Data in Brief 41 (2022) 107938

Contents lists available at ScienceDirect

Data in Brief

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

Data Article

A durum wheat recombinant inbred line (RIL) population: Data on β-glucans, grain protein content, grain yield per spike, and heading time

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ARTICLE INFO

Article history:
Received 17 January 2022
Revised 2 February 2022
Accepted 4 February 2022
Available online 11 February 2022

Keywords:
Durum wheat
β-glucans
Grain protein content
Grain yield per spike
Heading time
QTL

ABSTRACT

Data presented are on genetic variation of quality trait and production in a recombinant inbred line (RIL) population derived from a cross between two elite durum wheat cultivars grown in two different locations (Valenzano, metropolitan city of Bari -Italy) and Policoro (metropolitan city of Matera – Italy).

The data of the two environment include: 1. β-glucan content; 2. grain protein content; 3. grain yield per spike; 4. heading time. In addition data on high-density SNP-based genetic linkage map and linkage analysis are reported.

The data in this article support and augment information presented in the research article "Development of a high-density SNP-based linkage map and detection of QTL for β-glucans, protein content, grain yield per spike and heading time in durum wheat" (Int J Mol Sci. 18(6):1329, 2017, https://doi.org/10.3390/ijms18061329).

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https://doi.org/10.1016/j.dib.2022.107938

Specifications Table

Subject	*Biological sciences*
Specific subject area	*Genetics: General* *Plant Science: General*
Type of data	Tables Graphs
How the data were acquired	Samples were hand-harvested at maturity and grain yield per spike was determined dividing grain yield per row by the number of spikes per row (about 70-80 spikes). The β-glucan (percentage w/w) content in whole grain was assayed using the Mixed-Linkage β-glucan Assay Kit (Megazyme International Ireland Ltd, Wicklow, Ireland) based on the accepted method by McCleary and Codd [1] and included the industrial standard for barley (4.1% of β-glucan). Grain protein content, expressed as a percentage of protein on a dry weight basis, was determined on a 2 g sample of whole-meal flour using InfraAlyzer spectrophotometer (near-infrared reflectance spectroscopy). Grain yield per spike (GYS) was determined dividing grain yield per row by the number of spikes per row (about 70–80 spikes). The heading time was reported as the number of days from 1 April, 2014, until the ears of ca. 50% of the tillers had emerged from the flag-leaf sheaths by approximately half of their length, corresponding to stage 55 of the Zadoks scale [2].
Data format	Analyzed Filtered
Description of data collection	A randomized complete block design was used in both field experiments (Valenzano and Policoro) with three replications and plots consisting of 1-m rows, 30 cm apart, with 80 germinating seeds per plot. During the growing season, 10 g of nitrogen per m^2 and standard cultivation practices were adopted.
Data source location	Department of Agricultural and Environmental Science, University of Bari "Aldo Moro", Via G. Amendola 165/A, 70126 Bari, Italy Locations of the durum wheat field of Valenzano (metropolitan city of Bari –Italy): lat. 41.0438° N, long. 16.8842° E, elevation 85m above sea level. Locations of the durum wheat field of Policoro (metropolitan city of Matera): lat. 40°12′45"00 N, long. 16°40′24″24 E, elevation 25 m above sea level.
Data accessibility	Repository name: Mendeley data Data identification number: DOI:10.17632/7npf76mk6k.1 Direct URL to data: https://data.mendeley.com/datasets/7npf76mk6k/1.
Related research article	I. Marcotuli, A. Gadaleta, G. Mangini, A.M. Signorile, S.A. Zacheo, A. Blanco, R. Simeone, P. Colasuonno, Development of a High-Density SNP-Based Linkage Map and Detection of QTL for β-Glucans, Protein Content, Grain Yield per Spike and Heading Time in Durum Wheat. Int. J. Mol. Sci. 18 (2017) 1329. https://doi.org/10.3390/ijms18061329

Value of the Data

- These data represent an added value to the durum wheat knowledge, which can be suitable for breeders to select the best genotypes among the RIL population for important trait and use to develop new lines.
- These data include additional information on QTL for important agronomic traits that could be useful to build new marker-assisted selection to obtain new genotypes with commercial and nutritional relevance.
- These data can be included in the group of information, which can enrich the lack of info concerning β-glucan content in relation to protein content and yield components in durum wheat.

1. Data Description

The kernel quality of wheat is important for the determination of the nutritional value of the derived end products. There is a wide variation for grain quality considering the different varieties due to the heritable genetic components, the environment and field management practices. There are interactions between genotype × environment and genotype × agronomic management, which have strong effect on phenotype [3].

Tables 1–4 showed the mean of β-glucan content, β-glucans, grain protein content, grain yield per spike, heading time, respectively, determined in three field replicates for each parent and RIL grown in two fields. Table 5 reported the 5,477 SNP markers obtained after the remotion of failed, monomorphic and missing data >10% and used for the construction of the biparental map and the performing of the linkage analysis. For each SNP, the chromosome location and position were reported.

Fig. 1 showed the number and distribution of SNP markers in the Duilio × Avonlea map.

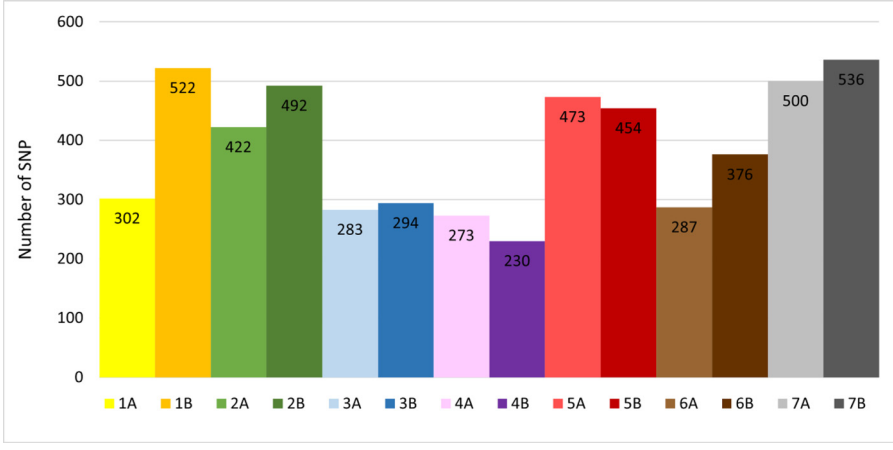

Fig. 1. Number and distribution of SNP markers in the Duilio × Avonlea map.

2. Experimental Design, Materials and Methods

2.1. RIL population

RIL population "Duilio x Avonlea" was obtained by advancing random individual F2 plants to the F7 generation by the single-seed descent procedure. The parents and the RILs were evaluated for all the traits in two replicated trials and in three different biological replication per trial.

2.2. β-glucan

Analyses of (1,3;1,4)-β-glucan in wheat were performed using the Mixed-Linkage β-Glucan Assay Kit (Megazyme International Ireland Ltd, Wicklow, Ireland) based on the accepted method McCleary and Codd [1]) and the industrial standard for barley. For each sample, 15 mg of wholemeal flour were used for the analyses. The method included two washes with 1 ml 70% ethanol at 97°C for 30 min, and a wash with 1 ml 100% ethanol followed by 30 min extraction at 90°C in 1 ml 20 mM sodium phosphate buffer (pH 6.5), 1.5h incubation at 50°C with 40 µl 50 U/ml Lichenase, and addition of 0.4 ml 200 mM acetate buffer (pH 4.0). A volume of 50 µl of each

sample was dispensed into a set of three wells of a 96 deep well Eppendorf plate, one containing 50 µl of acetate buffer and two with 50 µl 2 U/ml β-glucosidase. This was incubated for 30 min, 1.5 ml glucose oxidase-peroxidase reagent was added and an aliquot was read on a spectrophotometer ($\lambda = 510$ nm).

2.3. Grain protein content

Grain protein content, expressed as a percentage of protein on a dry weight basis, was determined on a 2g sample of whole-meal flour using near-infrared reflectance spectroscopy. The analysis is based on the interaction of infrared rays with the sample molecules. The sample, in fact, is irradiated with infrared (NIR) at a specific wavelength selected by high-precision filters. The NIR light directed towards the sample is partly absorbed and partly reflected. The reflected light is captured and measured by an internal detector: the information obtained is specific to each sample and allows to determine particularly the protein percentage and the humidity percentage for each flour. The data obtained were used to estimate the protein content on the dry matter of the sample, using the following formula:

$$\frac{\%protein}{(100 - \%humidity)} \times 100$$

2.4. Grain yield per spike

To obtain the grain yield per spike, the number of spikes were counted in a linear meter row, the seeds were trashing with a mini-harvester, taking care to keep the kernels of each line separate, and finally the grain were weighed and related to the number of spikes.

2.5. Heading time

The heading date was determined as duration of the period from sprouting to heading. For all plants, the recording of the date of heading was done subsequently as the date when 1/3 of spike appeared from the flag leaf. The number of days from the sprouting to heading date were taken as the days of heading. For each line, 15 plants were used to determine the average value of heading date.

2.6. Statistical data analysis

The mean data of 5 randomly selected plants for each genotype of the RIL and parent lines were used to determine the range of agronomic traits and the overall mean of each environment. All the collected phenological data were used to perform the ANOVA using GenStat (18th version) [4]. The genetic variance (s^2_G) and broad-sense heritability (h^2) of the traits were determined and reported for the RIL population in the main article. Linkage analysis between markers and determination of the linear order of loci was performed by JoinMap 4.0 [5] using the regression mapping algorithm. To determine the interaction between genotype and phenotype, QGene 8.3.16 was used with inclusive composite interval mapping [6]. The number and distribution of SNP markers in the Duilio × Avonlea map were used to construct the Fig. 1 using excel graphing features.

Ethics Statements

No ethics statement

CRediT Author Statement

Ilaria Marcotuli: Data curation, Software, Validation, Writing – original draft preparation; **Stefania Lucia Giove:** Data curation; **Angelica Giancaspro:** Data curation; **Agata Gadaleta:** Conceptualization, Supervision, Writing – review & editing.

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.

Data Availability

A durum wheat recombinant inbred line (RIL) population: data on β-glucans, grain protein content, grain yield per spike, and heading time (Reference data) (Mendeley Data).

Acknowledgments

Projects PRIMA 2019 “CEREALMED”; project “Attraction and International Mobility” PON-AIM1812334-1 (Ministero dell’Istruzione, dell’Università e della Ricerca, Italy)

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