Data in Brief

Iso-Seq analysis of *Nepenthes ampullaria*, *Nepenthes rafflesiana* and *Nepenthes × hookeriana* for hybridisation study in pitcher plants

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Abstract

Tropical pitcher plants in the species-rich Nepenthaceae family of carnivorous plants possess unique pitcher organs. Hybridisation, natural or artificial, in this family is extensive resulting in pitchers with diverse features. The pitcher functions as a passive insect trap with digestive fluid for nutrient acquisition in nitrogen-poor habitats. This organ shows specialisation according to the dietary habit of different *Nepenthes* species. In this study, we performed the first single-molecule real-time isoform sequencing (Iso-Seq) analysis of full-length cDNA from *Nepenthes ampullaria* which can feed on leaf litter, compared to carnivorous *Nepenthes rafflesiana*, and their carnivorous hybrid *Nepenthes × hookeriana*. This allows the comparison of pitcher transcriptomes from the parents and the hybrid to understand how hybridisation could shape the evolution of dietary habit in Nepenthes. Raw reads have been deposited to SRA database with the accession numbers SRX2692198 (*N. ampullaria*), SRX2692197 (*N. rafflesiana*), and SRX2692196 (*N. × hookeriana*).

1. Direct link to deposited data

   http://www.ncbi.nlm.nih.gov/sra/SRX2692198.
   http://www.ncbi.nlm.nih.gov/sra/SRX2692197.
   http://www.ncbi.nlm.nih.gov/sra/SRX2692196.

2. Value of the data

   - There is still limited molecular genetics information on different species of *Nepenthes* pitcher plants.
   - The lack of transcriptomes from this genus hinders further studies on the molecular mechanism and evolution of their carnivory habit.
   - This dataset provides the first full-length transcriptome sequences from pitcher tissues of three well-studied *Nepenthes* species, which is important for guiding functional genomics and proteomics studies.
   - This will further improve our understanding on the Nepenthaceae evolutionary history and contribute to gene mining for useful digestive enzymes for industrial applications.

3. Data

   Full-length cDNA transcriptome profiles of three *Nepenthes* species (*N. ampullaria*, *N. rafflesiana* and *N. × hookeriana*) were generated from the polyA-enriched cDNA libraries prepared from total RNA extracted from whole pitchers. The sequences generated using PacBio RS II platform from SMRTbell libraries were processed using the SMRT Analysis Server. Raw data for this project were deposited in the SRA database with the accession numbers SRX2692198 (http://www.ncbi.nlm.nih.gov/sra/SRX2692198) for *N. ampullaria*, SRX2692197 (http://www.ncbi.nlm.nih.gov/sra/SRX2692197) for *N. rafflesiana*, and
4.1. Plant materials

All three species of pitcher plants were growing together on a terrace (2°55′11.5″N 101°47′01.4″E) next to experimental plots at Universiti Kebangsaan Malaysia, Bangi. Whole mature pitchers were collected in the morning within 24 h of pitcher opening in June 2015, emptied and frozen in liquid nitrogen before stored in −80 °C for further use.

4.2. Total RNA extraction and quality control, library preparation and Iso-Seq

Total RNA from all samples were extracted using modified method of CTAB [1]. Quantity and Integrity of extracted total RNA were determined using NanoDrop (Thermo Fisher Scientific Inc., USA) and Agilent 2100 bioanalyzer (Agilent Technologies, USA), respectively.

One sample for each species was sequenced using on the Pacific Biosciences RS II platform with one SMRT cell v3 each based on P6-C4 chemistry after standard full-length cDNA (1–3 kb) library preparation protocol (SMRTbell Template Preparation Kit 1.0) at Icahn Medical Institute (Mount Sinai, New York City, USA) [2].

4.3. Read analysis

Sequence movie files from all three data sets were processed and analysed through Iso-Seq pipeline (RS_IsoSeq protocol) using PacBio SMRT Analysis Server v2.3.0 (http://www.pacb.com/products-and-services/analytical-software/smrta-analysis/) to filter out polymerase read reads < 50 bp and quality < 0.75 with 0 minimum full passes (Table 1). Filtered reads were further classified (≥ 300 bp, full-length reads do not require poly-A tails, and 0 maximum number of paths per isoform/read), and clustered using ICE algorithm (estimated cDNA size ≥ 1–2 kb) with quiver polishing (quality ≥ 0.99) to generate consensus isoform sequences. Further information on the different reads generated can be found in PacBio wiki (https://github.com/PacificBiosciences/cDNA_primer/wiki/Understanding-PacBio-transcriptome-data). Statistics of the filtered sequences from each transcriptome library is showed in Table 2. The consensus isoform sequences can be used as full-length transcriptome references for the three species of carnivorous pitcher plants for further studies.

Conflict of interest

All the authors have approved submission and there are no conflicts of interest.

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References

[1] S.-H. Kim, T. Hamada, Rapid and reliable method of extracting DNA and RNA from sweetpotato, Ipomona batatas (L.) Lam, Biotechnol. Lett. 27 (2005) 1841–1845.
[2] S.E. Abdel-Ghany, M. Hamilton, J.L. Jacobs, P. Ngam, N. Devitt, F. Schilkey, A. Ben-Hur, A.S.N. Reddy, A survey of the sorghum transcriptome using single-molecule long reads, Nat. Commun. 7 (2016) 11706.