Data Article

Genomic data of two Greek Vitis varieties

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A R T I C L E   I N F O

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A B S T R A C T

The genetic material of Vitis varieties is crucial for the wine sector. In addition, genomic technologies applied in vitis germplasm characterization are important for the conservation of indigenous genetic reservoirs. Until recently the most common method to genetically identify vitis varieties was the use of Simple Sequence Repeats (SSR) along with SNP chips. Yet, with the progress in Next Generation Sequencing (NGS) technologies and the reduced sequencing cost per base, a twist in plant species genetic identification methods has occurred. Among them, the low coverage Whole-Genome Sequencing (lcWGS) method with downstream bioinformatic analysis for variant discovery and phylogenetic characterization is gaining scientific attention. In this dataset, shotgun sequencing data of two different Greek Vitis varieties, ‘Razaki’ and ‘Vlahiko’ are presented. Vitis cultivars were collected from the Aristotle University of Thessaloniki’s (AUTH) ampelographic collection and have been previously phenotypically and genetically characterized. WGS libraries were sequenced on an Illumina\textsuperscript{®} NovaSeq 6000 platform with the Illumina\textsuperscript{®} NovaSeq 6000 S2 Reagent Kit (300 cycles). Raw sequence data used for analysis are available in NCBI under the Sequence Read Archive (SRA), with BioProject ID PRJNA805368. Reads were aligned to the reference genome of Vitis vinifera available from the EnsemblPlants database and formal analysis was conducted with the Genome Analysis Toolkit 4 (GATK4) pipeline. Data can be used to enrich our knowledge related to the genetic background of vitis cultivars.

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and can also serve as a threshold in the scientific community towards the construction of a genomic database of vitis cultivars.

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Specifications Table

| Subject | Biological sciences: Omics: Genomics |
|---------|--------------------------------------|
| Specific subject area | Low coverage whole genome sequencing of two Greek vitis cultivars for cultivar identification and variant discovery |
| Type of data | Tables and Figures |
| How the data were acquired | WGS libraries were constructed using Illumina's Nextera DNA Flex library preparation kit. Sequencing was performed on an Illumina® NovaSeq 6000 platform using the Illumina® NovaSeq 6000 S2 Reagent Kit (300 cycles). The variant discovery was conducted using the Genome Analysis Toolkit 4 pipeline. |
| Data format | Raw and Analyzed |
| Description of data collection | Leaves from two grapevine varieties, ‘Razaki’ (white grape variety) and ‘Vlachiko’ (red grape variety), were obtained from the Ampelographic Collection of the Aristotle University of Thessaloniki. |
| Data source location | Institution: Institute of Applied Biosciences – Centre for Research and Technology Hellas |
| | City: Thessaloniki |
| | Country: Greece |
| | Latitude and longitude for analyzed data: 40.56806, 22.99713 |
| Data accessibility | Repository name: NCBI SRA |
| | Data identification number: PRJNA805368 |
| | Direct URL to data: |
| | https://www.ncbi.nlm.nih.gov/bioproject/PRJNA805368, |
| | https://www.ncbi.nlm.nih.gov/sra/?term=SRR17982062, |
| | https://www.ncbi.nlm.nih.gov/sra/?term=SRR17982063 |

Value of the Data

• Data add new knowledge on Vitis genetic variation at the level of variety.
• Data provides information on the genomic background of two Greek vitis varieties that can be used for future identification of unknown grapevine varieties.
• Viticulturists will benefit from results related to the functional characteristics of each variety through genetic selection.
• The data produced contribute to the preservation and the adoption of these vitis varieties in plant breeding schemes.

1. Data Description

Genomic sequencing data were generated with Illumina® NovaSeq 6000® platform using two paired-end libraries with insert size of approx. 300 bp. In total, 25.62 Gbases were generated with >Q30 of 98%; 12.91 Gbases for ‘Razaki’ variety and 12.71 Gbases for ‘Vlachiko’ variety (Table 1). Total coverage for each variety’s genome was greater than 25x, which is sufficient to identify single nucleotide polymorphisms (SNPs) and insertions/deletions (indels) across their genomes [1]. Raw sequencing data are available under the BioProject accession PRJNA805368 at NCBI’s sequence read archive.

The majority of the discovered variants were SNPs with approximately $5.8 \times 10^6$ events in each variety and insertions/deletions with over $900 \times 10^3$ events per variety (Table 2). These
numbers include SNPs and InDels found in unique sequences of the reference genome as well as in the repetitive genome fractions. The SNPs were primarily found in intergenic regions in contrast to the indels that were mainly found in intragenic regions causing frameshifts. Frameshift variants due to the indels are 6,847 in ‘Razaki’ and 7,024 in ‘Vlachiko’. Missense variants due to the SNPs are 119,532 in ‘Razaki’ and 126,314 in ‘Vlachiko’. SNPs and indels responsible for the gain of stop codons are 2,882 in ‘Razaki’ and 2,910 in ‘Vlachiko’. The number and the type of variants of the affected Sequence Ontologies (SO) are presented in detail in Table 3 and Fig. 1.

2. Experimental Design, Materials and Methods

2.1. Sampling and library construction

Leaf tissues were obtained from two grapevine varieties ‘Razaki’ and ‘Vlachiko’, which are a part of the Ampelographic Collection of the Aristotle University of Thessaloniki. Leaves were ground to a fine powder in the presence of liquid nitrogen and subsequently, DNA extraction was conducted using the NucleoSpin Plant II kit (MACHEREY-NAGEL, Düren, Germany), according to the manufacturer’s instructions. The quality of extracted DNA was assessed on a 0.8% agarose gel stained with 0.5 μg/ml ethidium bromide. DNA concentration was estimated by a fluorometric method on a Qubit 4.0 Fluorimeter using the Qubit® dsDNA BR assay kit (Invitrogen, Carlsbad, CA, USA).

Libraries were prepared with the Nextera DNA Flex library preparation kit following the manufacturer’s instructions for an average insert size of 300 bp. Initially, libraries were quantified with the Qubit dsDNA BR kit and their average size was estimated by capillary fragment electrophoresis on a 5400 Fragment Analyzer system (Agilent Technologies, Santa Clara, CA, USA) using the DNF-477-0500 kit. Finally, library quantification was performed by qPCR using the KAPA Library Quantification kit for Illumina® sequencing platforms (Kapa Biosystems: Roche Diagnostics Corporation, Indianapolis, IN, USA) on a Rotor-Gene Q thermocycler (Qiagen, Hilden, Germany), and normalized in relation to their size. Libraries were sequenced on an Illumina® NovaSeq 6000® platform using the NovaSeq 6000 S2 Reagent Kit (300 cycles).
Fig. 1. Heatmap of variants for ‘Razaki’ and ‘Vlachiko’ varieties. Rows depict the affected Sequence Ontologies and columns the SNPs and InDels for each variety. Color scale refers to log10((variants)+1).
Table 3
The number of variants and the affected Sequence Ontologies (SO).

| Sequence Ontologies (SO) affected | Razaki InDels | Razaki SNPs | Vlachiko InDels | Vlachiko SNPs |
|----------------------------------|---------------|-------------|----------------|---------------|
| 3_prime_UTR_truncation            | 3             | 44,682      | 2              | 0             |
| 3_prime_UTR_variant               | 10,404        | 0           | 11,375         | 48,289        |
| 5_prime_UTR_premature_start_codon_gain_variant | 0 | 3,776 | 0 | 3,889 |
| 5_prime_UTR_truncation            | 4             | 0           | 2              | 0             |
| 5_prime_UTR_variant               | 4,571         | 23,523      | 4,792          | 24,673        |
| bidirectional_gene_fusion         | 1             | 0           | 0              | 0             |
| conservative_inframe_deletion     | 786           | 0           | 794            | 0             |
| conservative_inframe_insertion    | 807           | 0           | 907            | 0             |
| disruptive_inframe_deletion       | 1,335         | 0           | 1,391          | 0             |
| disruptive_inframe_insertion      | 952           | 0           | 1,012          | 0             |
| downstream_gene_variant           | 371,034       | 1,811,783   | 386,922        | 1,906,153     |
| exon_loss_variant                 | 13            | 0           | 13             | 0             |
| frameshift_variant                | 6,847         | 0           | 7,024          | 0             |
| gene_fusion                       | 1             | 0           | 3              | 0             |
| initiator_codon_variant           | 0             | 51          | 0              | 50            |
| intergenic_region                 | 686,851       | 4,261,933   | 709,662        | 4,401,118     |
| intragenic_variant                | 5             | 0           | 0              | 0             |
| intron                            | 203,918       | 1,154,763   | 1,241,972      | 1,241,972     |
| missense_variant                  | 119,532       | 0           | 126,314        | 0             |
| non_coding_transcript_exon_variant | 968          | 122         | 1,216          | 133           |
| non_coding_transcript_variant     | 0             | 307         | 0              | 331           |
| splice_acceptor_variant           | 545           | 356         | 554            | 340           |
| splice_donor_variant              | 522           | 428         | 570            | 422           |
| splice_region_variant             | 14,691        | 3,220       | 16,125         | 3,346         |
| start_lost                        | 405           | 181         | 412            | 170           |
| start_retained_variant            | 0             | 15          | 0              | 16            |
| stop_gained                       | 2,591         | 291         | 2,628          | 282           |
| stop_lost                         | 517           | 133         | 524            | 129           |
| stop_retained_variant             | 231           | 25          | 253            | 35            |
| synonymous_variant                | 95,902        | 0           | 103,131        | 0             |
| upstream_gene_variant             | 1,973,306     | 412,606     | 2,045,032      | 423,890       |

2.2. Bioinformatics and data analysis

The quality of the reads was evaluated with the FastQC [2]. Raw reads were aligned to the reference genome of *Vitis vinifera* (12x) from EnsemblPlants (http://ftp.ensemblgenomes.org/pub/plants/release-52/fasta/vitis_vinifera/dna/) with MiniMap2 [3] and the command line options `-x sr -a -R '@R@tID:<variety>@tLB:<variety>@tPL:ILLUMINA@tPM:NOVASEQ@tSM:<variety>’ without removing duplicate reads in this step. For variant discovery, Genome Analysis Toolkit 4 (GATK4) [4] pipeline was used. In detail, the duplicates duplicate reads were marked with the *MarkDuplicatesSpark* and the variants were recalibrated with the *BaseRecalibrator* using the filtered variants. The first round of variant discovery performed with *HaploTypeCaller*. Identified variants were filtered with *VariantFiltration* in order to filter out the variants with values of QD<2.0, FS>60.0, MQ<40.0, SOR>4.0, MQRankSum<-12.5 and ReadPosRankSum<-8.0. Final variants were obtained after the filtration of technical variants with the *BaseRecalibrator* and *ApplyBSQR* tools. The annotation of the final variants was performed with *SnpEff* [5].

Ethics Statements

The authors declare that they have no known competing financial interests or personal relationships which have or could be perceived to have influenced the work reported in this article.
CRediT Author Statement

**George Tsiolas:** Methodology, Analysis, Writing and Editing **Sofia Michailidou:** Methodology, Writing, Review and Editing. **Antiope Tsoureki:** Analysis. **Anagnostis Argiriou:** Conceptualization, Review, Funding Acquisition, Project Administration.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships which have, or could be perceived to have, influenced the work reported in this article.

Data Availability

Greek Vitis (Original data) (SRA NCBI).

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