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HISTORICAL DATA OF SOME DESCRIPTORS IN A BARLEY COLLECTION DURING THE 1957-2022 PERIOD

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Introduction

- The most valuable sources of traits useful within the breeding barley programs are genetic resources. The scarce knowledge of main descriptor characterization usually restricts the usage of accessions in breeding (Gonzalez et al., 2018) and in obtaining new varieties with desired traits to alleviate climatic changes.
- The main purpose of this paper is to assess five descriptors with high agronomical relevance during the 1957-2022 period (seed regeneration of barley *ex-situ* collection).

Material and methods

- The metadata search and retrieval from notebooks (1957 to 2022), and digital curation of some descriptors: yield (Y), specific weight (SW), lodging (Lod), protein (P), and starch content (S) from different season cycles, and geographic regions (with available longitude and latitude) were used (47 years, 5 locations, 83 experiments for spring barley and 57 years, 15 locations, 92 experiments for winter barley).
- Data were analyzed using (Table 1) Data Analysis Tool Pack MS Excel 2016 (t-test, mean, standard error, standard deviation, sample variance, kurtosis, skewness, minimum, maximum at 95% level of confidence)

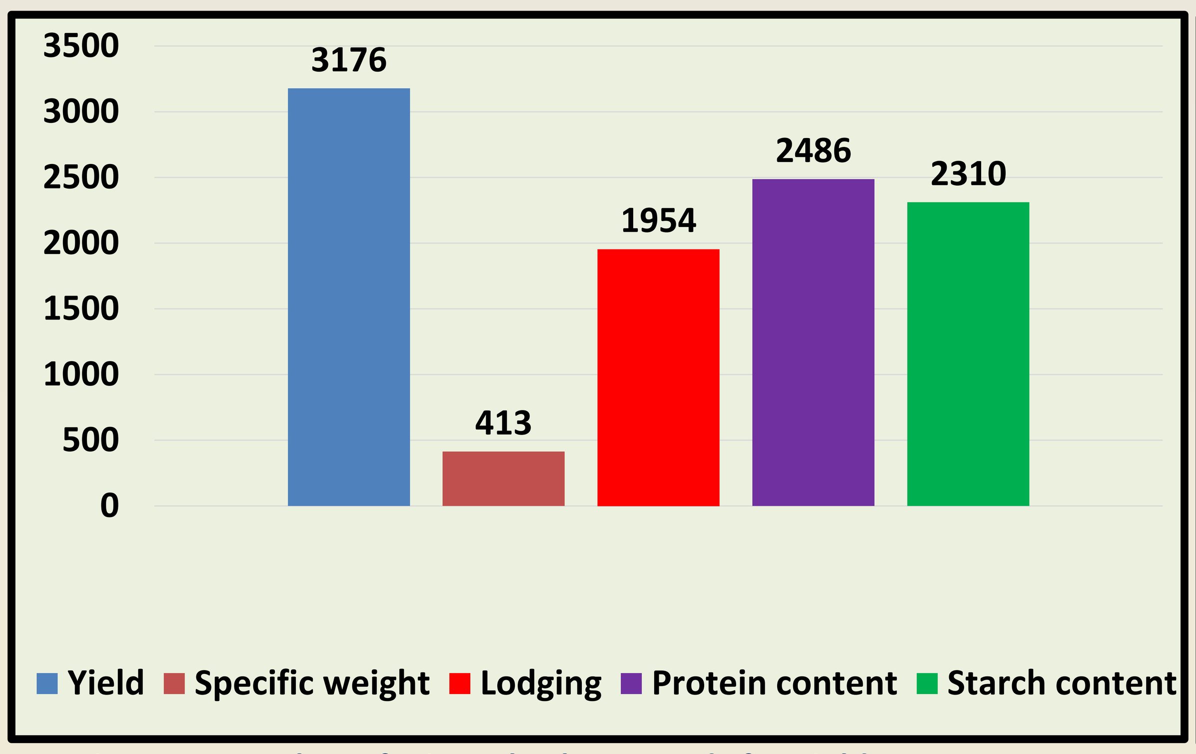

Figure 1. Number of winter barley records for yield, specific weight, lodging, protein, and starch content for the period from 1957 to 2021

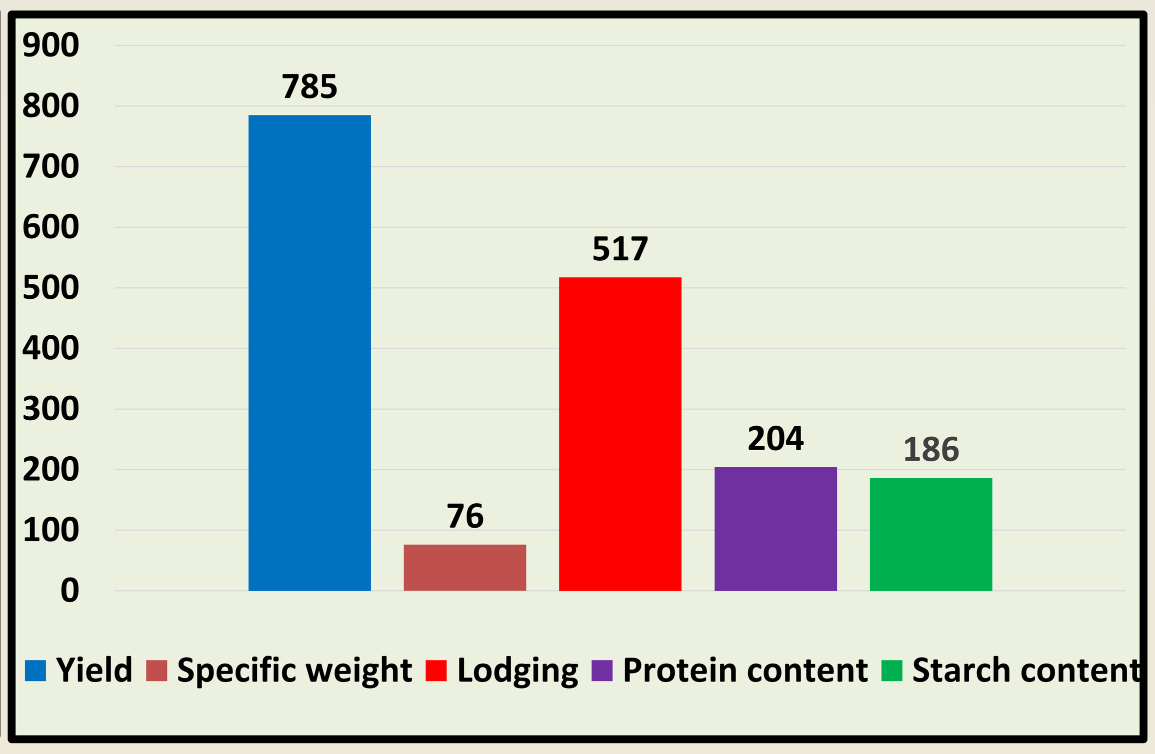

Figure 2. Number of spring barley records for yield, specific weight, lodging, protein, and starch content for the period from 1957-2022

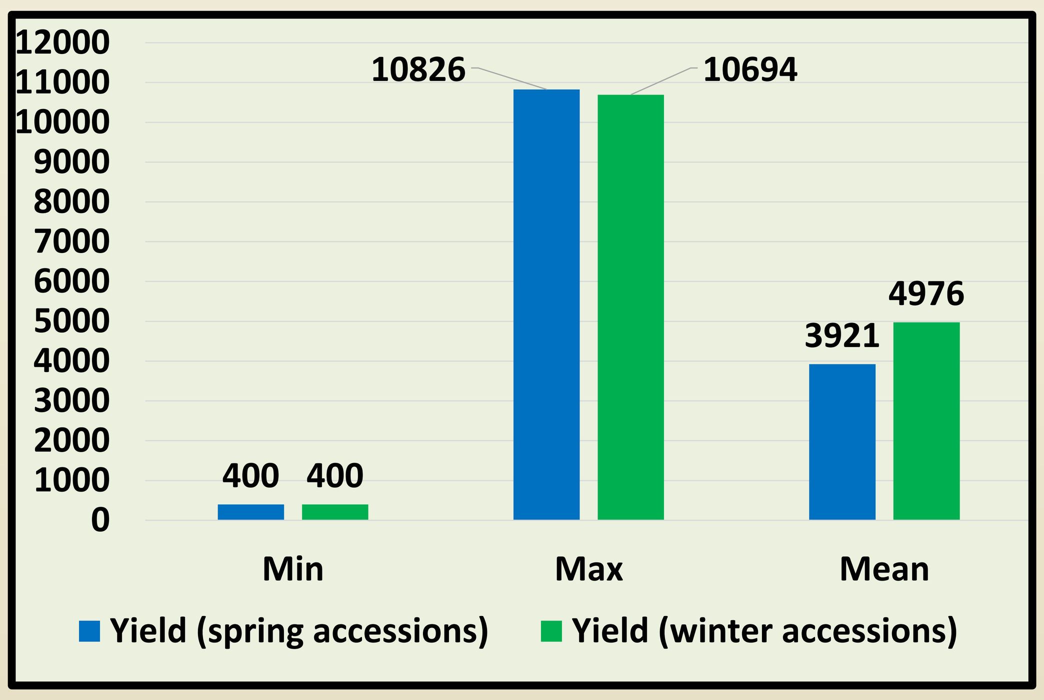

Figure 3. Spring and winter barley minim, maxim, and average values for registered yield (kg/ha), 1957-2022

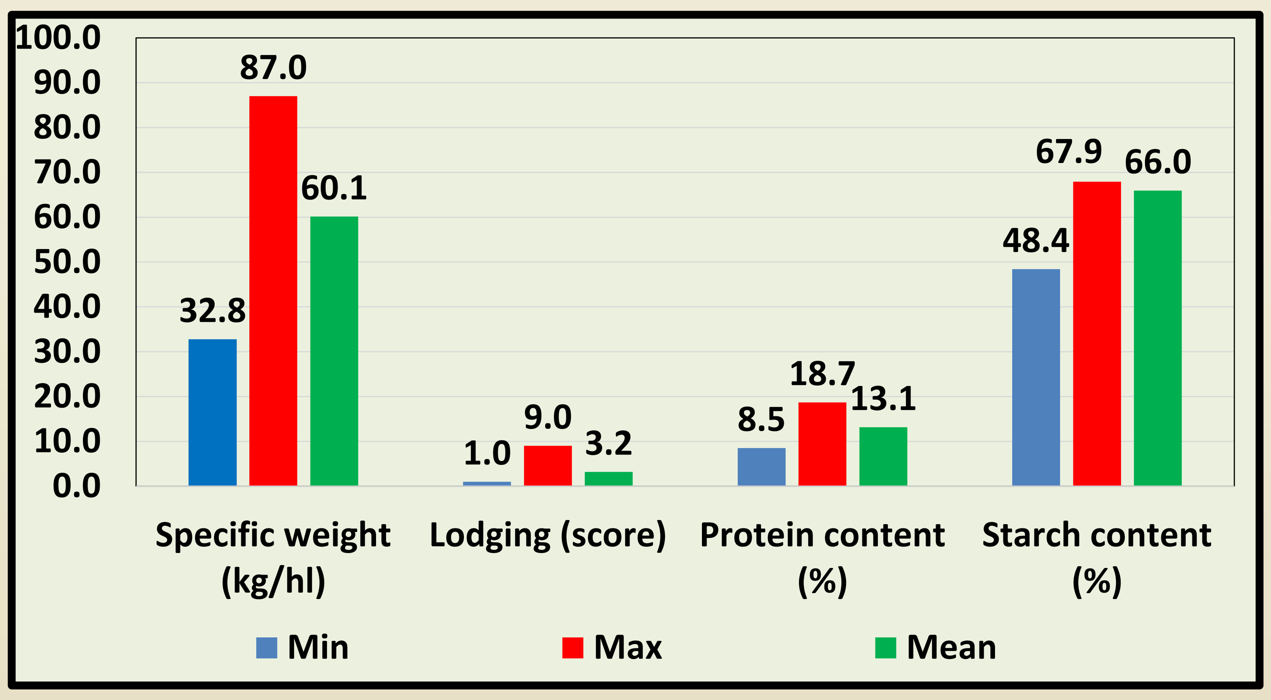

Figure 4. Minim, maxim, and average values of winter barley traits, 1957-2021

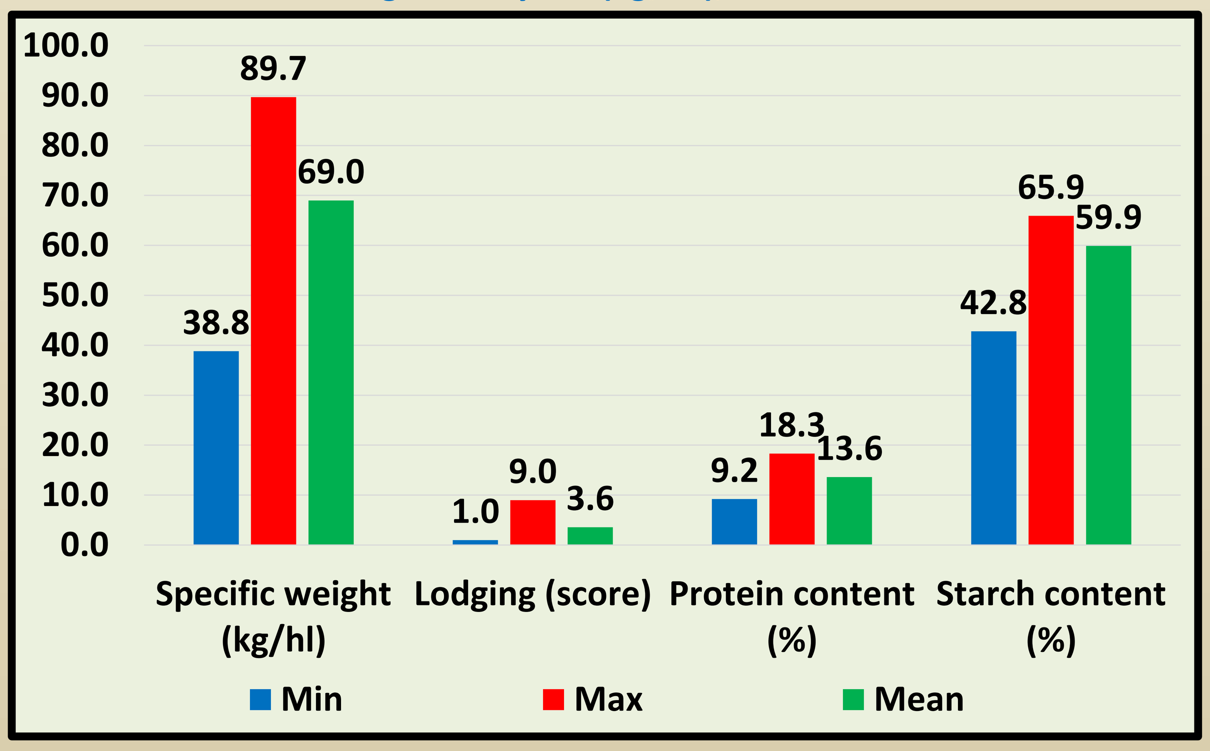

Figure 5. Minim, maxim, and average values of spring barley traits, 1957-2022

Results and discussion

- To determine whether the mean of each variable in the dataset is significantly different from the specified test value, the one-sample t-tests were conducted. For all the variables, the t-test at a 1.0% level of significance, suggests a statistically significant difference between the mean of the variables and the specified test values (p-value 0.0000).

Table 1. Descriptive statistics for the studied spring accession

Descriptors/Variables	Dry matter yield	Specific weight	Lodging	Protein content	Starch content
Mean	3921.28	69.15	3.57	13.61	59.91
Standard Error	51.52	0.91	0.10	0.15	0.26
Median	3718.00	67.60	3.00	13.90	60.52
Mode	4000.00	66.80	1.00	15.90	60.40
Standard Deviation	1443.47	7.97	2.20	2.18	3.52
Sample Variance	2083608.23	63.51	4.86	4.76	12.42
Kurtosis	1.5027	1.6763	-0.5583	-0.9863	3.2053
Skewness	0.8388	-0.4334	0.5208	-0.1964	-1.4687
Minimum	400.00	38.81	1.00	9.20	42.80
Maximum	10826.00	89.70	9.00	18.32	65.90
Count	785	76	517	204	186
Confidence Level (95.0%)	101.133	1.821	0.190	0.301	0.510

- Winter and spring barley data over 7 decades were collected and 5 descriptors were available for 1376 accessions. The accessions were characterized (Figures 1, 2, and 3) for yield (Y), lodging (Lod), specific weight (SW), protein (P), and starch content (S). Regarding the number of historical data collected in the EXCEL template, there are in total of 10339 records for winter barley accessions (3176 for Y, 413 for SW, 1954 for Lod, 2486 for P, and 2310 for S) and 1768 records for spring barley accessions (785 for Y, 76 for SW, 517 for Lod, 04 for p, and 186 for S).
- The range value (min, max, and mean) of each winter and spring barley descriptor value is presented in Figures 4 and 5.
- The obtained results underlined significant differences between winter and spring barley descriptors, especially for maximum SW value (between winter and spring the maximum difference is 2.7 units, higher for spring accessions) which can illustrate the different density packs of seed and minimum protein content (lower for winter and higher for spring) exhibiting for spring accessions a lower request of nitrogen fertilizer comparing with winter accessions.
- The mean starch content value of winter accessions showed there are a higher number of accessions with better resistance to biotic and abiotic stress and translocation of assimilates to the seeds.

Conclusions

- The data were gathered under different climatic conditions and cycles of seed regeneration so to enhance the quality of data, the outlier values have to be taken into consideration for each descriptor, approached with the Bonferroni-Holm test and computing BLUEs value for accessions in the R program.
- The phenotyping process under different climatic conditions followed by passport data digitalization of winter and spring barley genetic resources will allow a proper choice of accessions by the breeders for barley crop improvement.
- Also, these kinds of data can be used for genomic prediction to boost the utilization of barley genetic resources.

Acknowledgments

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Refferences

González, M.Y., Weise, S., Zhao, Y., Philipp, N., Arend, D., Börner, A., Oppermann, M., Graner, A., Reif, J.C., Schulthess, A.W., 2018. Unbalanced historical phenotypic data from seed regeneration of a barley (*Hordeum sp.*) *ex situ* collection. Scientific Data, 5: 180278. DOI: 10.1038/sdata.2018.278