

Data Submission Standards

Submission of a manuscript to Tree Genetics and Genomes implies that readily reproducible materials described in the manuscript, including all relevant raw data, will be freely available to any scientist wishing to use them for non-commercial purposes. Nucleic acid sequences, protein sequences, genetic maps, SNPs, expression data, etc. must be deposited in the databases detailed below.

Enforcement of sequence submissions will occur during the review process. It is recommended that authors submit all relevant data types to the NCBI repositories in advance of submission to TGG (due to the longer timeline involved for formatting/submission). Submissions to organism-specific databases (for genetic maps and association studies) can be completed during the review/in response to reviews. Final acceptance of a manuscript into TGG is contingent on all relevant accession numbers being made available in text. In all cases, public release of the data itself can be held by the respective databases until publication.

In addition to including relevant accession numbers in the manuscript text, authors are required to list the data types and the accession numbers (or indication of submissions in progress) in the cover letter.

Nucleotide sequences

Nucleotide sequences must be deposited with the [DNA Data Bank of Japan](#) (DDBJ), [European Molecular Biology Laboratory \(EMBL/EBI\) Nucleotide Sequence Database](#), or [GenBank](#) (National Center for Biotechnology Information).

Next-Generation Sequencing Reads

Raw sequence data must be submitted to NCBI's [Short Read Archive](#) (SRA).

Transcriptome assemblies should be submitted to NCBI's [Transcriptome Shotgun Assembly Sequence Database](#) (TSA). Note: Sequences in dbEST/SRA are single-pass reads determined by different sequencing techniques. TSA sequences are computationally assembled sequences from these single-pass reads.

Sequence Alignments

Aligned sequence sets used for population genetics analysis must be submitted to [PopSet](#).

Protein sequences

Protein sequences must be deposited with [SwissProt](#) or the [Protein Information Resource](#) (PIR).

SNPs

Single nucleotide polymorphisms must be deposited into the [European Variation Archive](#) (EVA). Note: EVA requires the reference sequence to be [INSDC](#) registered. Please submit all genotypes to TreeGenes or Genome Database for Rosaceae.

Genetic Maps

Genetic maps must be submitted to the relevant organism-specific database.

For forest tree species, submit all marker/position data to the [TreeGenes database](#). Please contact treegenesdb@gmail.com for submission assistance.

For horticulture tree species, please follow instructions and submit all marker/position data to the [Genome Database for Rosaceae](#) (GDR) or the [Citrus Genome Database](#). Please contact tgg@bioinfo.wsu.edu for submission assistance.

Association, Population/Diversity, and Common Garden Studies (Genotype/Marker, Phenotype, Environment)

Supplemental files in the form of marker/genotype data, phenotype data, and environmental descriptors should be submitted to the relevant organism database.

For forest tree species, submit files and metadata to the [TreeGenes Database](#). Please contact treegenesdb@gmail.com for submission assistance.

For horticulture tree species, submit formatted files to the [Genome Database for Rosaceae](#) (GDR) or the [Citrus Genome Database](#). Please contact tgg@bioinfo.wsu.edu for submission assistance.

Gene Expression data

Where appropriate, authors should adhere to the standards proposed by the [Microarray Gene Expression Data Society](#) and must deposit microarray data in one of the two public repositories: [ArrayExpress](#) or [Gene Expression Omnibus](#) (GEO). GEO also accepts ChIP-Seq, methyl-Seq, RNA-Seq and small RNA profiling.

Computational modeling

We encourage authors to prepare models of biochemical reaction networks using the [Systems Biology Markup Language](#) and to deposit the model with the [BioModels database](#).

Other Supplemental Data

For supplemental files that do not fit into one of the categories above, please send this information as flat files to Dryad: <http://datadryad.org/depositing>