# **The USDA-ARS Hemp Germplasm Repository**

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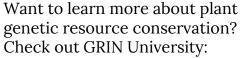
The hemp germplasm collection plays a crucial role in safeguarding biodiversity, supporting research, and ensuring the availability of genetic material for breeding programs, agriculture, and conservation efforts. There are currently 581 accessions housed in Geneva, NY.



A diversity of hemp seeds included in the germplasm repository: https://npgsweb.ars-grin.gov/gringlobal/search

# How hemp germplasm is collected, stored, and distributed:

- 1. Hemp materials are received from all over the world. Highly-detailed metadata is collected on all materials received and imputed into GRIN Global as "passport information".
- 2. Seeds are dried at 4°C for 6 weeks. They are then packaged into envelopes and stored in a -20 °C cold room for long-term storage.
- 3. Germplasm is regenerated for 4-5 months indoors to make new seeds with the intent of preserving the allelic diversity of each population.
- 4. New seeds are evaluated for many traits including fiber quality, seed oil quality, pathogen resistance, cannabinoids, and more in a highly collaborative way. Germplasm is screened for regulatory compliance (less than 0.3% THC). These traits are linked to the accessions within the GRIN global website.
- 5. Researchers and breeders can go online to GRIN Global and add material to their shopping cart. Seeds can be mailed anywhere in the world to be used for research projects for free.







An interview with Zachary Stansell, the hemp germplasm curator and research geneticist at the National Plant Germplasm System. Zach says the Geneva, NY hemp collection is "both a challenge and an opportunity".



## What is the purpose of including feral hemp and landraces in the collection?

Crop wild relatives have much greater genetic diversity than the crops themselves which have undergone selection pressure throughout the years. To the best of our knowledge, we don't know of any crop wild relatives for hemp. However, it is possible to find landraces that have undergone far less selection pressure. Additionally, feral populations, many from the American Midwest, have promise of segregating for interesting traits and may be a secondary source of diversity.

# Because hemp lacks much of the historical context associated with other crops, how do you plan to develop rich datasets?

A lot of the previous work in germplasm collections is pre-genomics era. Now we have an opportunity to start things with a blank slate and utilize advanced technology and methodologies. This spring, we plan to do long-read whole genome sequencing on every accession in our collection. From GRIN Global, folks will be able to find seeds with a phenotype of interest, click a button, and download its genome. This is unheard of in genebank work.

#### How is genetic purity maintained within each population of seeds?

One of our major goals is to increase our throughput so we can regenerate more accessions faster while maintaining genetic purity. When we receive seeds, we often don't have information on whether the seeds are from a highly-inbred line or if they are from a population that is segregating for specific traits. Therefore, I incorporate as many individuals as possible into the regeneration process. Hemp is wind-pollinated and typically dioecious, so we can't regenerate it outdoors like we would with insect-pollinated seed crops. In addition to building more growth chambers, we are beginning to invent "hemp huts", outdoor structures that can exclude pollen.

### Do you have any other big goals for the hemp germplasm collection?

I am very interested in creating a core collection that will allow us to best capture hemp genetic diversity with the fewest number of accessions. Each member of the core collection will be as genetically-distinct from one another as possible. The offspring from core collection-derived inbred lines can be used to map numerous traits. This will allow researchers to draw from a much larger pool of genetic diversity in hemp with confidence.