Papatheodorou et al., 2018) |
| Ensemble Plants | Access to plant genome annotation  | (Kersey et al., 2018) |
| Reactome | Access to plant reaction data | (Fabregat et al., 2018) |

**Supplementary Table 3. Experimental factors related to plant biology studies within the TOAST Metadata app.** Manual curation of the metadata associated with the spaceflight-related experiments inTOAST 4.5.

See attached Excel file

**Supplementary Table 4. Significantly differentially expressed transcripts in spaceflight vs those also seen in the “high light early” clade of the ROS wheel analysis.** DET, differentially expressed transcripts. The “high light early” clade in the ROS wheel analysis consists of 8.89K genes identified by meta analysis of publicly available microarray data (Willems et al., 2016).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Dataset | Sample | Light/darkgrown | DETP<0.05 | “High Light Early” clade members |
| GLDS-7 | Seedling, Ws | Light | 2.96K  | 1.25K |
| GLDS-17 | Seedling, Col | Dark | 1.34K | 719 |
| GLDS-37 | Seedling, Ler | Dark | 451 | 179 |
| GLDS-37 | Seedling, Cvi | Dark | 2.27K | 1.02K |
| GLDS-37 | Seedling, Ws | Dark | 903 | 380 |
| GLDS-44 | Seedling, Col | Dark | 6.32K | 2.87K |
| GLDS-121 | Seedling, Ler | Dark | 239 | 144 |

**Supplementary Table 5.** Orthologous loci responding to spaceflight in Arabidopsis and rice cell cultures grown during spaceflight. Orthologs defined using Orthologous Matrix (Altenhoff et al., 2018) mapping within TOAST 4.5. Table shows Arabidopsis gene symbol, Arabidopsis gene ID, orthologous rice gene ID, % identity between Arabidopsis and rice ortholog and adjusted P-value (Q-value) for the Arabidopsis data and the orthologous rice gene’s data. Table 5.1 compares genes significantly differentially expressed (P<0.05) in spaceflight vs ground controls in Arabidopsis and rice cell cultures described in Fengler et al. (2015). Table 5.2 filters these gene lists for Q<0.05 for both Arabidopsis and rice datasets. Table 5.3 shows genes significantly differentially expressed (P<0.05) in Arabidopsis and rice cultures in flight (microgravity) samples versus samples in the 1 x *g* on-board centrifuge. Table 5.4 filters the data in Table 5.3 on Q-value <0.05 and then compares the genes that are significantly differentially expressed (P<0.05, Q<0.05) in both Arabidopsis and rice cell cultures in the flight vs ground control comparison with those significantly differentially expressed (P<0.05, Q<0.05) in both Arabidopsis and rice cell cultures in the flight vs centrifuge dataset.

See attached Excel Spreadsheet

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