Data Article

Dataset for transcriptome analysis of abscisic acid degrading bacterium *Novosphingobium* sp. P6W

Natalia E. Gogoleva\(^a\), Tatiana A. Konnova\(^a\), Timur T. Ismailov\(^a\), Alexander S. Balkin\(^c\), Andrey A. Belimov\(^d\), Yuri V. Gogolev\(^a,b,*\)

\(^a\) Kazan Institute of Biochemistry and Biophysics, Kazan Scientific Center of RAS, 2/31 Lobachevsky St., Kazan 420111, Russian Federation
\(^b\) Institute of Fundamental Medicine and Biology, Kazan (Volga Region) Federal University, 18 Lenina St., Kazan 420021, Russian Federation
\(^c\) Center of Shared Scientific Equipment “Persistence of Microorganisms”, Institute for Cellular and Intracellular Symbiosis, Ural Branch of Russian Academy of Sciences, Orenburg, Russian Federation
\(^d\) All-Russia Research Institute for Agricultural Microbiology, 3 Sh. Podbelskogo St., Saint Petersburg 196608, Russian Federation

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**A B S T R A C T**

Plant growth-promoting rhizobacteria (PGPR) improve plant productivity and stress resistance. The mechanisms involved in plant-microbe interactions include the modulation of plant hormone status. The *Novosphingobium* sp. strain P6W was previously described as the bacterium capable of abscisic acid (ABA) degradation, and its inoculation decreased ABA concentrations in planta. The metabolic pathway for the ABA degradation in bacteria is still unknown. Here we present transcriptome data of *Novosphingobium* sp. P6W grown in the medium supplemented with ABA or fructose as the carbon source. Cleaned FASTQ files for the RNA-seq libraries are deposited in the NCBI Sequence Read Archive (SRA, Identifier: SRP189498) and have been assigned BioProject accession PRJNA529223.

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1. Data description

The dataset contains cleaned sequencing data obtained through the transcriptome sequencing of *Novosphingobium* sp. P6W grown in the medium supplemented with ABA or fructose as the sole carbon source and under carbon starvation conditions. Samples for transcriptome profiling were collected at the exponential and stationary growth phases. Cleaned FASTQ files were deposited in NCBI Sequence Read Archive and accessible through the BioProject PRJNA529223. Information about bacterial culture samples is presented in Table 1. Reads were mapped onto the reference genome sequence and the coverage data were obtained. Statistics of sequence reads and sequence coverage data are shown in Table 2. PCA plot of RNA-seq data presented in Fig. 1 demonstrates the variance between sample groups and sample replicates according to gene expression levels. Each dot in the Fig. 1 indicates particular sample.

2. Experimental design, materials, and methods

2.1. Bacterial strains and growth conditions

The *Novosphingobium* sp. P6W strain was initially isolated from the rhizosphere of rice (*Oryza sativa* L.) seedlings [1]. Complete genome sequencing for this strain was performed previously [2]. Bacterial cells were grown aerobically at 28 °C in a minimal medium (g L⁻¹: MgSO₄•7H₂O - 0.3; NH₄NO₃ - 0.5; KH₂PO₄ - 1.36; FeCl₃ - 0.002; pH 6.7) supplemented with 250 mg/L (±)-abscisic acid (Sigma) or 250 mg/L D-fructose (Sigma) as a sole carbon source.

2.2. Experiment design

To identify the genes involved in ABA metabolism, the transcriptome profiles of exponential phase cultures growing in the minimal medium supplemented with ABA or fructose were compared. To exclude genes associated with stress adaptation, samples of cultures incubated under carbon starvation conditions for 24 and 48 hours were taken as corresponding controls. It was important to obtain
information about the genes that decrease activity at the substrate depletion. For this purpose, samples of cultures grown in the ABA supplemented medium at the stationary phase were also taken.

2.3. Library construction and sequencing

Bacterial cultures were fixed with an equal volume of cold RNA-stabilizing solution (19% ethanol, 1% acidic phenol, pH 5.5) on ice for 30 minutes. Cells were harvested by centrifugation and RNA isolation was performed using RNA Extract Reagent (Evrogen, Russia) according to the manufacturer’s protocol. DNA contaminants were removed using RNase-free DNase I kit (Ambion, USA). The integrity of the RNA was checked by Agilent 2100 bioanalyzer (USA). For rRNA removal the Ribo-Zero kit for Gram-negative bacteria (Illumina, USA) was used.

NEBNext Ultra Directional RNA Library Prep Kit for Illumina was used to prepare RNA-seq libraries. The resulting average size of the cDNA libraries was approximately 300 bp. Libraries were sequenced using the Illumina HiSeq 2500 sequencing platform.

Table 1
Samples of the *Novosphingobium* sp P6W cultures.

| Sample name                      | Biological replicates | Carbone source | Duration of cultivation, hours | Culture density, OD | Accession number |
|----------------------------------|-----------------------|----------------|--------------------------------|---------------------|------------------|
| ABA exponential phase            | ABA_1                 | ABA            | 24                             | 0.23                | SRX5577386       |
|                                  | ABA_2                 | ABA            | 24                             | 0.21                | SRX5577385       |
|                                  | ABA_3                 | ABA            | 24                             | 0.21                | SRX5577384       |
|                                  | ABA_4                 | ABA            | 24                             | 0.24                | SRX5577383       |
|                                  | ABA_5                 | ABA            | 24                             | 0.21                | SRX5577391       |
|                                  | ABA_6                 | ABA            | 24                             | 0.20                | SRX5577381       |
| ABA stationary phase             | ABA_7                 | ABA            | 48                             | 0.55                | SRX5577382       |
|                                  | ABA_8                 | ABA            | 48                             | 0.51                | SRX5577380       |
| Carbon starvation exponential phase | NoCarbon_1           | absent         | 24                             | 0.13                | SRX5577387       |
| Carbon starvation stationary phase | NoCarbon_2           | absent         | 24                             | 0.10                | SRX5577392       |
| Carbon starvation exponential phase | NoCarbon_3           | absent         | 48                             | 0.16                | SRX5577379       |
| Fructose exponential phase       | Fructose_1            | fructose       | 18                             | 0.25                | SRX5577390       |
|                                  | Fructose_2            | fructose       | 18                             | 0.28                | SRX5577389       |
|                                  | Fructose_4            | fructose       | 18                             | 0.25                | SRX5577388       |

Table 2
Cleaned reads and reads mapped on reference genome.

| Library    | Number of cleaned reads | Number of reads mapped on genome | % Mapped reads |
|------------|-------------------------|----------------------------------|----------------|
| ABA_1      | 10,899,064              | 10,346,749                       | 94.93          |
| ABA_2      | 10,757,369              | 10,281,619                       | 95.58          |
| ABA_3      | 9,060,795               | 8,713,460                        | 96.17          |
| ABA_4      | 12,313,428              | 11,778,892                       | 95.66          |
| ABA_5      | 9,715,928               | 9,659,951                        | 99.42          |
| ABA_6      | 11,740,625              | 10,636,562                       | 90.60          |
| ABA_7      | 12,473,706              | 12,413,817                       | 99.52          |
| ABA_8      | 6,292,959               | 5,820,562                        | 92.49          |
| NoCarbon_1 | 9,325,126               | 9,184,277                        | 98.49          |
| NoCarbon_2 | 4,655,901               | 4,254,299                        | 91.37          |
| NoCarbon_3 | 6,234,953               | 5,123,816                        | 82.18          |
| NoCarbon_4 | 4,468,833               | 4,286,867                        | 95.93          |
| Fructose_1 | 12,282,002              | 11,014,354                       | 89.68          |
| Fructose_2 | 10,869,930              | 9,944,951                        | 91.49          |
| Fructose_4 | 12,513,546              | 10,247,348                       | 81.89          |
2.4. Sequence QC and filtering

144,262,494 reads were obtained in total with a length of 60 nucleotides (Table 1). FastQC software (Version 0.11.5) [3] was used to assess the quality of the raw Fastq files and clean reads. Raw reads were filtered using BBDuk (v. 37.23, http://jgi.doe.gov/data-and-tools/bb-tools/) to remove Illumina adapters, NEB indexes and to quality-trim right end to Q20 (ktrim = r k = 23 mink = 11 hdist = 1 tpe tbo minlen = 25 qtrim = r trimq = 20). Thereafter, the rRNA reads were eliminated by using SortMeRNA v2.1 program [4].

2.5. Reads alignment to the reference genome

The high-quality reads were mapped onto the genome sequence of the *Novosphingobium* sp. P6W strain (assembly: GCA_000876675.2) (ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/876/675/GCF_000876675.2_ASM87667v2/GCF_000876675.2_ASM87667v2_genomic.fna.gz). HISAT2 version 2.1.0 [5] was used to build index of reference genome and align clean reads to reference genome with the following parameters: hisat2 -p -dta -x -U -S. SAM files of alignments created by HISAT2 were converted to BAM files using SAM-tools view [6]. Coverage estimates and reads mapping statistics are presented in Table 2. DESeq2 [7] was used to assess variance between sample groups and sample replicates using principle component analysis (PCA). PCA plot shown in the Fig. 1 demonstrates the overall quality of our sample collection, library preparation, and sequencing.

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**Appendix A. Supplementary data**

Supplementary data to this article can be found online at https://doi.org/10.1016/j.dib.2019.105001.
Conflict of 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.

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