

U.S. Submission of views and information on “Digital Sequence Information” on Plant Genetic Resources for Food and Agriculture

Terminology used

The United States recognizes that there is not a common understanding of the term “digital sequence information” on plant genetic resources for food and agriculture. We understand “DSI” on PGRFA to refer to the genetic sequence data (GSD) that describe the order of nucleotides in DNA or RNA in genetic material of plant origin of actual or potential value for food and agriculture. We therefore use the term GSD instead of DSI in our response, and suggest the Governing Body use the more precise and broadly understood term going forward.

We note that GSD are neither genetic material nor a genetic resource. It is essential to maintain a conceptual and definitional distinction between genetic material itself and data associated with that material.

Uses of GSD describing PGRFA and implications for the Treaty’s objectives

Use of GSD directly contributes to all three objectives of the International Treaty on Plant Genetic Resources for Food and Agriculture (the Treaty). Researchers around the world rely on GSD describing PGRFA as an essential tool for advancing scientific knowledge and technological innovation. The use and exchange of GSD describing PGRFA are critical for efforts to improve crop productivity and resilience, which are essential for ending hunger and poverty around the world and achieving shared development goals. Any move to unreasonably restrict or impede access to and use of GSD on PGRFA could slow or halt such basic and applied research. Such moves could have serious, adverse consequences for the conservation and sustainable use of PGRFA, economic development, and food security, and indeed for the feasibility of conducting any research related to PGRFA, in the public or private sectors.

Broadly speaking, researchers depend upon GSD describing PGRFA to (1) define, distinguish, and identify plant populations, (2) characterize genetic diversity within and between plant populations, and (3) better understand plant traits of interest. All of these uses can inform decisions related to the conservation, management and use of PGRFA in a manner that promotes food security and economic development.

GSD can be used to define, distinguish, and identify plant populations of interest based on genetic sequence signatures. Therefore, researchers rely on GSD to distinguish between plant populations that may seem identical in appearance, behavior, and other properties but are genetically distinct. This is especially relevant for advancing the conservation of PGRFA. For example, crop genebanks look at differences in diagnostic nucleotide sequences to identify unknown samples, maintain these samples genetically true-to-type, and choose the best samples for specific research or breeding purposes.

In addition to defining specific distinct populations, researchers use GSD describing PGRFA to establish the degree of genetic divergence and diversity within and between populations.

Understanding and quantifying diversity within a population is essential for adaptation; researchers can use GSD to determine whether a population has the ability to adapt to environmental changes, contributing to the development of resilient production systems. For example, new modeling tools developed under the Feed the Future Applied Wheat Genomics Innovation Lab, a U.S. government collaborative research program involving researchers in Pakistan, India, Bangladesh and Nepal, are using GSD, along with rainfall and soil information, to improve the precision of selecting candidate wheat varieties across South Asia. This program also demonstrates the contribution of GSD, and other information, to benefit-sharing. By harnessing these shared data, countries are able focus precious resources on the specific wheat varieties most likely to work in their production environments.

Knowledge of the genetic diversity within and between plant populations is also useful for maintaining and leveraging genetic diversity in collections, and reducing undesired inbreeding, both of which are important for selective breeding and conservation activities like cryopreservation. In plant breeding, knowledge of genetic interrelationships of parental lines is a prerequisite for success, especially for producing hybrids of maize, sorghum, sunflowers, and other vegetable and fruit crops. Hybrid vigor in these crops results in yield and product quality that substantially exceed those of non-hybrid plants. The availability of GSD and other descriptive information make PGRFA more useful for research and breeding.

Researchers also use GSD describing PGRFA to study traits of interest in agricultural production, such as disease resistance, product quality, production efficiency, and resilience to extreme conditions. GSD can advance discovery and development of new crop varieties, with enhanced outcomes for food security.

GSD describing PGRFA are incorporated extensively in crop development, especially for breeding drought- and pest-resistant crops and crops with enhanced nutritional and economic value. Access to GSD has enabled researchers to rapidly identify markers for genes associated with drought tolerance and other important traits in sorghum, maize, wheat and other crops. Scientists are also applying GSD to breed beans that cook more quickly, which could reduce fuel use and therefore economic and environmental costs associated with preparing this food staple in low and middle income countries. Researchers can use GSD describing PGRFA to accelerate the progress of genetically improving dietary staples, enabling productivity and quality gains that underpin food security by allowing for the production of more abundant, high-quality food.

As described above, GSD describing PGRFA contribute to the achievement of the Treaty's objectives of conservation and sustainable use. GSD describing PGRFA also contributes to the achievement of the fair and equitable sharing of benefits arising from the use of PGRFA. The generation and exchange of data and information associated with PGRFA are important modes of benefit-sharing, and the Treaty explicitly recognizes exchange of information as a mechanism for benefit-sharing (Article 13.2). Article 17 further sets out that Parties will cooperate to develop a global information system to facilitate information exchange "with the expectation that such exchange of information will contribute to the sharing of benefits" (Article 17.1). The Treaty also states that available non-confidential descriptive information associated with PGRFA should be made available with materials provided through the Multilateral System, subject to applicable law (Article 12.3 c). Any action to restrict the

exchange and use of publicly available GSD and other information associated with PGRFA potentially hinders achievement of the Treaty's objectives.

As part of research best-practices, GSD are routinely made openly available via international data repositories such as GenBank and the International Nucleotide Sequence Database Collaboration, as well as in journals found in print and online. Additionally, scientists make large amounts of GSD freely available through sector and species specific online databases, such as the Genome Database for Rosaceae (link: <https://www.rosaceae.org/>), Gramene (link: <http://www.gramene.org/>), GrainGenes (link: <https://wheat.pw.usda.gov/GG3/>), and SoyBase (link: <https://www.soybase.org/>), to name a few.

These repositories and journals further engender collaboration by providing a free flow of GSD describing PGRFA to both researchers and to the general public. Open access and collaboration are key benefits of the use of GSD describing PGRFA. Regulations that would restrict or preclude access to and sharing of GSD describing PGRFA would likely lead to a significant reduction in data sharing through these and other such mechanisms, stifle innovation, slow agricultural research and development, and impede responses to crises affecting crop production, with negative impacts for global food security.