



UNIVERSITÀ POLITECNICA DELLE MARCHE
Repository ISTITUZIONALE

Mobilizing Crop Biodiversity

This is the peer reviewed version of the following article:

Original

Mobilizing Crop Biodiversity / Mccouch, S.; Navabi, Z. K.; Abberton, M.; Anglin, N. L.; Barbieri, R. L.; Baum, M.; Bett, K.; Booker, H.; Brown, G. L.; Bryan, G. J.; Cattivelli, L.; Charest, D.; Eversole, K.; Freitas, M.; Ghamkhar, K.; Grattipaglia, D.; Henry, R.; Valadares Inglis, M. C.; Islam, T.; Kehel, Z.; Kersey, P. J.; King, G. J.; Kresovich, S.; Marden, E.; Mayes, S.; Ndjiondjiop, M. N.; Nguyen, H. T.; Paiva, S. R.; Papa, R.; Phillips, P. W. B.; Rasheed, A.; Richards, C.; Rouard, M.; Amstalden Sampaio, M. J.; Scholz, U.; Shaw, P. D.; Sherman, B.; Staton, S. E.; Stein, N.; Svensson, J.; Tester, M.; Montenegro Valls, J. F.; Varshney, R.; Visscher, S.; von Wettberg, E.; Waugh, R.; Wenzl, P.; Bieseberg, L. H. - In: MOLECULAR PLANT. - ISSN 1674-2052. - 13:10(2020), pp. 1341-1344. [10.1016/j.molp.2020.08.011]

Publisher:

Published

DOI:10.1016/j.molp.2020.08.011

Terms of use:

The terms and conditions for the reuse of this version of the manuscript are specified in the publishing policy. The use of copyrighted works requires the consent of the rights' holder (author or publisher). Works made available under a Creative Commons license or a Publisher's custom-made license can be used according to the terms and conditions contained therein. See editor's website for further information and terms and conditions.

This item was downloaded from IRIS Università Politecnica delle Marche (<https://iris.univpm.it>). When citing, please refer to the published version.

note finali coverage

(Article begins on next page)

Title: Mobilizing Crop Biodiversity

Authors: Susan McCouch¹, Katy Navabi^{2,34}, Michael Abberton³, Noelle L Anglin⁴, Rosa Lia Barbieri⁵, Michael Baum⁶, Kirsten Bett⁷, Helen Booker⁸, Gerald L Brown⁹, Glenn J Bryan¹⁰, Luigi Cattivelli¹¹, David Charest¹², Kellye Eversole¹³, Marcelo Freitas⁵, Kioumars Ghamkhar¹⁴, Dario Grattapaglia⁵, Robert Henry¹⁵, Maria Cleria Valadares Inglis⁵, Tofazzal Islam¹⁶, Zakaria Kehel⁷, Paul J Kersey¹⁷, Stephen Kresovich¹⁸, Emily Marden¹⁹, Sean Mayes²⁰, Marie Noelle Ndjiondjop²¹, Henry T Nguyen²², Samuel Paiva⁵, Roberto Papa²³, Peter W B Phillips²⁴, Awais Rasheed²⁵, Christopher Richards²⁶, Mathieu Rouard²⁷, Maria Jose Amstalden Sampaio⁵, Uwe Scholz²⁸, Paul D Shaw¹⁰, Brad Sherman²⁹, S Evan Staton³⁰, Nils Stein²⁸, Jan Svensson³¹, Mark Tester³², Jose Francisco Montenegro Valls⁵, Rajeev Varshney³³, Stephen Visscher³⁴, Eric von Wettberg³⁵, Robbie Waugh¹⁰, Peter W B Wenzl³⁶, Loren H. Rieseberg*³⁰

Affiliations:

1 Plant Breeding and Genetics, School of Integrated Plant Sciences, Cornell University, Ithaca, NY, 14853, USA

2 DivSeek, Global Institute for Food Security, 110 Gymnasium Place, University of Saskatchewan, Saskatoon, SK, S7N 0W9, Canada

3 International Institute of Tropical Agriculture (IITA), PMB 5320, Oyo Rd, Ibadan, Nigeria

4 International Potato Center (CIP) 1895 Avenida La Molina, Lima Peru 12, Lima 15023, Peru

5 Embrapa Genetic Resources and Biotechnology, Parque Estação Biológica, Final Av W5 Norte, Caixa Postal 02372, 70770-917 - Brasília DF, Brazil

6 International Center for Agricultural Research in the Dry Areas (ICARDA), Station Exp. INRA-Quich. Rue Hafiane Cherkaoui. Agdal. Rabat – Instituts, 10111, Rabat, Morocco

7 University of Saskatchewan, 51 Campus Dr., Saskatoon, SK S7N 5A8, Canada

8 University of Guelph, Rm 316, Crop Science Bldg, 50 Stone Rd E, Guelph, ON, N1G 2W1, Canada

9 Genome Prairie, 111 Research Drive, Suite 101, Saskatoon, SK, S7N 3R2, Canada

10 The James Hutton Institute, Errol Road, Invergowrie, Dundee, DD2 5DA, UK

11 CREA, Research Centre for Genomics and Bioinformatics, via San Protaso 302, Fiorenzuola d'Arda, 29017, Italy

12 Genome British Columbia, 400-575 West 8th Avenue, Vancouver, BC, V5Z 0C4, Canada

13 International Wheat Genome Sequencing Consortium 2841 NE Marywood Ct, Lee's Summit, MO, 64086, USA

14 AgResearch Forage, Science, Grasslands Research Centre, AgResearch, Palmerston North, 4410, New Zealand

15 Queensland Alliance for Agriculture and Food Innovation, Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Brisbane, QLD, 4072, Australia

- 16 Institute of Biotechnology and Genetic Engineering (IBGE), Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur 1706, Bangladesh
- 17 Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3AE, UK
- 18 Feed the Future Lab for Crop Improvement, 431 Weill Hall, Cornell University, Ithaca, NY, 14853, USA
- 19 University of British Columbia, 3083 Alma St, Vancouver, BC, V6R 3S9, Canada
- 20 Crops For the Future (UK) CIC 76-80 Baddow Road, Chelmsford, Essex, CM2 7PJ, UK
- 21 Africa Rice Center (AfricaRice), Mbe Research Station, Bouaké, 01 BP 2511 Bouaké, Côte d'Ivoire
- 22 University of Missouri, Division of Plant Sciences, 25 Agriculture Lab Bldg, College of Agriculture, Food and Natural Resources, University of Missouri, Columbia, MO 65211, USA
- 23 Università Politecnica delle Marche, Via Brece Bianche, 60131, Ancona, Italy
- 24 Johnson Shoyama Graduate School of Public Policy, University of Saskatchewan, 101 Diefenbaker Place, Saskatoon, S7N 5B8, Canada
- 25 CIMMYT-China office, Beijing 100081, Beijing, P.R. China
- 26 USDA-ARS National Laboratory for Genetic Resources Preservation, 1111 South Mason St, Fort Collins, CO, 80521, USA
- 27 Bioversity International, Parc Scientifique Agropolis II, 34397, Montpellier, Cedex 5, France
- 28 Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Corrensstr. 3, D-06466 Stadt Seeland, Germany
- 29 Law School, University of Queensland, St Lucia, QLD, 4072, Australia
- 30 Department of Botany and Biodiversity Research Centre, University of British Columbia, Vancouver, BC, V6R 2A5, Canada
- 31 NordGen, Smedjevagen 3, 230 53 Alnarp, Sweden
- 32 King Abdullah University of Science & Technology (KAUST), Thuwal, 23955-6900, Saudi Arabia
- 33 International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru - 502 324, Telangana State, India
- 34 Global Institute for Food Security, 110 Gymnasium Place, University of Saskatchewan, Saskatoon, SK, S7N 4J8, Canada
- 35 University of Vermont, 63 Carrigan Drive, Jeffords Hall, Burlington, VT, 05405, USA
- 36 Centro Internacional de Agricultura Tropical (CIAT), Km 17 Recta Cali-Palmira, 763537 Cali, Colombia
- * Correspondence: Loren H. Rieseberg,

Contact Information: lriesebe@mail.ubc.ca

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/) 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.

References

Bernal-Galeano V, N.G., Ellis D, Anglin NL, Hareau G, Smale M, Jamora N, Alwang J, Pradel W. (2020). The effect of Andean potato diversity conserved in the International Potato Center genebank helps develop agriculture in Uganda: the example of Victoria. *Food Security Journal*, <https://doi.org/10.1007/s12571-020-01037-8>

Canady, M.A., Ji, Y., and Chetelat, R.T. (2006). Homeologous recombination in *Solanum lycopersicoides* introgression lines of cultivated tomato. *Genetics* 174:1775–1788.

Fernandes, J.B., Séguéla-Arnaud, M., Larchevêque, C., Lloyd, A.H., and Mercier, R. (2018). Unleashing meiotic crossovers in hybrid plants. *Proceedings of the National Academy of Sciences USA* 115:2431-2436.

Harlan, J.R. (1972). Genetics of Disaster. *Journal of Environmental Quality* 1:212-215.

Johnsson, M., Gaynor, R.C., Jenko, J., Gorjanc, G., de Koning, D.-J., and Hickey, J.M. (2019). Removal of alleles by genome editing (RAGE) against deleterious load. *Genetics Selection Evolution* 51:14.

König, P., Beier, S., Basterrechea, M., Schüler, D., Arend, D., Mascher, M., Stein, N., Scholz, U., and Lange, M. (2020). BRIDGE - A visual analytics web tool for barley genebank genomics. *Frontiers in Plant Science* 11:701-701.

- Laird, S., Wynberg, R., Rourke, M., Humphries, F., Muller, M.R., and Lawson, C. (2020). Rethink the expansion of access and benefit sharing. *Science* 367:1200.
- Lassoued, R., Macall, D.M., Smyth, S.J., Phillips, P.W.B., and Hessel, H. (2019). Risk and safety considerations of genome edited crops: Expert opinion. *Current Research in Biotechnology* 1:11-21.
- Lippman, Z.B., Semel, Y., and Zamir, D. (2007). An integrated view of quantitative trait variation using tomato interspecific introgression lines. *Current Opinion in Genetics & Development* 17:545-552.
- Mackill, D.J., Ismail, A.M., Singh, U.S., Labios, R.V., and Paris, T.R. (2012). Development and rapid adoption of submergence-tolerant (Sub1) rice varieties. *Advances in Agronomy* 115:299-352.
- Marden, E. (2018). International agreements may impact genomic technologies. *Nature Plants* 4:2-4.
- McCouch, S., Baute, G.J., Bradeen, J., Bramel, P., Bretting, P.K., Buckler, E., Burke, J.M., Charest, D., Cloutier, S., Cole, G., et al. (2013). Feeding the future. *Nature* 499:23-24.
- Mir, R.R., Reynolds, M., Pinto, F., Khan, M.A., and Bhat, M.A. (2019). High-throughput phenotyping for crop improvement in the genomics era. *Plant Science* 282:60-72.
- Pingali, P.L. (2012). Green Revolution: Impacts, limits, and the path ahead. *Proceedings of the National Academy of Sciences USA* 109:12302-12308.
- Pommier, C., Michotey, C., Cornut, G., Roumet, P., Duchêne, E., Flores, R., Lebreton, A., Alaux, M., Durand, S., Kimmel, E., et al. (2019). Applying FAIR principles to plant phenotypic data management in GnpIS. *Plant Phenomics* 2019:1671403.
- Sherman, B., and Henry, R.J. (2020). The Nagoya Protocol and historical collections of plants. *Nature Plants* 6:430.
- Tanksley, S.D., and McCouch, S.R. (1997). Seed banks and molecular maps: unlocking genetic potential from the wild. *Science* 277:1063-1066.
- Vavilov, N.I. (1992). *Origin and geography of cultivated plants*. New York, NY, USA: Cambridge University Press.
- Zsögön, A., Cermak, T., Naves, E., Notini, M., Edel, K., Weinl, S., Freschi, L., Voytas, D., Kudla, J., and Peres, L. (2018). *De novo* domestication of wild tomato using genome editing. *Nature Biotechnology* 36:1211–1216.

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.



