Data in Brief 66 (2026) 112812

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Small RNA sequencing datasets from caryopses and flag leaves of multiple rice genotypes exposed to high nighttime temperature stress

David Payne[a], Yongfang Li[a], Julie Thomas[b], Anuj Kumar[b], Andy Pereira[b], Ramanjulu Sunkar[a,*]

[a] Department of Biochemistry and Molecular Biology, Oklahoma State University, Stillwater, OK 74078, USA
[b] Department of Crop, Soil, and Environmental Sciences, University of Arkansas, Fayetteville, AR 72701, USA

ARTICLE INFO

Article history:
Received 20 March 2026
Revised 19 April 2026
Accepted 28 April 2026
Available online 6 May 2026

Dataset link: small RNA datasets (Original data)

Keywords:
Caryopses
Chalkiness
Degradome
Flag leaf
Small RNAs

ABSTRACT

The increasing frequency and severity of High Nighttime Temperature (HNT) threatens to damage rice quality by inducing the chalky grain phenotype. To better understand the roles that small RNAs (sRNAs) play in HNT-induced chalkiness in rice, we sequenced sRNA libraries from the R6-stage caryopses samples and flag leaves of 8 rice genotypes differing in their HNT-induced chalkiness (low chalky [LC] or high chalky [HC]) under Control Nighttime Temperature (CNT) and HNT conditions. These efforts allowed us to deposit 84 high-quality sRNA libraries for 8 varieties. Additionally, high-quality degradome libraries were generated for the caryopses and flag leaves of the Cypress variety under both CNT and HNT conditions. Our sRNA sequencing data is likely to be useful in detecting potential relationships between sRNA regulation and the HNT-induced chalky phenotype, while the degradome sequencing data will be useful in identifying sRNA targets relevant to the tissues and conditions analysed. Both the sRNA and degradome sequencing libraries have been deposited in the Sequence Read Archive, so they can be further analysed in future studies investigating the

* Corresponding author.
E-mail address: ramanjulu.sunkar@okstate.edu (R. Sunkar).

https://doi.org/10.1016/j.dib.2026.112812

importance of HNT-altered sRNAs not only on grain quality, but also for many other important agronomic traits.

Specifications Table

Subject	Biology
Specific subject area	Plant abiotic stress and specifically high nighttime temperature stress
Type of data	Small RNA-seq from caryopses and flag leaves of 8 rice varieties both under control nighttime temperature stress (CNT) and high nighttime temperature stress. The 8 rice varieties used differed in their chalkiness (low chalky or high chalky) under high nighttime temperature stress. Similarly, degradome-seq data from caryopses and flag leaves of Cyp variety exposed to CNT and HNT conditions was generated.
Data collection	Total RNA was extracted using TRIzol reagent. Small RNA Libraries were prepared according to TruSeq® Small RNA Sample Preparation Guide and sequenced using Illumina Novaseq™ 6000 platform. Degradome Libraries were prepared using poly(A) RNA. An RNA adaptor containing EcoP15I recognition site was ligated to uncapped 5′ phosphate containing mRNA fragments. Reverse transcription was performed on the ligated product using an oligo(dT)-tailed adapter (RT-primer) and then amplified the product using 5 PCR cycles. The dsDNA was digested using EcoP15I restriction enzyme, and a 3′ds-DNA adapter was ligated to the digested DNA. Finally, 10 cycle PCR was used and sequenced.
Data source location	Seeds were obtained from Genetic Stocks Oryza and cultivated in growth chambers at the University of Arkansas, Fayetteville.
Data accessibility	Repository name: Sequence Read Archive (SRA) Data identification number: PRJNA1372752 Direct URL to data: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1372752
Related research article	Payne, D., Li, YF., Ng, PJ., Govindan, G., Thomas, J., Kumar, A., Rohila, JS., Pereira, A. and Sunkar, R (2026). High Nighttime Temperature (HNT)-Responsive MicroRNA profiles in Developing Caryopses and Flag Leaves of 13 Rice Varieties, Plant Stress, 20, 101,320. doi.org/10.1016/j.stress.2026.101320

1. Value of the Data

- This dataset provides high-quality small RNA sequencing data for rice caryopses and flag leaves under Control Nighttime Temperature (CNT) and High Nighttime Temperature (HNT) for eight genotypes. These lines differed in their chalkiness (some are low chalky [LC] whereas others are high chalky [HC] lines) under HNT.
- The dataset allows the analyses and exploration of the small RNA profiles from eight rice varieties in two specific tissues (caryopses and flag leaves) under CNT and HNT. Most importantly, how microRNA and other small RNA profiles are affected by HNT in rice genotypes. This allows for identifying small RNA regulation patterns associated with either the LC or HC phenotype under HNT.
- This dataset also includes four high quality degradome libraries for the caryopses and flag leaves of Cypress variety under CNT and HNT conditions.
- The degradome libraries will aid in identification and validation of known and novel small RNA targets in rice caryopses and flag leaves under CNT and HNT conditions.
- The small RNA and degradome sequencing files are deposited in Sequence Read Archive for use in future analyses.

2. Background

Increasing global temperatures threaten to decrease the yield and quality of *Oryza sativa*. The increasing incidence and severity of high temperatures, in particular, negatively affects grain

quality by inducing the chalky phenotype, which primarily results from impairments in the grain filling process. Rice varieties vary in their susceptibility to HNT-induced chalkiness and can therefore be classified as low-chalkiness (LC) or high-chalkiness (HC) genotypes. While transcriptomic and metabolomic factors associated with the HNT-induced chalky phenotypes have been frequently investigated, the involvement of small RNAs remains a relatively unexplored field. In this report, we describe small RNA datasets generated for 8 rice varieties exposed to HNT [1]. We have previously investigated small RNAs especially miRNA responses in rice varieties under High Daytime Temperature (HDT) [2]. The HNT effects are notably different from HDT and more detrimental to rice yield and quality [3–7]. We profiled small RNAs under CNT and HNT conditions for both the R6-stage caryopsis and flag leaf samples from several LC and HC rice varieties. We selected two important tissues (caryopses and flag leaves) that are relevant for examining HNT-induced chalkiness. The caryopses are the site of grain filling, and the flag leaf serves as the primary source of sucrose that is used for starch biosynthesis during grain filling in the caryopses.

Additionally, for identifying sRNA targets, we sequenced four high quality degradome libraries from both tissues under CNT and HNT conditions for the Cypress (Cyp) variety. Overall, the data is useful for identifying common (conserved) or different (non conserved geneotype-specific, if any) small RNAs and their regulatory patterns among these genotypes that differ in HNT-induced chalkiness. Additionally, the data is useful for identifying genotype, tissue, or stress-specific sRNAs that may affect other agronomic traits in rice. The degradome data is also useful for identifying any additional sRNA targets that may occur in a tissue- and condition-specific manner.

3. Data description

3.1. Sequencing of small RNA libraries

Small RNA-seq files for the flag leaves were generated for thirteen rice varieties [Cypress (Cyp), Kaybonnet (Kay), LaGrue (Lag), RoyJ (Roy), Starbonnet (Sta), Wells (Wel), Bengal (Ben), Nipponbare (NB), GSOR 311,258 (258), GSOR 310,080 (080), GSOR 310,039 (039), GSOR 310,045 (045) and GSOR 310,337 (337)]. These varieties differed in their HNT-induced grain chalky phenotype, i.e. seven LC varieties (Cyp, Kay, Roy, Sta, Ben, 045, and 080) and six HC varieties (Lag, Wel, NB, 039, 258, and 337). For caryopses samples, except for Ben, NB, and 080, the remaining ten genotypes were sequenced. For each tissue of each variety, three replicates were used for both CNT and HNT treatments. However, sRNA libraries from five genotypes (258, 080, 039, 045, and 337) could not pass the qualitative analyses of typical sRNA libraries. This was largely due to low quality of the isolated RNA, which in turn was due to high sugar accumulation in these tissues which interferes with the isolations and drastically decreases the overall RNA quality. Though the sRNA libraries from five genotypes (258, 080, 039, 045, and 337) were also sequenced but because of their suboptimal quality, they were not deposited for public use. Therefore, a total of 48 small RNA-seq libraries for the flag leaves (from 8 genotypes - Cyp, Kay, Lag, Roy, Sta, Wel, Ben and NB) and 36 small RNA-seq libraries for the caryopses (from 6 genotypes - Cyp, Kay, Lag, Roy, Sta, and Wel) [Table 1, Fig. 1] were deposited as fastq files in Sequence Read Archive with the BioProject ID PRJNA1372752 for further analyses.

Principal component analysis (PCA) of the small RNA libraries showed generally good clustering by genotype, although some overlap was observed, particularly among flag leaf samples (Fig. 1). In the caryopsis tissue, PC1 separated Kay from the other varieties, whereas in the flag leaves, PC1 separated Ben and NB from the remaining varieties.

Beyond the miRNA profiles as we reported recently [1], these large scale small RNA libraries from caryopses and flag leaves for eight rice varieties under two conditions (CNT and HNT), are a valuable resource for identifying additional classes of regulatory sRNAs, including phasiRNAs, tasiRNAs, and heterochromatic-siRNAs, identifying PHAS loci and phasing patterns, characterizing tissue- and stress-responsive sRNA populations, and integrating with degradome and RNA-seq data to define biologically active sRNA-target regulatory modules.

Table 1
Summary of sRNA-seq libraries [1].

Tissue	Variety	Condition	Average depth of cleaned libraries	Average % of reads aligned to genome	Average % of reads aligned to miRNAs
Caryopsis	Cyp	CNT	10,858,364	91.65	1.90
		HNT	10,999,216	90.61	2.62
	Kay	CNT	6533,348	88.90	3.31
		HNT	7593,632	91.03	2.87
	Lag	CNT	8236,848	91.65	2.05
		HNT	10,683,774	91.24	3.10
	Roy	CNT	25,890,174	90.07	3.16
		HNT	16,315,728	90.94	3.42
	Sta	CNT	8640,327	93.21	2.69
		HNT	9551,475	92.08	2.69
	Wel	CNT	12,099,061	90.58	4.62
		HNT	17,623,780	89.30	2.22
Flag leaf	Ben	CNT	6830,749	92.63	17.61
		HNT	5023,695	89.31	7.46
	Cyp	CNT	12,316,713	89.44	8.11
		HNT	10,300,646	86.96	6.36
	Kay	CNT	9656,711	93.33	6.89
		HNT	10,212,125	93.61	6.48
	Lag	CNT	11,038,340	92.00	6.53
		HNT	11,955,567	93.06	10.53
	NB	CNT	6995,464	93.60	13.60
		HNT	8618,816	90.73	9.43
	Roy	CNT	8827,387	92.21	8.60
		HNT	9862,260	93.07	11.11
	Sta	CNT	10,620,182	93.19	11.66
		HNT	8955,612	92.48	5.53
	Wel	CNT	15,342,481	91.35	7.85
		HNT	9897,362	92.94	7.52

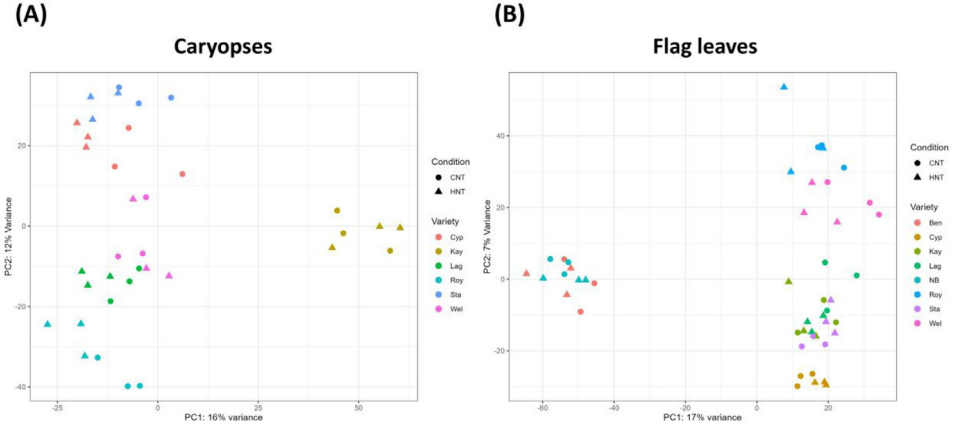

Fig. 1. PCA plots for sRNA-seq libraries of the rice **(A)** caryopses and **(B)** flag leaf tissues.

3.2. Sequencing degradome libraries

A total of four degradome libraries (one each from caryopses and flag leaves collected from CNT and HNT conditions) were generated for the Cyp variety [1] [Table 2]. The sequencing depth highly varied between these two tissues. The sequenced caryopses degradome libraries

Table 2
Summary of degradome libraries generated for Cyp Variety [1].

Tissue	Condition	Average depth of cleaned libraries	Average % of reads aligned to transcriptome
Caryopsis	CNT	25,883,338	83.14%
	HNT	26,317,769	75.85%
Flag leaf	CNT	168,713,978	87.96%
	HNT	158,219,309	86.64%

yielded approximately 25 million reads whereas the flag leaves libraries depth was almost six-fold greater. These differences could be attributed to the quality of RNA isolations, since the high sugar accumulation in the caryopses tend to interfere with high quality isolations, which is critical for poly(A) RNA isolation. While conventional degradome sequencing [8] typically yields 20-nt long reads for mapping on to the target mRNAs, the method [9] used here yields slightly longer reads (25–27-nt long), enabling better alignment to the individual mRNAs, which in turn decreases the incidences of multi-mapping to gene family members. These files are available as fastq files in Sequence Read Archive with the BioProject ID PRJNA1372752 for further analyses.

Apart from validating miRNA targets, degradome libraries could be used for many other applications. For example, in identifying novel sRNA and phasiRNA targets including miRNA-guided trigger sites on phasiRNA precursors for initiating the phasiRNA biogenesis, and in determining tissue and condition-specific targeting. More recently, degradome data has also been used to investigate the RNA turnover and endonucleolytic cleavages analyses across transcripts etc [10]. Thus, degradome libraries generated from R6-stage caryopses and flag leaves under CNT and HNT conditions could be used in multiple analyses.

4. Experimental Design, Materials and Methods

4.1. Experimental conditions for growing rice varieties

A panel of 13 accessions consisting of Wel, Lag, Cyp, Roy, Sta, Kay, NB, Ben, 039, 045, 080, 258, and 337 were used for generating these datasets, but the quality of the datasets from the later five genotypes was extremely poor for any type of analyses, thus could not be deposited. These genotypes were grown in the greenhouse under controlled conditions [(30 °C Day/22.2 °C nighttime temperatures, 13/11-h light/dark photoperiod with 800–1000 µmol Photosynthetically Active Radiation (PAR) m^2 s^{-1} and 60–65% Relative Humidity (RH)]. A total of 30 seeds per variety were germinated in plastic pots with a 3:1 mixture of Sun Gro potting mix and field soil. The 2-week-old seedlings were transplanted into larger pots and grown in the greenhouse under controlled conditions for up to 5 days after flowering which coincides with R5–6 stage of reproductive development. A completely randomized design (CRD) was used with three biological replicates, each consisting of a single plant in a pot, and fertilized as per local rice growing recommendations for vegetative growth. To ensure environmental consistency during the treatments, HOBO® data loggers (Onset HOBO®, Cape Cod, MA, USA) were installed in each chamber to monitor the control and treatment temperature regimes continuously throughout the experimental period.

4.2. High nighttime temperature (HNT) stress treatment

At the R5–6 stage, the pots which were tagged for HNT stress, were transferred to growth chamber to impose HNT stress treatment. For the HNT treatment, the plants were subjected to a day/night temperature cycle of 30 °C during the day (13 h; 7:00 am to 8:00 pm) and 28 °C at night (11 h; 8:00 pm to 7:00 am), mimicking elevated nighttime conditions. In contrast, the

control treatment maintained a day/night regime of 30 °C/22.2 °C to simulate optimal nighttime temperatures. At the R6-stage (approximately 10 days after flowering), the control (CNT) and HNT-exposed caryopses samples as well as flag leaves were collected, immediately frozen in liquid nitrogen, and stored at −80 °C until total RNA was isolated.

4.3. Small RNA sequencing

Total RNA was extracted from all these samples using TRIzol reagent (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's protocol. The quality and quantity of total RNA were analysed using Agilent Bioanalyzer 2100 and Nanodrop ND-1000. Small RNA Libraries were prepared according to TruSeq® Small RNA Sample Preparation Guide (Illumina) as described previously [8,11] and sequenced using Illumina Novaseq™ 6000 platform. The quality of each raw fastq sRNA-seq library was examined using fastqc [12], and trimmomatic [13] was used to remove adapters, low quality reads, and the reads which were shorter than 18 nt. Three replicate libraries for each variety grown under CNT or HNT conditions were generated for sRNA-sequencing [Table 3].

Sequence alignments were carried out using the Bowtie [14] bioinformatic software, allowing for 1 mismatch to the rice genome (obtained from http://rice.uga.edu/downloads.shtml) or to primary miRNA sequences (obtained from miRBase [15]). In the latter case, the –norc option was used. ShortStack [16] was used with the default settings on all good quality sRNA-seq libraries to perform sRNA clustering and to obtain read counts for each cluster in all samples. In DESeq2 [17], the sRNA clusters were filtered for those with at least ten sRNA reads in at least a third of the samples. Afterwards, the PCA values were determined using the plotPCA command, and ggplot2 [18] was used to create the visualizations.

4.4. Degradome sequencing

Degradome libraries from the caryopses and flag leaves of the Cyp variety were prepared according to our published protocol [9] [Table 4]. Briefly, total RNA was isolated from plant tissues and poly(A) RNA was enriched. An RNA adaptor containing the EcoP15I recognition site (5′-GUU CAG AGU UCU ACA GUC CGA UCAGCAGC 3′) was ligated to the poly(A) RNA with 5′ monophosphate (indicative of miRNA/siRNA guided Argonaute-mediated cleavage), and reverse transcription was performed using an oligo(dT)-tailed adapter (RT-primer). Next, 5 cycle PCR was used to amplify the RT-PCR product. This dsDNA was digested using EcoP15I and then ligated to a ds-DNA adapter. The ligated product was PCR-amplified using 10 cycles, which were sequenced. Alignments to the rice transcriptome (obtained from http://rice.uga.edu/downloads.shtml) were performed using Bowtie [14] with the –norc option enabled and one mismatch allowed.

Limitations

While sRNA-seq libraries were generated for additional rice varieties (GSOR 311,258, GSOR 310,080, GSOR 310,039, GSOR 310,045 and GSOR 310,337), the quality of these sRNA libraries was extremely poor. Therefore, we did not deposit them for public use. The poor quality was attributable to suboptimal RNA quality during RNA isolations, probably due to high sugar accumulation in these tissue samples especially in these genotypes.

Several rice degradome libraries were reported previously for several other rice tissue types such as seedlings and leaves as well as other tissues. Thus far no degradome libraries from rice R6-stage caryopses samples were generated, which is one of the tissues that we used in analysing the role of HNT-induced grain chalkiness in rice genotypes [1]. Generating extensive number of degradome libraries from R6-stage caryopses and flag leaves for all genotypes used

Table 3
List of sRNA-seq libraries deposited at Sequence Read Archive (PRJNA1372752) [1].

Run	Biological Replicate	Variety	Library Name	Tissue	Treatment
SRR36277529	1	Cyp	Cyp_C_sRNA_CNT_1	Caryposis	CNT
SRR36277528	2	Cyp	Cyp_C_sRNA_CNT_2	Caryposis	CNT
SRR36277517	3	Cyp	Cyp_C_sRNA_CNT_3	Caryposis	CNT
SRR36277506	1	Cyp	Cyp_C_sRNA_HNT_1	Caryposis	HNT
SRR36277495	2	Cyp	Cyp_C_sRNA_HNT_2	Caryposis	HNT
SRR36277484	3	Cyp	Cyp_C_sRNA_HNT_3	Caryposis	HNT
SRR36277525	1	Kay	Kay_C_sRNA_CNT_1	Caryposis	CNT
SRR36277524	2	Kay	Kay_C_sRNA_CNT_2	Caryposis	CNT
SRR36277523	3	Kay	Kay_C_sRNA_CNT_3	Caryposis	CNT
SRR36277522	1	Kay	Kay_C_sRNA_HNT_1	Caryposis	HNT
SRR36277521	2	Kay	Kay_C_sRNA_HNT_2	Caryposis	HNT
SRR36277520	3	Kay	Kay_C_sRNA_HNT_3	Caryposis	HNT
SRR36277512	1	Lag	Lag_C_sRNA_CNT_1	Caryposis	CNT
SRR36277511	2	Lag	Lag_C_sRNA_CNT_2	Caryposis	CNT
SRR36277510	3	Lag	Lag_C_sRNA_CNT_3	Caryposis	CNT
SRR36277509	1	Lag	Lag_C_sRNA_HNT_1	Caryposis	HNT
SRR36277508	2	Lag	Lag_C_sRNA_HNT_2	Caryposis	HNT
SRR36277507	3	Lag	Lag_C_sRNA_HNT_3	Caryposis	HNT
SRR36277499	1	Roy	Roy_C_sRNA_CNT_1	Caryposis	CNT
SRR36277498	2	Roy	Roy_C_sRNA_CNT_2	Caryposis	CNT
SRR36277497	3	Roy	Roy_C_sRNA_CNT_3	Caryposis	CNT
SRR36277496	1	Roy	Roy_C_sRNA_HNT_1	Caryposis	HNT
SRR36277494	2	Roy	Roy_C_sRNA_HNT_2	Caryposis	HNT
SRR36277493	3	Roy	Roy_C_sRNA_HNT_3	Caryposis	HNT
SRR36277486	1	Sta	Sta_C_sRNA_CNT_1	Caryposis	CNT
SRR36277485	2	Sta	Sta_C_sRNA_CNT_2	Caryposis	CNT
SRR36277483	3	Sta	Sta_C_sRNA_CNT_3	Caryposis	CNT
SRR36277482	1	Sta	Sta_C_sRNA_HNT_1	Caryposis	HNT
SRR36277481	2	Sta	Sta_C_sRNA_HNT_2	Caryposis	HNT
SRR36277480	3	Sta	Sta_C_sRNA_HNT_3	Caryposis	HNT
SRR36277472	1	Wel	Wel_C_sRNA_CNT_1	Caryposis	CNT
SRR36277471	2	Wel	Wel_C_sRNA_CNT_2	Caryposis	CNT
SRR36277470	3	Wel	Wel_C_sRNA_CNT_3	Caryposis	CNT
SRR36277469	1	Wel	Wel_C_sRNA_HNT_1	Caryposis	HNT
SRR36277468	2	Wel	Wel_C_sRNA_HNT_2	Caryposis	HNT
SRR36277467	3	Wel	Wel_C_sRNA_HNT_3	Caryposis	HNT
SRR36277459	1	Ben	Ben_F_sRNA_CNT_1	Flag leaf	CNT
SRR36277458	2	Ben	Ben_F_sRNA_CNT_2	Flag leaf	CNT
SRR36277457	3	Ben	Ben_F_sRNA_CNT_3	Flag leaf	CNT
SRR36277456	1	Ben	Ben_F_sRNA_HNT_1	Flag leaf	HNT
SRR36277455	2	Ben	Ben_F_sRNA_HNT_2	Flag leaf	HNT
SRR36277454	3	Ben	Ben_F_sRNA_HNT_3	Flag leaf	HNT
SRR36277473	1	Cyp	Cyp_F_sRNA_CNT_1	Flag leaf	CNT
SRR36277462	2	Cyp	Cyp_F_sRNA_CNT_2	Flag leaf	CNT
SRR36277451	3	Cyp	Cyp_F_sRNA_CNT_3	Flag leaf	CNT
SRR36277442	1	Cyp	Cyp_F_sRNA_HNT_1	Flag leaf	HNT
SRR36277527	2	Cyp	Cyp_F_sRNA_HNT_2	Flag leaf	HNT
SRR36277526	3	Cyp	Cyp_F_sRNA_HNT_3	Flag leaf	HNT
SRR36277519	1	Kay	Kay_F_sRNA_CNT_1	Flag leaf	CNT
SRR36277518	2	Kay	Kay_F_sRNA_CNT_2	Flag leaf	CNT
SRR36277516	3	Kay	Kay_F_sRNA_CNT_3	Flag leaf	CNT
SRR36277515	1	Kay	Kay_F_sRNA_HNT_1	Flag leaf	HNT
SRR36277514	2	Kay	Kay_F_sRNA_HNT_2	Flag leaf	HNT
SRR36277513	3	Kay	Kay_F_sRNA_HNT_3	Flag leaf	HNT
SRR36277505	1	Lag	Lag_F_sRNA_CNT_1	Flag leaf	CNT
SRR36277504	2	Lag	Lag_F_sRNA_CNT_2	Flag leaf	CNT
SRR36277503	3	Lag	Lag_F_sRNA_CNT_3	Flag leaf	CNT
SRR36277502	1	Lag	Lag_F_sRNA_HNT_1	Flag leaf	HNT
SRR36277501	2	Lag	Lag_F_sRNA_HNT_2	Flag leaf	HNT

(*continued on next page*)

Table 3 (*continued*)

Run	Biological Replicate	Variety	Library Name	Tissue	Treatment
SRR36277500	3	Lag	Lag_F_sRNA_HNT_3	Flag leaf	HNT
SRR36277453	1	NB	NB_F_sRNA_CNT_1	Flag leaf	CNT
SRR36277452	2	NB	NB_F_sRNA_CNT_2	Flag leaf	CNT
SRR36277450	3	NB	NB_F_sRNA_CNT_3	Flag leaf	CNT
SRR36277449	1	NB	NB_F_sRNA_HNT_1	Flag leaf	HNT
SRR36277448	2	NB	NB_F_sRNA_HNT_2	Flag leaf	HNT
SRR36277447	3	NB	NB_F_sRNA_HNT_3	Flag leaf	HNT
SRR36277492	1	Roy	Roy_F_sRNA_CNT_1	Flag leaf	CNT
SRR36277491	2	Roy	Roy_F_sRNA_CNT_2	Flag leaf	CNT
SRR36277490	3	Roy	Roy_F_sRNA_CNT_3	Flag leaf	CNT
SRR36277489	1	Roy	Roy_F_sRNA_HNT_1	Flag leaf	HNT
SRR36277488	2	Roy	Roy_F_sRNA_HNT_2	Flag leaf	HNT
SRR36277487	3	Roy	Roy_F_sRNA_HNT_3	Flag leaf	HNT
SRR36277479	1	Sta	Sta_F_sRNA_CNT_1	Flag leaf	CNT
SRR36277478	2	Sta	Sta_F_sRNA_CNT_2	Flag leaf	CNT
SRR36277477	3	Sta	Sta_F_sRNA_CNT_3	Flag leaf	CNT
SRR36277476	1	Sta	Sta_F_sRNA_HNT_1	Flag leaf	HNT
SRR36277475	2	Sta	Sta_F_sRNA_HNT_2	Flag leaf	HNT
SRR36277474	3	Sta	Sta_F_sRNA_HNT_3	Flag leaf	HNT
SRR36277466	1	Wel	Wel_F_sRNA_CNT_1	Flag leaf	CNT
SRR36277465	2	Wel	Wel_F_sRNA_CNT_2	Flag leaf	CNT
SRR36277464	3	Wel	Wel_F_sRNA_CNT_3	Flag leaf	CNT
SRR36277463	1	Wel	Wel_F_sRNA_HNT_1	Flag leaf	HNT
SRR36277461	2	Wel	Wel_F_sRNA_HNT_2	Flag leaf	HNT
SRR36277460	3	Wel	Wel_F_sRNA_HNT_3	Flag leaf	HNT

Table 4
List of degradome libraries deposited at sequence read archive (PRJNA1372752) [1].

Run	Variety	Library Name	Tissue	Treatment
SRR36277446	Cyp	Cyp_C_deg_CNT	Caryposis	CNT
SRR36277445	Cyp	Cyp_C_deg_HNT	Caryposis	HNT
SRR36277444	Cyp	Cyp_F_deg_CNT	Flag leaf	CNT
SRR36277443	Cyp	Cyp_F_deg_HNT	Flag leaf	HNT

in our study is exhaustive as well as cost-prohibitive for addressing our aim. The major objective of degradome libraries was to identify and validate miRNA targets specifically in R6-stage caryopses and flag leaf tissues of rice, and as a representative of these tissue-specific degradome libraries, we chose one genotype, i.e., Cyp grown under CNT and HNT conditions.

Ethics Statement

The authors have read and follow the ethical requirements for publication in Data in Brief and confirming that the current work does not involve human subjects, animal experiments, or any data collected from social media platforms.

CRediT Author Statement

David Payne: Investigation, Software, Methodology, Original draft preparation, Visualization. **Yongfang Li**: Formal analyses, Investigation, Methodology. **Julie Thomas**: Methodology, Investigation. **Anuj Kumar**: Methodology, Investigation. **Andy Pereira**: Methodology, Investigation, Resources. **Ramanjulu Sunkar**: Conceptualization, Supervision, Writing, Reviewing and Editing.

Data Availability

small RNA datasets (Original data) (SRA))

Acknowledgements

This research was funded by NSF EPSCoR award 1826836 and Stevens Endowed Chair of Agricultural Biotechnology, Oklahoma State University to R.S.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

[1] D. Payne, Y.F. Li, P.J. Ng, G. Govindan, J. Thomas, A. Kumar, J.S. Rohila, A. Pereira, R. Sunkar, High nighttime temperature (HNT)-responsive MicroRNA profiles in developing caryopses and flag leaves of 13 rice varieties, Plant. Stress. 20 (2026) 101320, doi:10.1016/j.stress.2026.101320.
[2] D. Payne, Y. Li, G. Govindan, A. Kumar, J. Thomas, C.A. Addo-Quaye, A. Pereira, R. Sunkar, High daytime temperature responsive MicroRNA profiles in developing grains of rice varieties with contrasting chalkiness, Int. J. Mol. Sci. 24 (2023) 11631, doi:10.3390/ijms241411631.
[3] A.A. Ambardekar, T.J. Siebenmorgen, P.A. Counce, S.B. Lanning, A. Mauromoustakos, Impact of field-scale nighttime air temperatures during kernel development on rice milling quality, Field Crops Res. 122 (2011) 179–185, doi:10.1016/j.fcr.2011.03.012.
[4] N.T.W. Cooper, T.J. Siebenmorgen, P.A. Counce, Effects of nighttime temperature during kernel development on rice physicochemical properties, Cereal. Chem. 85 (2008) 276–282, doi:10.1094/CCHEM-85-3-0276.
[5] P.A. Counce, R.J. Bryant, C.J. Bergman, R.C. Bautista, Y.J. Wang, T.J. Siebenmorgen, K.A.K. Moldenhauer, J.F.C. Meullenet, Rice milling quality, grain dimensions, and starch branching as affected by high night temperatures, Cereal Chem. 82 (2005) 645–648, doi:10.1094/CC-82-0645.
[6] S. Peng, J. Huang, J.E. Sheehy, R.C. Laza, R.M. Visperas, X. Zhong, G.S. Centeno, G.S. Khush, K.G. Cassman, Rice yields decline with higher night temperature from global warming, Proc. Natl. Acad. Sci. U.S.A. 101 (2004) 9971–9975, doi:10.1073/pnas.0403720101.
[7] Q. Su, J.S. Rohila, S. Ranganathan, R. Karthikeyan, Rice yield and quality in response to daytime and nighttime temperature increase – a meta-analysis perspective, Sci. Total Environ. 898 (2023) 165256, doi:10.1016/j.scitotenv.2023.165256.
[8] D. Formey, L.P. Iñiguez, P. Peláez, Y.F. Li, R. Sunkar, F. Sánchez, J.L. Reyes, G. Hernández, Genome-wide identification of the phaseolus vulgaris sRNAome using small RNA and degradome sequencing, BMC Genom. 16 (2015) 423, doi:10.1186/s12864-015-1639-5.
[9] Y.F. Li, M. Zhao, M. Wang, J. Guo, L. Wang, J. Ji, Z. Qiu, Y. Zheng, R. Sunkar, An improved method of constructing degradome library suitable for sequencing using Illumina platform, Plant Method. 15 (2019) 134, doi:10.1186/s13007-019-0524-7.
[10] D.R. Ganguly, Y.F. Li, S.S. Bhat, T. Tiwari, P.J. Ng, B.D. Gregory, R. Sunkar, mRNA adenosine methylase promotes drought tolerance through N^6-methyladenosine-dependent and independent impacts on mRNA regulation in Arabidopsis, New Phytologist. 245 (2025) 183–199, doi:10.1111/nph.20227.
[11] G. Jagadeeswaran, P. Nimmakayala, Y. Zheng, K. Gowdu, U.K. Reddy, R. Sunkar, Characterization of the small RNA component of leaves and fruits from four different cucurbit species, BMC Genom. 13 (2012) 329, doi:10.1186/1471-2164-13-329.
[12] Andrews, S., 2010. Fastqc: a quality control tool for high throughput sequence data.
[13] A.M. Bolger, M. Lohse, B. Usadel, Trimmomatic: a flexible trimmer for Illumina sequence data, Bioinformatics 30 (2014) 2114–2120, doi:10.1093/bioinformatics/btu170.
[14] B. Langmead, C. Trapnell, M. Pop, S.L. Salzberg, Bowtie: an ultrafast memory-efficient short read aligner, Genome Biol. 10 (3) (2009) R25.
[15] S. Griffiths-Jones, The microRNA registry, Nucl. Acids. Res. 32 (suppl_1) (2004) 109D–1111, doi:10.1093/nar/gkh023.
[16] M.J. Axtell, Shortstack: comprehensive annotation and quantification of small RNA genes, RNA 19 (2013) 740–751, doi:10.1261/rna.035279.112.
[17] M.I. Love, W. Huber, S. Anders, Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2, Genome Biol. 15 (12) (2014) 550, doi:10.1186/s13059-014-0550-8.
[18] Wickham, H., 2016. Elegant graphics for data analysis. 10.1007/978-3-319-24277-4