



DATA NOTE

The complete genome sequence of *Toxicodendron radicans*, Eastern Poison Ivy

[version 1; peer review: 2 approved, 1 approved with reservations]

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Abstract

Eastern Poison Ivy (*Toxicodendron radicans*, Anacardiaceae) is well known in Eastern North America for causing contact dermatitis, an itchy and painful rash in most people who come in contact with it. We present the whole genome sequence and annotation of this species. A total of 96,255,779 paired-ends reads consisting of 28.9 G bases were obtained by sequencing one leaf from a wild-collected plant. The reads were assembled by a *de novo* method followed by alignment to related species. Annotation was performed via GenMark-ES. The raw and assembled data is publicly available via GenBank: Sequence Read Archive (SRR10325927) and Assembly (GCA_009867345).

Keywords

Toxicodendron radicans, Eastern Poison Ivy, genome, assembly, annotation

Open Peer Review

Approval Status

	1	2	3
version 1			
20 Aug 2020	view	view	view

1. **Rongxi Sun**, Jiangxi Agricultural University, Nanchang, China
2. **Xuming Zhou**, Chinese Academy of Sciences, Beijing, China
3. **Hyungtaek Jung**, The University of Queensland, St Lucia, Australia

Any reports and responses or comments on the article can be found at the end of the article.

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Author roles: Pirro T: Resources; Pirro S: Data Curation, Funding Acquisition, Investigation, Methodology, Writing – Original Draft Preparation, Writing – Review & Editing

Competing interests: No competing interests were disclosed.

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Introduction

Eastern Poison Ivy (*Toxicodendron radicans*, Anacardiaceae) is well known in the Eastern United States, Canada, Mexico and parts of China for causing contact dermatitis, an itchy and painful rash in most of the human population (Barceloux, 2008). The rash, along with accompanying blisters, is caused by urushiol, an oil compound in the plant's sap. Urushiol-induced allergic rashes are a Type IV hypersensitivity reaction (Kalish & Johnson, 1990). This type of reaction is a cell-mediated response and can take hours to days to produce symptoms (Williams *et al.*, 1999). Approximately 15% of people have no allergic reaction to urushiol, but most people experience a reaction from between 5–12 days after exposure. Allergic reactions can increase in duration and severity after each incident (Bonnekoh *et al.*, 2019).

Exposure to the urushiol in *Toxicodendron radicans* can cause hypersensitivity in related plants, such as mango, *Mangifera indica* (Yoo & Carius, 2019), and the Chinese Lacquer Tree, *Toxicodendron vernicifluum*. Consumer products made from the Chinese Lacquer Tree are manufactured by curing the urushiol-containing sap to a clear, hard, waterproof substance. Improperly cured products can cause contact dermatitis in urushiol-hypersensitive people several years after manufacture, and present an ongoing health challenge to lacquerware workers (Ma *et al.*, 2012).

A complete genome sequence for this species will allow the insight into the evolution of the urushiol biosynthetic pathway.

Methods

A leaf from a single wild-collected *Toxicodendron radicans* plant was used as the source of genomic DNA. Extraction was performed on tissue from a single leaf using the Qiagen DNeasy genomic extraction kit for plants, using the standard

process. A paired-end sequencing library was constructed using the Illumina TruSeq kit, according to the manufacturer's instructions. The library was sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150bp format.

The resulting fastq files were trimmed of adapter/primer sequence and low-quality regions with Trimmomatic (v0.33) (Bolger *et al.*, 2014). The trimmed sequence was assembled by SPAdes (v2.5) (Bankevich *et al.*, 2012) followed by a finishing step using RagTag (v1.0.0) (Alonge, 2020) to make additional contig joins based on conserved regions in related plant species: *Mangifera indica* (mango, GCA_011075055) and *Pistacia vera* (pistachio, GCA_008641045). Default procedures were used for all assembly steps.

Annotation was performed using GeneMark-ES (v2.0) (Lomsadze *et al.*, 2005). Annotation was performed fully *de novo* without a curated training set and default parameters.

Results

The genome assembly yielded a total sequence length of 454,874,194 bp over 270,263 scaffolds with an N50 of 1,945,245. The GeneMark-ES annotation resulted in 42,021 genes.

Data availability

Underlying data

Raw and assembled data is publicly available via GenBank:

Raw genome of *Toxicodendron radican*, Accession number SRR10325927: <https://www.ncbi.nlm.nih.gov/sra/?term=SRR10325927>

Assembly of *Toxicodendron radican*, Accession number GCA_009867345: https://www.ncbi.nlm.nih.gov/assembly/GCA_009867345.1/

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Open Peer Review

Current Peer Review Status:   

Version 1

Reviewer Report 07 July 2021

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Hyungtaek Jung

School of Biological Sciences, The University of Queensland, St Lucia, Qld, Australia

The authors have assembled the genome by employing Illumina sequencing technology using the leaf tissue of *T. radicans*. There is no doubt that the data generated in the current study will make a valuable contribution to the scientific community, however, I have several concerns about the analyses and/or the interpretation of the data as it currently stands.

Methods:

The fact is Illumina-based genome assemblies contain many misassemblies. Given the circumstances, why did authors choose Illumina reads over PacBio and Oxford Nanopore? What's the overall sequencing and assembly summary? Any chloroplast DNA contamination? If yes, how did you treat them? Where are the executed scripts? Annotation with GeneMark-ES without any RNA-Seqs?

Results:

How did you evaluate the assembly accuracy (e.g. BUSCO)? Where are the structural (RepeatMasker) and functional annotations? It needs more explanation.

Is the rationale for creating the dataset(s) clearly described?

Partly

Are the protocols appropriate and is the work technically sound?

Partly

Are sufficient details of methods and materials provided to allow replication by others?

Partly

Are the datasets clearly presented in a useable and accessible format?

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Genomics and Bioinformatics

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Reviewer Report 24 June 2021

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Xuming Zhou

Key Laboratory of Animal Ecology and Conservation Biology, Chinese Academy of Sciences, Beijing, China

This study reported the complete genome sequence of *Toxicodendron radicans*, which could help future research of this species. The manuscript is well written and should be considered for indexing prior to two questions:

1. The author should provide more details about the annotation, for example, how *de novo* and homologous approaches were performed.
2. The author should compare their genome quality to their relative species.

Is the rationale for creating the dataset(s) clearly described?

Yes

Are the protocols appropriate and is the work technically sound?

Yes

Are sufficient details of methods and materials provided to allow replication by others?

No

Are the datasets clearly presented in a useable and accessible format?

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Genomics, Phylogenetics, Aging

I confirm that I have read this submission and believe that I have an appropriate level of

expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 13 November 2020

<https://doi.org/10.5256/f1000research.28204.r73876>

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Rongxi Sun

Jiangxi Agricultural University, Nanchang, China

I have now thoroughly reviewed the manuscript "The complete genome sequence of *Toxicodendron radicans*, Eastern Poison Ivy". Given urushiol in this plant's sap causing dermatitis, an itchy and painful rash in most of the human population, the new assembly of complete genome sequence of this species helps to understand the evolution of the urushiol biosynthetic pathway. However, there are still some flaws in the manuscripts which the authors may consider to change:

1. Method: What is the source of the leaf used for sequencing, such as tree age and specific location.
2. Results : How accurate is this high-throughput genome sequence? Whether there are indicators related to accuracy in the results.
3. In results, the annotation should be more discussed.

Is the rationale for creating the dataset(s) clearly described?

Partly

Are the protocols appropriate and is the work technically sound?

Partly

Are sufficient details of methods and materials provided to allow replication by others?

Yes

Are the datasets clearly presented in a useable and accessible format?

Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Genetic diversity and phylogeography

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

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