

New knowledge in history: Evaluating seven decades of ex situ seed regeneration

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Seed multiplication of genetic resources of the Gene Bank. Credit: Christoph Martin / IPK Gatersleben

The Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben has been promoting the transition of gene banks into bio-

digital resource centres—the aim is the preparation and collation of the phenotypic and genetic information for all stored accessions. As an important step for the further development of the Federal Ex situ Gene Bank, which is being hosted by the IPK in Gatersleben, researchers have been evaluating the historical data which has been accrued by the gene bank over the last 70 years. Not only is the resulting published data an important new resource for researchers and plant breeders, the publications also provide blueprint strategies for the preparation of correlated datasets from which other gene banks and research facilities will be able to draw.

Gene banks have long outgrown their role as mere "storage facilities" of different plant accessions. With the increasing need for new and improved crop species due to [climate change](#) and the continuously growing world population, their importance as providers of novel phenotypic and genetic resources for plant breeders and researchers is becoming clearer. The steady progression of omics-technologies and the efforts of researchers worldwide have already started driving the evolution of the gene banks into the envisioned all-encompassing bio-digital resource centres. A group of scientists from the IPK in Gatersleben has been supporting the evolution of the Federal Ex situ Gene Bank by analysing the historical phenotypic data of different crops which was compiled over the last seven decades and making the data available to the public in a highly structured manner.

Analysing large amounts of phenotypic data is no small feat, considering that the gene bank hosted by the IPK with its collection of roughly 151,000 accessions counts as one of the ten largest gene banks worldwide. In addition, about 5% of the collection need to be regrown annually to regenerate the seeds. Due to this, further questions arise such as how to deal with non-orthogonal experimental designs, changes in agronomic practices or in weather patterns? And how to assess the quality of data which has been collected over such long periods of time

and with different methods? Over a series of papers, the IPK researchers led by Prof. Dr. Jochen Reif have been examining and finding solutions to these challenges.

Focusing on the agronomic traits flowering time, plant height, and thousand grain weight, the scientists developed statistical models with which they were able to leverage maximal information from the available datasets. Employing innovative approaches for data analysis (for further reading see their 2018 *Frontiers* publication), they established an outlier corrected dataset as well as ready-to-use processed phenotypic data in the form of "Best Linear Unbiased Estimations" (BLUEs). The BLUEs data now complement the passport information of a large number of accessions stored at the Gene Bank and allows the direct comparison of accessions across the different regeneration years.

The scientists had previously processed the historical data of the majority of the barley accessions stored at the Ex situ Gene Bank. A new paper, published in "*Scientific Data*", now sheds new light on the phenotypic data of 12,754 spring and winter wheat accessions whose seeds have been stored and continuously regenerated at the Gene Bank over the last 70 years.

Even though the [historical data](#) behind barley and wheat is now being prepared for further use by plant researchers and breeders, there is still plenty of phenotypic data for different accessions but also for different crops left—as well at the Federal Ex situ Gene Bank but also at the other gene banks worldwide. The data publications by the IPK researchers showcase methodologies which can be adapted for such further data evaluation-projects.

And whilst their results may stimulate new avenues for barley and wheat research and breeding, they also show how much potential and knowledge can be hidden away in seemingly dusty records—once the

correct methods to unlock the hidden data have been found.

More information: Norman Philipp et al, Historical phenotypic data from seven decades of seed regeneration in a wheat ex situ collection, *Scientific Data* (2019). [DOI: 10.1038/s41597-019-0146-y](https://doi.org/10.1038/s41597-019-0146-y)

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