

Supplemental Table 1. Available Omics Data of Eucalyptus

Organism	Omics	Details	Tissue	Reference
<i>Eucalyptus grandis</i>	Transcriptomics	RNA-seq	Shoot tips, young leaves, mature leaves, floral buds, roots, phloem, immature xylem	https://doi.org/10.1038/nature13308
<i>Eucalyptus grandis</i>	Transcriptomics	RNA-seq	Xylem, immature xylem, phloem, shoot tips, young leaf, mature leaf	https://doi.org/10.1186/1471-2164-11-681
<i>Eucalyptus grandis</i>	Transcriptomics	RNA-seq of <i>E. grandis</i> resistant and susceptible to the pest <i>Leptocybe invasa</i>	Leaf	https://doi.org/10.1093/pcp/pcv064
<i>Eucalyptus grandis</i>	Transcriptomics	RNA-seq	Xylem	https://doi.org/10.1093/database/bax079
<i>Eucalyptus globulus</i>	Transcriptomics	RNA-seq. 18 libraries were prepared, corresponding to six temperature and CO2 combinations (three temperatures and two CO2 concentrations), using three biological replicates	Stem	https://doi.org/10.1007/s11295-022-01537-y
<i>Eucalyptus grandis</i>	Transcriptomics	RNA-seq. 18 libraries were prepared, corresponding to six temperature and CO2 combinations (three temperatures and two CO2 concentrations), using three biological replicates	Stem	https://doi.org/10.1007/s11295-022-01537-y
<i>Eucalyptus grandis</i>	Transcriptomics	RT-qPCR. Transcriptomic analysis of <i>E. grandis</i> bark	Bark	https://doi.org/10.1186/s12870-016-0839-8

		during summer (wet) and winter (dry)		
<i>Eucalyptus grandis</i>	Proteomics	2-D-LC-MS/MS. Isolation of proteins of <i>Eucalyptus grandis</i> , at three ages of growth (6-month-old seedlings, 3- and 6-year-old trees)	Stem of seedling, xylem and phloem	DOI 10.1002/pmic.200600989
<i>Eucalyptus grandis</i>	Proteomics	MS-UPLC. Samples of leaves were collected 0, 6, 12, 18 and 24 hours after inoculation of fungus <i>Austropuccinia psidii</i> in rust-resistant and rust-susceptible <i>E. grandis</i> plants	Leaf	https://doi.org/10.3389/fpls.2020.604849
<i>Eucalyptus grandis</i>	Proteomics	MS. Proteome analysis was carried out in the stem of <i>E. grandis</i> after its cultivation at 10 °C (LT), 22 °C (MT) and 32 °C (HT)	Stem	https://doi.org/10.1016/j.phytochem.2017.01.017
<i>Eucalyptus globulus</i>	Proteomics	MS. Proteome analysis was carried out in the stem of <i>E. grandis</i> after its cultivation at 10 °C (LT), 22 °C (MT) and 32 °C (HT)	Stem	https://doi.org/10.1016/j.phytochem.2017.01.017
<i>Eucalyptus grandis</i>	Proteomics	MS. Proteomic analysis of <i>E. grandis</i> plants that were subjected to two acclimatization regimes	Leaf	https://doi.org/10.1016/j.plaphy.2020.05.026
<i>Eucalyptus grandis</i>	Proteomics	2-DE gels and LC-MS/MS. Proteomic analysis of <i>E. grandis</i> bark during summer (wet) and winter (dry)	Bark	https://doi.org/10.1186/s12870-016-0839-8
<i>Eucalyptus grandis</i>	Metabolomics	LC-MS. Samples of leaves were collected 0, 6, 12, 18 and 24 hours after inoculation of fungus	Young leaf	https://doi.org/10.3389/fpls.2020.604849

<i>Austropuccinia psidii</i> in rust-resistant and rust-susceptible <i>E. grandis</i> plants				
<i>Eucalyptus globulus</i>	Metabolomics	MS-UPLC. Metabolic profiles of both healthy <i>Eucalyptus globulus</i> and those infected with the <i>Mycosphaerella</i> leaf disease	Leaf	DOI 10.1007/s11306-014-0666-6
<i>Eucalyptus pauciflora</i>	Metabolomics	GC-MS. Metabolite profiling to examine the response of leaf metabolites to a long (2 month) and severe water stress	Leaf	DOI 10.1007/s11306-011-0299-y
<i>Eucalyptus dumosa</i>	Metabolomics	GC-MS. Metabolite profiling to examine the response of leaf metabolites to a long (2 month) and severe water stress	Leaf	DOI 10.1007/s11306-011-0299-y
<i>Eucalyptus grandis</i>	Metabolomics	GC-MS. Metabolomic analysis of <i>E. grandis</i> plants that were subjected to two acclimatization regimes	Leaf	https://doi.org/10.1016/j.plaphy.2020.05.026
<i>Eucalyptus grandis</i>	Metabolomics	GC-MS. Metabolomic analysis of <i>E. grandis</i> bark during summer (wet) and winter (dry)	Bark	https://doi.org/10.1186/s12870-016-0839-8