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### Mobilizing Crop Biodiversity

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**Title: Mobilizing Crop Biodiversity**

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1 Over the past 70 years, the world has witnessed extraordinary growth in crop productivity, enabled by a  
2 suite of technological advances, including higher yielding crop varieties, improved farm management,  
3 synthetic agrochemicals, and agricultural mechanization. While this “Green Revolution” intensified crop  
4 production, and is credited with reducing famine and malnutrition, its benefits were accompanied by  
5 several undesirable collateral effects (Pingali, 2012). These include a narrowing of agricultural  
6 biodiversity, stemming from increased monoculture and greater reliance on a smaller number of crops and  
7 crop varieties for the majority of our calories. This reduction in diversity has created vulnerabilities to  
8 pest and disease epidemics, climate variation, and ultimately to human health (Harlan, 1972).

9 The value of crop diversity has long been recognized (Vavilov, 1992). A global system of genebanks (e.g.  
10 [www.genebanks.org/genebanks/](http://www.genebanks.org/genebanks/)) was established in the 1970s to preserve the abundant genetic variation  
11 found in traditional “landrace” varieties of crops and in crop wild relatives (Harlan, 1972). While  
12 preserving crop variation is a critical first step, the time has come to make use of this variation to breed  
13 more resilient crops. The DivSeek International Network (<https://divseekintl.org/>) is a scientific, not-for-  
14 profit organization that aims to accelerate such efforts.

15

#### 16 **Crop diversity: value, barriers to use, and mitigation strategies**

17 There are >1750 national and international genebanks worldwide. They house ~7 million crop germplasm  
18 accessions (<http://www.fao.org/3/i1500e/i1500e00.htm>), including samples of diverse natural  
19 populations, with many more managed *in situ*. These accessions arguably represent one of humanity’s  
20 greatest treasures, as they contain genetic variation that can be harnessed to create better tasting, higher  
21 yielding, disease/pest resistant, and climate resilient cultivars that require fewer agricultural inputs (Figure  
22 1).

23 Unfortunately, most genebank accessions are poorly characterized, and few have been utilized in  
24 breeding. Yet when a serious effort has been made to search genebanks for traits of interest, the effort has  
25 been highly rewarded. Examples include the discovery of a submergence-tolerant landrace used to breed  
26 new, high-yielding, submergence-tolerant rice varieties currently grown on tens of millions of acres  
27 (Mackill et al., 2012) and durable resistance to late blight, a devastating pathogen of potato, derived from  
28 a wild relative (Bernal-Galeano, 2020). Given the high value of the genetic diversity found in crop wild  
29 relatives and traditional landraces, why are these genetic resources not more widely employed in breeding  
30 programs?

31 One reason for the limited use of genebank holdings is the paucity of information about them, which  
32 increases the time, expense, and risk associated with mining genebank diversity. To address this

33 deficiency, we support the development of digital catalogs that provide essential information about the  
34 genetic composition, phenotypic diversity and phylogenetic relationships of genebank holdings, along  
35 with traditional passport data, images of whole plant morphology, growth habit, physiological data  
36 showing response to biotic/abiotic stress, nutrient profiles, and other information where available. Some  
37 genebanks have already begun building catalogs of their collections to improve the efficiency of  
38 genebank management, as well as to permit users to pre-screen for traits of interest, thereby facilitating  
39 variety development (König et al., 2020).

40 Another challenge to widespread use of genebank materials is the nature of genetic variation itself. Exotic  
41 germplasm often contains valuable cryptic variation, which is revealed only after crosses have been made  
42 with cultivated and elite breeding lines (Tanksley and McCouch, 1997). For example, wild populations  
43 frequently carry alleles that increase seed/ fruit/ tuber size or disease resistance when introduced into  
44 cultivars, but these are often masked by genes with opposing effects. Also, some traits that look  
45 promising in wild or landrace populations may not be expressed in adapted genetic backgrounds due to  
46 quantitative inheritance.

47 In addition, strategies are needed to overcome crossing barriers and to ameliorate the impacts of genetic  
48 material that is inadvertently introduced into cultivars along with traits/alleles of interest (i.e. linkage  
49 drag). Even when crosses are successful, specific chromosomal segments may fail to introgress if they  
50 underlie hybrid incompatibilities or experience reduced recombination, further exacerbating linkage drag  
51 (Canady et al., 2006). Lastly, traits and alleles introgressed from wild germplasm may exhibit incomplete  
52 penetrance or unexpected epistatic interactions, forfeiting expected gains from introgressions (Lippman et  
53 al., 2007).

54 Sorting through the myriad combinations of alleles generated in wild x elite crosses requires a systematic  
55 approach if it is to be productive. The use of structured populations, appropriate experimental designs,  
56 and effective use of reference varieties in combination with cost-effective genotyping, high throughput  
57 phenotyping, automated data capture and appropriate analyses make it possible to link genotype with  
58 phenotype, identify valuable haplotypes, drive recombination, and make predictions about offspring  
59 phenotypes. Techniques that enhance recombination and mitigate crossability barriers offer additional  
60 means for accessing diversity from divergent wild relatives while reducing linkage drag (Fernandes et al.,  
61 2018).

62 To address these challenges, we encourage communities of researchers to undertake systematic pre-  
63 breeding efforts to generate recombinant populations of introgressed lines in adapted cultivated  
64 backgrounds, evaluate them in diverse environments, and share the lines and associated information with  
65 breeders, farmers, researchers, and policy makers. The long time horizon and uncertainties associated

66 with “pre-breeding” often impede investment from private breeding programs. Therefore, we urge  
67 increased investment from foundations and the public sector to support such efforts across major crop  
68 families, expanding on recent efforts by the Global Crop Diversity Trust, CGIAR, and other  
69 organizations. As products of pre-competitive research, pre-bred lines could be deposited into genetic  
70 stock centers and made available to both public and private breeding programs with explicit procedures to  
71 fulfill access and benefit sharing obligations (see below).

72 An alternative approach to pre-breeding involves the use of genome editing, which can be used to re-  
73 introduce favorable alleles from wild and exotic relatives into crop plants, purge deleterious alleles, break  
74 linkage drag, or create new alleles designed to enhance plant performance and resilience (Johnsson et al.,  
75 2019; Zsögön et al., 2018). This approach allows researchers to explore natural variation as a key to  
76 resilience, and its application rests on a deep knowledge of the genetics and evolution of key traits and  
77 alleles. The use of genome editing also introduces a need for community discussion about regulatory  
78 requirements and international agreements to address the complex political, social, legal and economic  
79 concerns surrounding the use of this technology (Lassoued et al., 2019).

80 Lastly, national and international policies related to benefit sharing derived from the use of plant genetic  
81 resources impact how such resources and associated information are collected, stored, shared, studied,  
82 and used, creating additional obstacles to research and the utilization of crop diversity (Marden 2018;  
83 McCouch et al., 2013). The International Treaty for Plant Genetic Resources in Food and Agriculture  
84 facilitates multi-lateral access to plant genetic resources under mutually agreed-upon terms. It currently  
85 covers 64 crops, but ambiguity regarding benefit-sharing requirements impedes the use of genebank  
86 holdings by many plant breeders, researchers, and farmers (Sherman and Henry, 2020). There also are  
87 concerns that the benefit sharing provisions of the Treaty conflict with the long-accepted practice of  
88 providing open access to genetic sequence data (Marden 2018). In our view, open sharing of information  
89 about plant genetic resources, represents an essential form of benefit-sharing and provides a critical  
90 foundation for capacity building strategies that help address UN sustainable development goals. It is  
91 important that those employing genomic and phenomic information for crop research and breeding are  
92 fully aware of international treaties and comply with their requirements.

### 93 **Mission of DivSeek International Network**

94 The DivSeek International Network is a global, community-driven organization that facilitates the  
95 generation, integration and sharing of information related to plant genetic resources, thereby empowering  
96 genebank managers, researchers, breeders, and farmers to more effectively utilize genetic variation for  
97 research, accelerated crop improvement, and sustainable production. DivSeek comprises ~65 members  
98 from >30 countries, and includes a broad array of academic and research institutions, government

99 agencies, and inter-governmental organizations (<https://divseekintl.org/members/>). To help achieve its  
100 goals, DivSeek has established several Working Groups to engage members and assist them in addressing  
101 issues of importance to the DivSeek Community. The activities undertaken by DivSeek's three current  
102 Working Groups are summarized below.

103 *Genomics for Plant Genetic Resources:* DivSeek supports open-source genomic-assisted germplasm  
104 management and breeding, which represents a decentralized form of empowerment for genebanks and  
105 national breeding programs (Santantonio et al., 2020). Similar to the revolution in information technology  
106 that invented the internet and put cell phones in the hands of people throughout the world, open-source  
107 genomics tools, strategies and datasets are being developed and shared internationally. The tools provide  
108 data and information to support decisions about germplasm management and variety development, and  
109 the use and iterative improvement of these tools by communities of practice has the power to accelerate  
110 the deployment of crop diversity in farmers' fields, helping to address several of the UN's Sustainable  
111 Development Goals.

112 *Phenomics, ontologies and standards:* DivSeek promotes the use of new technologies for quantitative  
113 phenotypic evaluation of plant genetic resources across a network of test environments, and the  
114 application of community-based standards, ontologies and data management practices that help make data  
115 findable, accessible, interoperable and reusable (FAIR) (Pommier et al., 2019). Utilizing efficient and  
116 affordable technologies will be key to engaging genebanks and plant breeders in modern phenomics-  
117 based screening (Mir et al., 2019). Integration of diverse datasets boosts the power of global efforts to  
118 document phenotypic variation found in both genebank accessions and in breeding populations (Roitsch  
119 et al., 2019), and can greatly improve the accuracy of predictions about plant performance across  
120 environments. This is especially critical for accelerating the breeding of climate-resilient varieties in  
121 vulnerable environments.

122 *International Policies:* DivSeek aims to help members of the international plant community to understand  
123 the legal and policy framework for sharing information about plant genetic resources, lead discussions  
124 about the technological requirements for data-sharing across constituencies, and share perspectives on  
125 benefit sharing practices that are aligned with international treaties. All international agreements  
126 governing the utilization of plant genetic resources share the same basic objectives: conservation and  
127 sustainable use of resources, ease of access to them, and fair and equitable sharing of benefits derived  
128 from their use (<https://www.cbd.int/>; <http://www.fao.org/plant-treaty/en/>). However, rapid technological  
129 developments are changing the way scientists explore, utilize, and exchange information about plant  
130 genetic resources, creating new value for the information itself, and new opportunities for access and  
131 benefit-sharing, while at the same time challenging existing agreements (Marden 2018). In particular, new



132 breeding techniques that can take advantage of genomic and phenotypic data without accessing physical  
133 germplasm have led to a debate about open access to sequence data and the best ways to implement  
134 benefit-sharing requirements (Laird et al., 2020).

135

### 136 **Call for Global Participation**

137 International collaborative partnerships are essential for addressing global challenges, ranging from  
138 climate change to the control of pests and diseases to the conservation of biodiversity. DivSeek represents  
139 one such global partnership, focusing on the characterization and utilization of agricultural biodiversity  
140 and its impact on food and nutritional security.

141 The success of DivSeek will depend on attracting a broad coalition of members, observers, and  
142 stakeholders dedicated to discussion and constructive exchange of ideas, perspectives, and expertise. We  
143 are pleased to invite the global agricultural science community to join the DivSeek International Network,  
144 either as members or observers (<https://divseekintl.org/apply-to-join/>). By joining forces, we can mobilize  
145 the value of crop diversity to sustainably improve yields in farmers' fields and ensure that the benefits of  
146 our efforts are equitably distributed across the globe.

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Figure 1. Sunflower pre-bred line containing introgressions from wild *Helianthus annuus* performing well in drought stress trial in Uganda. Pre-bred lines developed by Greg Baute and Loren Rieseberg at the University of British Columbia. Drought stress trial performed by Walter Anyanga, National Semi-Arid Resources Research Institute, Uganda. Photo Credit: Walter Anyanga.





