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Data in Brief

Gene expression profiling of ramie roots during hydroponic induction and adaption to aquatic environment

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A B S T R A C T

Ramie (*Boehmeria nivea* (L.) Gaud.) is a traditionally terrestrial fiber crop. However, hydroponic technology can enhance the quantity and quality of disease free Ramie plant seedlings for field cultivation. To date, few studies have attempted to examine the hydroponic induction of ramie roots and the molecular responses of ramie roots to aquatic environment. In this study, ramie tender stems was grown in the soil or in a hydroponic water solution, and cultured in the same environmental conditions. Root samples of terrestrial ramie, and different developmental stages of hydroponic ramie (5 days, 30 days), were firstly pooled for reference transcriptome sequencing by Illumina Hiseq 2000. Gene expression levels of each samples were quantified using the BGISEQ500 platform to help understand the distribution of aquatic root development related genes at the macro level (GSE98903). Our data resources provided an opportunity to elucidate the adaptation mechanisms of ramie seedlings roots in aquatic environment.

Specifications [*standardized info for the reader*]	
Organism/cell line/tissue	Terrestrial or aquatic root tissues of *Boehmeria nivea* (L.) Gaud
Sex	N/A
Sequencer or array type	Illumina HiSeq 2000 and BGISEQ500 platform
Data format	Raw data
Experimental factors	Hydroponic induction of ramie roots
Experimental features	Gene expression profiling of terrestrial and aquatic roots. The root samples from hydroponic ramie were collected from 5-day-old seedlings (the early stage of root induction) and 30-day-old seedlings (the late stage of root induction). The roots of ramie seedlings in soil were collected for comparative analysis.
Consent	N/A
Sample source location	Institute of Bast Fiber Crops, Chinese Academy of Agricultural Sciences, Changsha, Hunan, China (GPS coordination: 112.907991,28.217469)

1. Direct link to deposited data

Deposited data can be found here: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE98903.

2. Introduction

Ramie (*Boehmeria nivea* (L.) Gaud.) is a commercially important plant species that is predominantly used for fabric production [1,2]. Due to the low survival rate of seedlings in the early stages, propagation by conventional means has been met with many difficulties. Hydroponic culture [3] is an excellent alternative method for the large scale and high quality production of this valuable crop. Several physiological and morphological investigations have been conducted to improve our understanding of the hydroponic culture of ramie. Here we report a de novo transcriptome assembly of ramie roots and gene expression profiling of ramie roots in an aquatic environment. Our aim was to obtain a high quality reference transcriptome of ramie root, elucidate the molecular response of ramie to aquatic environment, and find candidate waterlogging tolerance genes.

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Table. 1
Summary of the root transcriptome sequencing and assembly.

Index	Ramie roots
Number of assembled reads	66,209
Number of unigenes	43,541
Average unigene length (bp)	966
Unigenes annotated in Nr	31,066
Unigenes annotated in Nt	27,378
Unigenes annotated in Swiss Prot	22,887
Unigenes annotated in KEEG	24,522
Unigenes annotated in COG	15,513
Unigenes annotated in Interpro	24,071
Unigenes annotated in GO	18,486

3. Experimental design, materials and methods

3.1. Ramie cultivation and RNA sample preparation

The elite ramie cultivar "Zhongzhu 2", which can be hydroponically cultivated was used in this study. Ramie seedlings were cultivated in either soil or in a hydroponic environment with using the shoot-cutting propagation method. The root samples from hydroponic ramie were collected from the early (5-day-old seedlings) and late (30-day-old seedlings) stages of aquatic roots induction. The roots of ramie seedlings in soil were also collected for comparative analysis. The sample tissues were immediately frozen in liquid nitrogen and stored at − 80 °C until use. In order to increase the root transcriptome coverage, a mixture of the three samples were firstly pooled for RNA sequencing. Total RNA was extracted using TRIzol Reagent (Invitrogen, LifeTechnologies, USA) following the manufacturer's instructions, then treated with DNase I (Invitrogen, Life Technologies, USA). The RNA integrity was verified using an Agilent 2100 BioAnalyzer (Agilent, USA).

3.2. RNA sequencing

RNA-Seq libraries were constructed using the RNA Library Prep Kit for Illumina according to the manufacturer's instructions (NEB, USA). Library quality was assessed on the Agilent Bioanalyzer 2100 system. The libraries were sequenced on the Illumina HiSeq 2000 platform (Illumina, USA) based on sequencing by synthesis with 100 bp paired-end reads (Biomarker Technologies, Beijing). Whole RNA-Seq data were submitted to NCBI Sequence Read Archive and Gene expression Omnibus (series accession number GSE98903).

3.3. Root transcriptome assembly and gene functional annotation

Prior to assembly, the raw data were cleaned by trimming adaptor sequences and removing low quality sequences (Q < 20) with > 10% uncertain (N) bases using in-house perl scripts. These clean reads were then de novo assembled into unigenes using the short reads assembling program Trinity with min_kmer_cov set to 2 and all other parameters set to default [4,5]. The following databases were used to annotate the gene function: Nr (NCBI non-redundant protein sequences, NCBI blast 2.2.28 +, e-value = $1e^{-5}$); Nt (NCBI non-redundant nucleotide sequences, NCBI blast 2.2.28 +, e-value = $1e^{-5}$); Pfam (Protein family, http://pfam.sanger.ac.uk/, HMMER 3.0 package, hmmscan, e-value = 0.01); KOG/COG (Clusters of Orthologous Groups of proteins, http://www.ncbi.nlm.nih.gov/COG/, NCBI blast 2.2.28 +, e-value = $1e^{-3}$); Swiss Prot (a manually annotated and reviewed protein sequence database, http://www.ebi.ac.uk/uniprot/, NCBI blast 2.2.28 +, e-value = $1e^{-5}$); KO (KEGG Ortholog database, http://www.genome.jp/kegg/, KAAS, KEGG Automatic Annotation Server, e-value = $1e^{-10}$); and GO (Gene Ontology, http://www.geneontology.org/

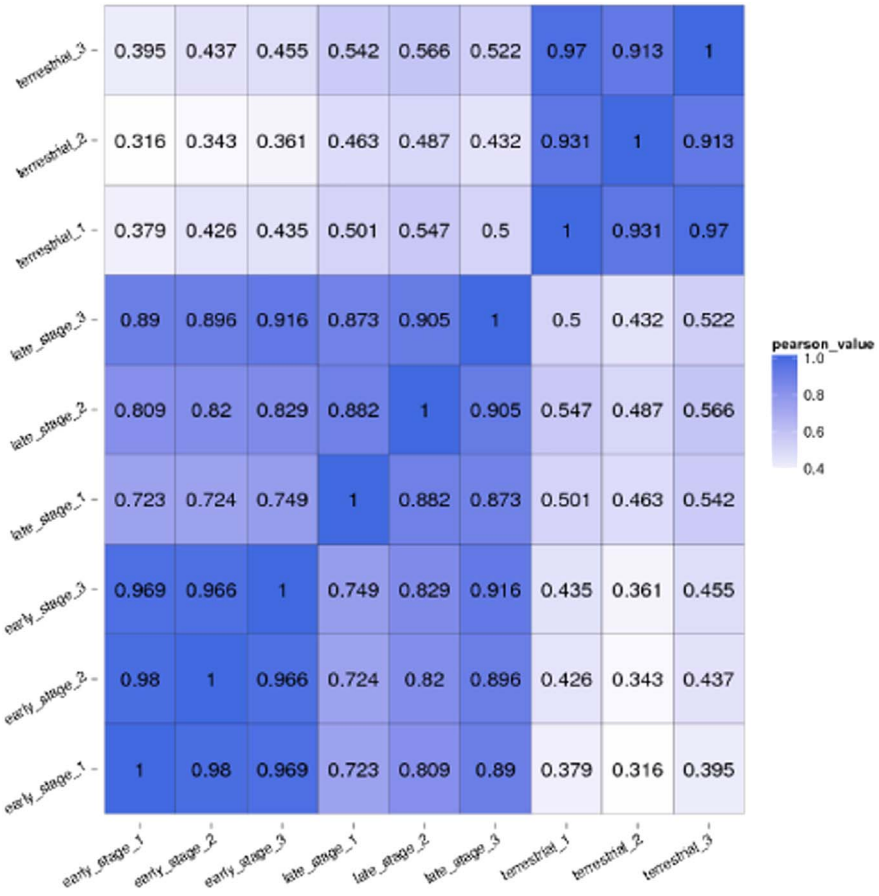

Fig. 1. Heatmap of correlation coefficient values across ramie root samples by growth condition and developmental stages. Gradient color barcode at the right top indicates the minimum value in white and the maximum in blue. If one sample is in highly similar with another one, the correlation value between them is very close to 1.

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