

Breeding for Mass in the Arctic Winter: An Analysis to Reveal the Volumes Genetically Accumulated During Three Winter Seasons

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Received: July 03, 2025 / Accepted: August 12, 2025 / Published: Vol. 10, Issue 11, pp. 19-24, 2025

This article reports on a genetic project that started in 2020 and ended in 2025. The specific project concerning the genetic accumulation of mass is a key project included in the portfolio of the TM2020 database, which is built around the sequence of the *T. Monococcum* genome. The purpose of the DB is to benefit human cultivation of wheat and provide an incontrovertible framework for both conservation and work through its data. It is believed that the genome genetically and materialistically embodies the extent of human nature. This article aims to explain some of the findings of the project and reason concerning the elements of those findings.

The article is not the product of a group or organization and does not represent the opinions, formal or informal, of anyone other than the author and Troms Oblat, the company owned by the author.

The wheat sown to produce this winter wheat was a haploid spring wheat adapted to the conditions of Northern Norway (i.e., 69°N). The sowing took place in the middle of October, a few weeks before the onset of winter. From the beginning, it was meant to be a solely genetic experiment where the aim was to use the wheat plant as an instrument to record and genetically encode the volumes preconditioned to accumulate during three winter cycles. These data would later be analyzed and conserved through a tailored DNA or RNA sequence. The sequence was meant to be a key aspect, together with the whole-genome sequencing (WGS) of *T. Monococcum*, of the construction of a large conservational database (i.e., TM2020).

The test field was a small plot on a very characteristic headland on one of the larger islands in Troms, Northern Norway. The field is very close to the sealine and receives sunlight day and night from around June 20 to August 20. Two narrow sand piers stretch out into the sea from both sides of the cape, reaching almost

200 m into the sound. From a satellite or plane, it is possible to see sand formations stretching out several miles on the seabed, especially toward the north.

The preliminary analyses revealed significantly higher than expected expression levels for several genes identified in the project when compared with the baseline expression of other genes. A comparative analysis utilizing the single α -locus model genome of Chinese Spring identified 10 genes exhibiting significantly elevated expression levels. These findings provide critical insights into the genetic adaptations and molecular mechanisms underlying responses to extreme northern environmental conditions (Yanez, 2025).

The studied wheat is said to be the northernmost wheat ever grown. Barley was grown in the study area only a few generations ago, both for fodder and for the baking of flat breads, although the very high risk of a wheat crop failing due to the short and cold summers caused farmers to avoid growing it (Halland, Thomsen, and Dalmannsdottir, 2018). The project reported in this article coincided with the longest and hottest summers ever recorded in Northern Norway. For instance, in 2024, there were 37 days where the temperature reached 20 degrees or higher, whereas a summer in Northern Norway typically has only 10–15 days where temperatures reach 20 degrees or higher. It is unknown whether this heat is man-made or due to natural causes (Tveito and Fjørland, 2010).

The growing and marking of the field were performed in the same way as Troms Oblat has done for over 10 years. The satellite data were mapped and clocked in QGIS, while the online plotting was conducted via Mergin Maps. The company's own algorithms were used to delineate the plotted satellite data to the fields, where new custom-tailored satellite data concerning the field were added from Metop-C twice a week, year round. The growing entailed an organic process, and all the supplements used accorded with this.

With the fifth chromosome arm in mind, preparations were made in autumn 2024 to sequence the third season's wheat—that is, the final product. This wheat had been given the name Khost, since the delineation algorithms in the field plots and the initial assemblies were K-based. This name was intended to reflect a product as allusive as a ghost but with a robust and “Norsk” (Norwegian) touch. After learning that Khost is also the name of a province and a town in Afghanistan, the wheat was nearly renamed Hard What; however, it was ultimately decided to keep the name as Khost.

Novogene offered to add an mRNA analysis to the database Troms Oblat had established with the *T. Monococcum* WGS the year before. Thus, around September 15, the author traveled to Cambridge and delivered the fresh samples. Three extractions were performed on three samples, and the sample with the densest RNA and the weight with the least odd numbers was chosen for sequencing. It was determined that this

was the most suitable and precise option for the material, as well as being very cost-effective when compared with sequencing several samples. Samples from the batch were tested for starch using potassium iodine (KI) before they were packed and taken to Novogene's lab. As expected, there were compliance problems due to the polarity and amount of the data, and solving these issues took a long time. Planning and organizing the sequencing at Novogene started months in advance and received a lot of attention and extra consideration in the Cambridge lab.

After Novogene had released the raw data, the decision was made to perform a quantitative analysis of it using *Arabidopsis Thaliana* as the reference. Not only would this assembly be in line with the conservation objectives of the project but this reference would also make the later comparative analysis easier. Parallel to this, another mRNA *T. Monococcum* analysis was conducted in the same lab, again using the *Arabidopsis Thaliana* reference.

Within the frames of the project and the conservation database the material was intended for, it was natural to assume that the volumes accumulated during the winter months would exist across the coding regions of the genome. These volumes emerged from natural ongoing and cyclic processes during the winter dormancy of the harvest-sown wheat. The stored masses in the genome were likely the minutest offsets of the products of the consumption and deformation taking place in the inherent genetic structures, and they likely also represented the natural growth and expansion of the cleaved peripheral regions during the winter seasons of the genetic project. The pressures and temperatures that occurred at the growing location and the atmospheres around there were denaturalized via K and carbon (C) in the same way as polymorphic processes. This was not impacted by the logic constraints of any genetic population built up in the genome.

It can be assumed that the promotor regions are central to the invalidation of the pressures, and rather than favor allelic designs in the genome, with the sustaining of the genes and establishment of these processes, the immediate impacts of the processes will primarily reside in changes to the top nomenclature and across variants. The physical locations of the presumed mass storages within the Khost genome were realistically envisioned spatially at the uppermost part, angularly affixed to its general structure scaffolding. The delineation and denaturalization of similar types of pressures are not yet governed by logic algorithms or electromagnetic radiation. Similar to pressures arising from tectonics, temperatures, or differences in atmospheric layers, these pressures also seem to play a role in the formation of the genomes of other model organisms (Wang et al., 2025). A very important example is the Chengdu wheat strain Chinese Spring, which is a sub-Himalayan strain that originates from just beneath the Tibetan Plateau and has factors unique to the

Sichuan Basin and its geological conditions, contributing to the features of the model genome Chinese Spring. Likewise, the Indian Punjabi strains are catalyzed by conditions similar to those of Chinese Spring, making the Punjab one of the most efficient wheat-producing areas of the world (Sardar and Bilar, 2023).

In short, there are many indicators that these pressures and volumes, when in a unresolved state, are important, especially to encoding the wheat genome (Ofria, Adami, and Collier, 2003). The assumption of volumes being accumulated during the winter and encoded in the genome is not only born from intuition but also from well-grounded knowledge and analytical information regarding the wheat genome and the human cultivation of wheat. The same is true concerning the notion of its resolvability through genomic decoding and the logical algorithms assembled inside the genome—that is, as part of a medication or via natural diffusion.

This project did not seek to measure the volumes exactly or to pinpoint the locations in the genome. These may be more appropriate tasks for a bioinformatician or someone working in another framework, as well as for after proper genetical conservation measurements have been taken. This is important to ensure that prior to blasting the data via massive computational analyses, the genome's natural proof condition is conserved and submitted to the DB. This would serve to secure both optimal computational reproducibility and precise genetical accession for future utilization (Sawchuk and Khair, 2021).

The projection of what was assumed would happen under the right conditions, in the right location, and given the right framework of underlying genetics and length of time has objectioned itself properly, rendering it more than adequate to be conserved in the database. From this DB, the Khost genome could be accessioned with the purpose of strengthening the biodiverse original co-ordinate landraces of lower altitudes, and it would also very likely benefit the already high-yielding hybrid strains to be crossed or modified with genes from Khost, stabilizing the strain's traits and thereby improving the health and overall quality of the plant.

The library linked to the logic algorithms of the genome is self-supported within the TM2020 DB. This makes working with the Khost genome easier when compared with strains that are not self-supported in a library. It practically feathers itself in; in particular, the K contours and K-outlined structures of the material will appear to be more accessible for rearrangement and distribution inside the library frame. In this case, the frame has been determined to be a haploid winter wheat manipulation of the K uptake and transport within the plant is a realistic approach to improving the K uptake efficiency, meaning that genetic improvements to acquire this are urgently required (Wang and Wu, 2015). The structuring processes of the volumes, as previously mentioned, contribute to a more detailed library. If it is believed that genes exist as natural elements from creation, it would be reasonable to determine that the strain library would favor the coding of storage over

the direct formation and sustainment of genes.

The keywords used for interpretation and differentiation in the analyses of the genetic mass storage were as follows:

A-mass: Dense, translated, allelic number within the range of the genome, constraining.

B-mass: Open, untranslated, library, provisioning.

A-arithmetic.

B-magnetic.

A link between the mechanic strain of this specific grain and the genetic isoforms is also quite possible, suggesting a finite and transportable form of self-deployable wheat mass. The wheat mass is the chalky and doughy substance found inside the wheat kernel. It is produced by the spike, claimed by the plant, and reclaimed by its genetics. If the masses affixed to it are said to be something other than inanimate entanglements with different origins, they must have common base-level compositions besides the molecular size and hydrodynamic radius. They must be encoded fully from the onset of deposition, either by the plant or by the genome of the plant.

In all cases, the genomic project was meant to run for three years of growth, with sowing in the autumn of one year and harvesting in the autumn of the next year. Then, the adapted F3 offspring were to be sequenced and analyzed.

There were some indications that the project was successful in capturing evidence that the accumulation and encoding of these volumes actually happened. These indications were based on alleged bioinformatic observations of this from a totally different part of the world. It was also a matter of belief and conviction. Most importantly, however, it was a human translation of a very probable natural construction created by more than one of the individual factors present.

This project was the first time that wheat had been grown so far north, and it was also the first time spring wheat used for developing the winter variety was grown for three seasons in the same location before the winter wheat project started. Hence, this project was the very first introduction of wheat to the polar region, except for the *T. Monococcum* wheat, which has been grown in the region for over a decade. The deterministic effects of growing wheat in this new territory for the first time would also make the hypothesis even more probable than if it was only a genetic prediction concerning a random production series grown in the same location and under the same conditions. The issue here is more likely to be whether the genetic material can be used outside its own growth zone or not. This project concluded that it can, and preliminary independent

analyses of the RNA sequence also revealed very exciting and promising results. The Khost genome can strengthen already high-yielding strains both molecularly and genetically, and it can also be used outside the database in the nascent technology of genetic library construction.

The Khost strain continued after the genetic project concluded, with the F4 batch from 2025 grown as cover for prior batches. The warmer climate makes it possible to grow wheat at such a latitude during a warm summer season and it is important to start developing strains that are adapted to Arctic growth conditions so that this resource can be explored for future far north grain production. The Khost project will, in addition to introducing new and important material for use in quantitative and conservation genetics and serving as a key aspect of the construction of the TM2020 database, continue to play a role in developing northern agronomics.

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