

## Submission of views and other information on “Digital sequence information”

### **Terminology used**

The term Digital Sequence Information has been widely used by Parties to the Treaty and CBD to describe certain data generated from activities aimed at understanding the molecular genetics of organisms. As such it is widely acknowledged that it has limitations (‘information’ is too broad, ‘sequence’ is very context dependent and whilst ‘digital’ is intended to distinguish such data from the physical resource, it too could have a number of interpretations; for example would digital images be included?). Furthermore, the ITPGRFA’s Global Information System already uses the phrase ‘Digital Object Identifier’ to catalogue physical PGRFA and facilitate access and benefit sharing. The CBD has stated that DSI should be used as a ‘placeholder’ phrase until broad agreement is reached on a more accurate term and associated definition (see decision COP13/16 and COP14/20). The WHO has adopted ‘Genetic Sequence Data’ as an alternative to DSI and some Parties to the ITPGRFA have expressed a preference for this phrase and associated acronym. The UK would be open to adopting such a phrase but recognises the importance of a science-based process to inform any multi-lateral decision.

### **Actors involved with DSI on PGRFA;**

All universities, institutes, companies and other organisations investigating the genetics of plants in the UK probably use DSI to a greater or lesser extent. Below are listed a few key users of DSI in the UK, with a particular focus on genebanks and genetic improvement. The crop Genetic Improvement Networks (GINs) are significant users of DSI, for the identification of new sources of resistance to pests and diseases as well as new sources of tolerance to abiotic stress (eg drought, water logging, nutrient deficiency etc)

- The Pea Genebank and Pulse Crop Genetic Improvement Network (PCGIN) at the John Innes Centre
- The Vegetable Genebank and Vegetable Genetic Improvement Network (VeGIN) at Warwick University
- The Oilseed Rape Genetic Improvement Network (OREGIN) at the University of York
- The Wheat Genetic Improvement Network (WGIN) at Rothamsted Research
- The National Fruit Collection at Brogdale
- The Genetic Resources Unit at John Innes Centre
- The Earlham Institute
- National Institute for Agricultural Botany
- The Millenium Seed Bank at Kew (Wakehurst Place)

### **Types and extent of uses of DSI on PGRFA**

In pre-breeding research, large scale manipulations of DSI data are undertaken using bioinformatics programmes. A multitude of genomics technologies have been developed which use DSI for understanding gene function and genetically characterising individual plants and populations towards the genetic improvement of

crop species (eg TILLING, Genome Wide Association Studies, Genotyping By Sequencing, Marker Assisted Selection, QTL mapping, KASP markers, multiplex PCR, qPCR, associative transcriptomics, exome/promotome capture, AgRenSeq and so on). These methodologies are routinely applied for capturing the genetic potential of the UK's genebanks and are fundamental to the UK's crop Genetic Improvement Networks (GINs)

In the UK, commercial breeders use DSI to assist the generation of higher yielding varieties. Publically funded research in the UK (such as the GINs) however is directed at producing crops which are resilient to food security threats such as pests, diseases and the weather. In the case of pulse crops, research is also aimed at improving seed quality, in an attempt to encourage greater adoption by growers within the arable rotation. The maintenance of the pre-breeding pipeline for these resilience traits is essential for the long term security, productivity and sustainability of the arable sector. In acknowledgement of this fact commercial breeders are key stakeholders working closely with the publically funded GINs to ensure end-user needs are met.

There is widespread recognition within the international research community that it would be useful to work towards harmonised bioinformatics systems, interoperable platforms and shared ontologies for the storage and sharing of DSI. Examples of initiatives that seek to achieve this include BrAPI, Germinate 3, DivSeek, Crop Trust, SeedStor, CIAT etc.

Whilst some developing countries may not have the resources available to generate and apply DSI for the conservation and improvement of native crop species, the UK, and other Parties to the Treaty, have substantial overseas development programmes (for example the UK's Global Challenges Research fund and the Darwin initiative) which foster the collaborations necessary to help in this area. The sharing of DSI is a vital component of these activities for the co-development of genetic maps and markers and the publication of scientific papers leading to advances in crop conservation and improvement.

### **Relevance of DSI on PGRFA for food security and nutrition**

The storage, sharing, characterisation and analysis of Digital Sequence Information (DSI) is a critical element of pre-breeding activities leading to the genetic improvement of crop species. Significant R&D investments are made worldwide in this area, to develop crops which are resistant to pests and diseases, more efficient at using nutrients, and better able to withstand extreme weather. This capability is becoming increasingly important in order to develop crops that continue to survive and perform in the increasingly unpredictable climatic extremes that the world is experiencing as a result of climate change.

Furthermore, part II of the Treaty outlines a number of specific activities in which DSI can play an important role. For example Article 5.1 paragraph a) mentions taking inventory and assessing the status and degree of variation associated with PGR, whilst paragraphs e) and f) describe the need for characterization, evaluation, and

monitoring the genetic integrity of collections. DSI can be employed to assist with these pursuits.

Recently three of the UK GINs (PCGIN, OREGIN and VeGIN) have begun to consider whether there may also be significant genetic potential within their germplasm collections to address issues related to nutritional density, commodity processing and shelf life of fresh produce.