Transcriptome of Russet Norkotah and its clonal selection, TXNS278

Julien Levy1*, Cecilia Tamborindeuy2, Giridhar Athrey3, Douglas C. Scheuring1, Jeffrey W. Koym4 and J. Creighton Miller Jr.1

Abstract

Objectives: Potato has a large genetic diversity. This diversity is in part due to somaclonal variability that appears within potato selections for which tubers are used as seeds. However, the potato tetraploid genome, as well as the use of tubers for crop propagation, does not allow for easy genetic studies. The objective is to gain knowledge at the genomic level from standard Russet Norkotah and a subclonal Russet Norkotah selection TXNS278.

Data description: In this report, we used RNA-seq, which allows genome-wide gene expression analysis to sequence the transcriptomes of the subclonal Russet Norkotah selection TXNS278 with standard Russet Norkotah grown in commercial fields. Among the selections, TXNS278 appeared in a multi-year analysis in Texas as a top No 1 yielding variety. Russet Norkotah and TXNS278 leaf and root transcriptomes were sequenced at two time points during growing season.

Keywords: Russet Norkotah, Clonal selection, RNA-seq, Genomic.
Breeding and Variety Development Program in the summer of 2013. The seeds of Russet Norkotah were obtained from Oregon State University—Klamath Basin Research & Extension Center. The seed of TXNS278 was obtained from Dr. David Holm, Colorado State University at the San Luis Valley Research Center in Colorado. The plots were planted April 1, 2013 from tuber seed obtained from certified seed growers. Tissues were sampled on July 6th (T1, 66 days after planting) and on July 24th (T2, 84 days after planting). Tissues were stored in a tube in RNAlater Stabilization Solution (Thermo Fischer Scientific, Waltham, MA) and placed on ice in a cooler before transportation to the laboratory, where tissues were frozen upon arrival and stored at −20 °C. Leaves and roots from different plants within the same plot were sampled independently at both time points. Plots of TXNS278 and RN were separated by two feet.

RNA extraction
RNA was isolated from individual samples using the Qiagen plant RNeasy kit. DNAse treatment was performed according to manufacturer recommendations (Qiagen, Hilden, Germany). RNA was quantified using an Infinite 200 PRO NanoQuant (Tecan, Mannedorf, Switzerland), and quality was verified by Bioanalyzer (Texas A&M AgriLife Genomics & Bioinformatics Service, College Station, TX).

RNA sequencing
A total of 24 RNA samples were submitted to the AgriLife Genomics & Bioinformatics Service. After RNA quality evaluation, three independent RNA samples (biological replicates) were pooled. Poly(A) RNA enrichment, library construction, and RNA sequencing from each pool were performed at the AgriLife Genomics & Bioinformatics Service.

One library was made for each potato cultivar (RN and TXNS278) at each time point (T1 and T2) and from each tissue (leaf and root). Therefore, a total of eight libraries were made using the TruSeq Kit (Illumina, San Diego, CA). The sequencing was performed using 100 single-end reads on one lane of the Illumina Hiseq-2000 platform. The libraries were made publicly available through NCBI and can be found at the following address https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?&acc=GSE87857. A summary of the sequencing results is described in Table 1.

Mapping of RN and TXNS278 transcriptomes to the potato genome
Leaf and root samples were collected from a commercial field near Springlake, TX in 2013. Two time points were tested, based on plant development: T1 (full flowering) and T2 (senescing plants).

Over 176 million reads that passed the quality filters were obtained (Additional file 1: Table S1), with an average of 22 million reads per library. The reads were mapped to the S. tuberosum double haploid DMI3.4 genome ensembl19 using Tophat2 in CyVerse (iplantcollaborative.org). Only 33% of the reads from the library RN-LeafT2 mapped to the potato genome (Table 1 data file 8). After exclusion of this library, a minimum of 66.3% of reads mapped to the potato genome, from which 55 to 68% were uniquely aligned reads (Additional file 1: Table S1). The samples used for the data file 8 were infected with potato virus and only 33% of the reads matched the potato genome. Consequently these data should be excluded from further analyses. Interestingly, a higher percentage of unique mapped reads were obtained from the root libraries (62–67%). This difference might be related to higher rRNA levels in leaves than in roots in spite of the mRNA enrichment.

Limitation
The libraries were sequenced on pooled samples from three biological replicates; this reduced the cost of sequencing multiple samples, but limited the statistical power of the analysis. Nevertheless, several studies

| Table 1 Overview of data files |
|-------------------------------|----------------|-----------------|--------------------------------|------|
| Label | Name of data file/data set | File types (file extension) | Data repository and identifier (DOI or accession number) | License |
| Data file 1 | GSM2341973 RN-Leaf-T1 | GTF (.gtf.gz) | NCBI GEO (GSM2341973) | N/A |
| Data file 2 | GSM2341974 TXNS278-Leaf-T1 | GTF (.gtf.gz) | NCBI GEO (GSM2341974) | N/A |
| Data file 3 | GSM2341975 TXNS278-Leaf-T2 | GTF (.gtf.gz) | NCBI GEO (GSM2341975) | N/A |
| Data file 4 | GSM2341976 RN-Root-T1 | GTF (.gtf.gz) | NCBI GEO (GSM2341976) | N/A |
| Data file 5 | GSM2341977 TXNS278-Root-T1 | GTF (.gtf.gz) | NCBI GEO (GSM2341977) | N/A |
| Data file 6 | GSM2341978 RN-Root-T2 | GTF (.gtf.gz) | NCBI GEO (GSM2341978) | N/A |
| Data file 7 | GSM2341979 TXNS278-Root-T2 | GTF (.gtf.gz) | NCBI GEO (GSM2341979) | N/A |
| Data file 8 | GSM2982237 RN-Leaf-T2 | GTF (.gtf.gz) | NCBI GEO (GSM2982237) | N/A |
have been published using pooled samples, and different software has been designed to analyze pooled samples. This sequencing provides valuable RNAseq data of Russet Norkotah genes for future sequencing of cultivated potato species and annotation of genes and transcripts.

**Additional file**

Additional file 1: Table S1. Overview of the mapping results.

**Abbreviations**

RN: Russet Norkotah; TXNS278: Texas Russet Norkotah Strain 278.

**Authors’ contributions**

JL carried out the experiments, DCS, JWK developed the material and collected the material. JL, CT, GA, JCM Jr participated in the design of the study and analyzed the data. All authors edited the final manuscript. All authors read and approved the final manuscript.

**Acknowledgements**

We thank Dr. Elizabeth A. Pierson for scientific conversation and continuous support.

**Competing interests**

The authors declare that they have no competing interests.

**Availability of data materials**

The data described in this Data note can be freely and openly accessed on (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?&acc=GSE87857). Please see Table 1 and reference list for details and links to the data.

**Consent for publication**

Not applicable.

**Data citation**

1. NCBI GEO Series: GSE87857.
2. Data file 1: GSM2341973.
3. Data file 2: GSM2341974.
4. Data file 3: GSM2341975.
5. Data file 4: GSM2341976.
6. Data file 5: GSM2341977.
7. Data file 6: GSM2341978.
8. Data file 7: GSM2341979.
9. Data file 8: GSM2982237.

**Ethics approval and consent to participate**

Not applicable.

**Funding**

This project was supported by a Texas A&M Potato Breeding and Variety Development Program grant.

**Publisher’s Note**

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Received: 23 January 2018 Accepted: 14 February 2018
Published online: 01 March 2018

**References**

1. Cromme N, Prakash AB, Lutaladio N, Ezeta F. Strengthening potato value chains. 2010. http://www.fao.org/docrep/013/i1710e/i1710e.pdf. Accessed 24 Feb 2018.
2. Miller JC. Selection of desirable somatic mutations; A means of potato improvement. Am Potato J. 1954;31:358–9.
3. NASS. National Agricultural Statistics Service. 2013. http://www.nass.usda.gov/Statistics_by_State/Washington/Publications/Potatoes/PT12_1.pdf. Accessed 24 Feb 2018.
4. Miller JC Jr, Scheuring DC, Miller JP, Fernandez GCJ. Selection, evaluation, and identification of improved Russet Norkotah strains. Am J Potato Res. 1999;76:161–7.
5. Miller JC Jr, Tai GCC, Ouellette B, Miller JP. Discriminating Russet Norkotah intraclonal selections using canonical and cluster analysis. Am J Potato Res. 2004;81:203–7.
6. Hale AL, Miller JC Jr, Renganayaki K, Fritz AK, Coombs JJ, Frank LM, Douches DS. Suitability of AFLP and microsatellite marker analysis for discriminating intraclonal variants of the potato cultivar Russet Norkotah. J Am Soc Hortic Sci. 2005;130:624–30.