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Data Article

Data of germination ability of tetraploid rice lines under multiple stress factors

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ABSTRACT

Rice production is affected by several environmental factors, such as cold, salinity and drought stress. These unfavourable factors could have a serious impact on germination as well as on later growth, causing many types of damage. Recently, polyploid breeding can offer an alternative opportunity to enhance the yield and abiotic stress tolerance in rice breeding. This article describes some germination parameters of 11 different autotetraploid breeding lines and their parental lines under different environmental stresses. Each genotype was grown in a climate chamber under controlled conditions: 13 °C for 4 weeks in the cold test and 30/25 °C for 5 days in control, salinity (150 mM NaCl) and drought (15% PEG 6000) treatments, respectively. The germination process was monitored throughout the experiment. The average data were calculated using three replicates. This dataset contains germination raw data and three calculated germination parameters, such as median germination time (MGT), final germination percentage (FGP), and germination index (GI). These data may provide reliable support to clarify whether the tetraploid lines can exceed the performance

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of their diploid parental lines under germination phase or not.

Specifications table

Subject	Agricultural Science/Agronomy and Crop Science
Specific subject area	Autotetraploid rice lines produced by androgenesis and their germination process under varied environmental stresses.
Type of data	Tables and Figures
How the data were acquired	The germination tests were carried out: **Cold test:** in a Lovibond TC 256 G thermo-statically controlled cabinet (Dortmund, Germany) for 4 weeks at 13 °C. Every week we counted the germinated seeds. **Salinity and drought test:** in a Binder Climatic/Photostability Test Chamber (KBWF 240, Germany) under 30/25 °C day/night temperature and 33.1–51 µmol/m^2/s light intensity for 5 days. The germination process was checked every 6 h. Basic mathematical analyses (mean and standard deviation) were run by Microsoft 365.
Data format	Germination raw data, and analysed (MGT, FGP and GI).
Description of data collection	Seeds of 11 different tetraploids and their parental lines (4) were germinated in controlled environments. Three replications were maintained throughout the experiment. Each replication contains 40 surface sterilised seeds.
Data source location	• Institution: Hungarian University of Agriculture and Life Sciences, Institute of Environmental Sciences, Research Centre for Irrigation and Water Management. • City/Town/Region: Szarvas • Country: Hungary • Latitude and longitude (and GPS coordinates, if possible) for collected samples/data: 46°52′16.3″N 20°31′38.6″E
Data accessibility	The data is provided in this article and Mendeley Data. Data identification number: https://data.mendeley.com/datasets/z7m5nb4krp or doi: 10.17632/z7m5nb4krp.4

Value of the Data

- This dataset provides basic knowledge and new resources for further research activities and future rice breeding. Autotetraploids can contain new mutations which may not exist in their parents' genome [1].
- The research outcome is advantageous for breeders and researchers because it provides baseline information on the tolerance properties of autopolyploid rice under germination stage. The research on polyploid rice is very up-to-date, tetraploid genetic stocks have been registered recently [2]. However, there are some unfavourable properties of tetraploids, especially low fertility, but due to the efforts of researchers, some new lines are already comparable with the diploid ones [3,4]. The importance of these germination data is considerable, because polyploids have enhanced tolerance of abiotic stress [5]. Despite this evidence, only a few papers confirmed that. Therefore, this article tries to fill this gap.
- This dataset can support other researchers in extending their analyses and making more detailed comparisons.

1. Objective

Polyploidization is one of the important ways of plant evolution. In rice, autotetraploids are discovered in 1933, but their bottleneck problem (low seed setting rate) hindered their use in breeding programs. However, it is widely accepted that poliploids have greater tolerance than diploid ones. In recent years, PMeS lines (2007) and neotetraploid rice lines (2017) with high fertility have been successively selected and opened a new prospect for polyploid rice breeding [6]. In vitro androgenesis is a reliable way to obtain polyploid lines [7]. Our aim was this study to supply baseline information about androgenesis generated tetraploids and to provide new germplasm resources for studying and breeding.

2. Data Description

The dataset presented in this article contains 5 Tables (supplemented tables). Two (Table 1 and Table 2) are raw data and the rest are derived, secondary data which were calculated from the raw data. The Table 1 provides the list of tetraploid rice genotypes with their parents and the cumulative number of germinated seeds under cold test. The Table 2 contains raw data of germination screening under control, saline and drought conditions. The number of each cell represents the cumulative number of germinated seeds from 40 surface sterilised seeds. The Table 3 represents the median germination time which shows the time necessary for the germination of 50% of the seeds (Fig. 1). Table 4 shows the final germination percentages (FGP) calculated at the end of the experiments (Fig. 2). The germination index (GI) values which combine the germination time and germination percentage, are described in Table 5, and presented in Fig. 3.

3. Experimental Design, Materials and Methods

The parental lines (Dáma - temperate japonica, Marilla - temperate japonica, IRAT 109 - tropical japonica and Nembo - temperate japonica) were chosen from the Rice Variety Collection maintained by MATE IES ÖVKI Galambos Rice Research Station (Szarvas, Hungary). The autotetrapoids were generated by in vitro anther culture in the Biotechnology Laboratory of Cereal Research Non-profit Ltd. (Szeged, Hungary [8]. The ploidy levels were determined using flow cytometric analyses. In our study, altogether 1800 seeds were investigated during the germination phase in each treatment (15 genotypes, 40 seeds in 3 replications). The germination test was carried out in Petri dishes between two layers of filter paper:

- in a Lovibond TC 256 G thermo-statically controlled cabinet for 4 weeks at 13 °C in the case of cold test.
- in a Binder KBW 240 climate chamber for 5 days at 30/25 °C temperature and 80% relative humidity in the control, salinity and drought test.

The seeds were separated in a 5% sodium chloride solution to avoid unfilled seeds. This step is important, especially in case of tetraploids, because their seed collection usually contain partially filled or deformed seeds. Afterwards, the seeds were surface sterilized with sodium hypochlorite (40 g/L) for ten minutes. The salinization was carried out with 150 mM NaCl solution (14.5 dS m^{-1}). To simulate the drought stress, 15% PEG 6000 was used. During our experiment, a seed was considered as germinated when radicle was observed as 1 mm long. The germinated seeds were counted every 7th days in the case of cold test, and every 6 h in the control, salinity and drought test. In the present study, three parameters were used to describe germination process of the selected rice varieties:

- Median germination time (MGT): time (in days) for 50% of germination [9].
- Final Germination Percentage (FGP): number of germinated seeds at the end of the experiments/total number of seeds *100

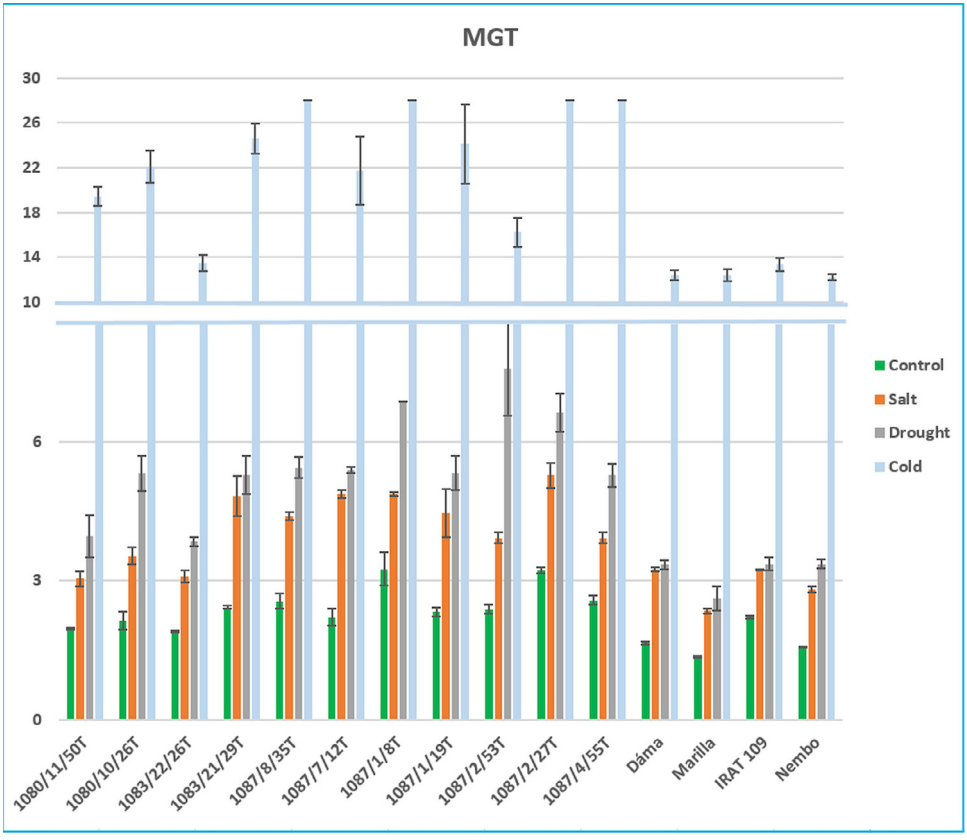

Fig. 1. Median Germination time of 15 different rice genotypes. The data show the means of three replicates.

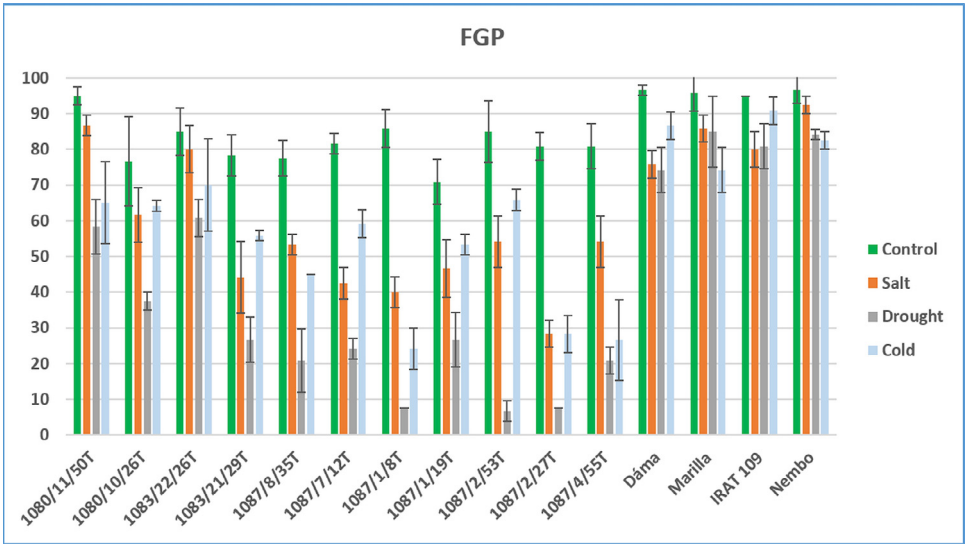

Fig. 2. The final germination percentage (%) at the end of the experiments (control, salinity, drought and cold). The data show the means of three replicates.

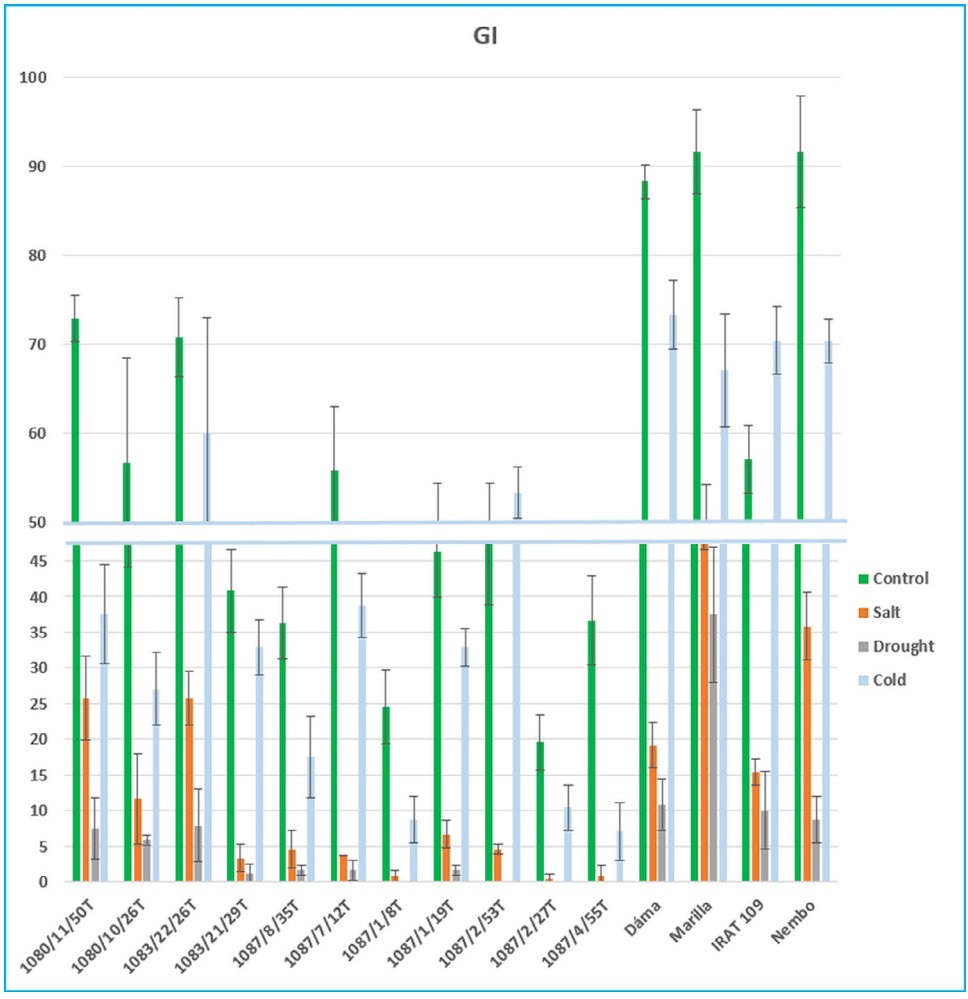

Fig. 3. The germination index (GI) of examined genotypes.

- Germination index (GI):
- Under cold conditions: GI = $(N_{14}+N_{21}/2)$ / 40 × 100, where N_{14} = number of germinated seeds 14 days after the beginning of the cold treatment; N_{21} = number of germinated seeds 21 days after the beginning of the cold treatment; 40 being the total number of seeds per genotypes per replications [10].
- Under control, salinity and drought conditions: We used modified formula of the equation above as follow: GI = $(N_2+N_3/2)$ / 40 × 100, where N_2 = number of germinated seeds 2 days after the beginning of the treatment; N_3 = number of germinated seeds 3 days after the beginning of the treatment; 40 being the total number of seeds per genotypes per replications.

Ethics statements

The authors declare that the study did not involve work with human subjects, animals experiments, or sensitive information from social media platforms.

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

Germination data of tetraploid rice lines under various environmental stresses. (Original data) (Mendeley Data).

CRediT Author Statement

Árpád Székely: Data curation, Writing – original draft, Writing – review & editing; **Tímea Szalóki:** Project administration, Investigation, Visualization, Writing – original draft; **Csaba Lantos:** Supervision, Project administration, Supervision, Writing – review & editing; **János Pauk:** Supervision, Project administration, Supervision, Writing – review & editing; **Mihály Jancsó:** Conceptualization, Methodology.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.dib.2023.109235.

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