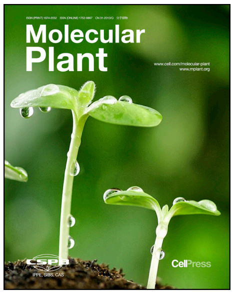

Mobilizing Crop Biodiversity

Susan McCouch, Katy Navabi, Michael Abberton, Noelle L. Anglin, Rosa Lia Barbieri, Michael Baum, Kirsten Bett, Helen Booker, Gerald L. Brown, Glenn J. Bryan, Luigi Cattivelli, David Charest, Kellye Eversole, Marcelo Freitas, Kioumars Ghamkhar, Dario Grattapaglia, Robert Henry, Maria Cleria Valadares Inglis, Tofazzal Islam, Zakaria Kehel, Paul J. Kersey, Stephen Kresovich, Emily Marden, Sean Mayes, Marie Noelle Ndjiondjop, Henry T. Nguyen, Samuel Paiva, Roberto Papa, Peter W.B. Phillips, Awais Rasheed, Christopher Richards, Mathieu Rouard, Maria Jose Amstalden Sampaio, Uwe Scholz, Paul D. Shaw, Brad Sherman, S Evan Staton, Nils Stein, Jan Svensson, Mark Tester, Jose Francisco Montenegro Valls, Rajeev Varshney, Stephen Visscher, Eric von Wettberg, Robbie Waugh, Peter W.B. Wenzl, Loren H. Rieseberg

PII: S1674-2052(20)30267-7
DOI: https://doi.org/10.1016/j.molp.2020.08.011
Reference: MOLP 984

To appear in: *MOLECULAR PLANT*
Accepted Date: 19 August 2020

Please cite this article as: **McCouch S., Navabi 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., Grattapaglia D., Henry R., Valadares Inglis M.C., Islam T., Kehel Z., Kersey P.J, Kresovich S., Marden E., Mayes S., Ndjiondjop M.N., Nguyen H.T, Paiva S., 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.W.B, and Rieseberg L.H.** (2020). Mobilizing Crop Biodiversity. Mol. Plant. doi: https://doi.org/10.1016/j.molp.2020.08.011.

Title: Mobilizing Crop Biodiversity

Authors: Susan McCouch[1], Katy Navabi[2, 34], Michael Abberton[3], Noelle L Anglin[4], Rosa Lia Barbieri[5], Michael Baum[6], Kirsten Bett[7], Helen Booker[8], Gerald L Brown[9], Glenn J Bryan[10], Luigi Cattivelli[11], David Charest[12], Kellye Eversole[13], Marcelo Freitas[5], Kioumars Ghamkhar[14], Dario Grattapaglia[5], Robert Henry[15], Maria Cleria Valadares Inglis[5], Tofazzal Islam[16], Zakaria Kehel[7], Paul J Kersey[17], Stephen Kresovich[18], Emily Marden[19], Sean Mayes[20], Marie Noelle Ndjiondjop[21], Henry T Nguyen[22], Samuel Paiva[5], Roberto Papa[23], Peter W B Phillips[24], Awais Rasheed[25], Christopher Richards[26], Mathieu Rouard[27], Maria Jose Amstalden Sampaio[5], Uwe Scholz[28], Paul D Shaw[10], Brad Sherman[29], S Evan Staton[30], Nils Stein[28], Jan Svensson[31], Mark Tester[32], Jose Francisco Montenegro Valls[5], Rajeev Varshney[33], Stephen Visscher[34], Eric von Wettberg[35], Robbie Waugh[10], Peter W B Wenzl[36], 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 Brecce 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

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

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

Crop diversity: value, barriers to use, and mitigation strategies

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

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

One reason for the limited use of genebank holdings is the paucity of information about them, which increases the time, expense, and risk associated with mining genebank diversity. To address this deficiency, we support the development of digital catalogs that provide essential information about the genetic composition, phenotypic diversity and phylogenetic relationships of genebank holdings, along with traditional passport data, images of whole plant morphology, growth habit, physiological data showing response to biotic/abiotic stress, nutrient profiles, and other information where available. Some genebanks have already begun building catalogs of their collections to improve the efficiency of genebank management, as well as to permit users to pre-screen for traits of interest, thereby facilitating variety development (König et al., 2020).

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

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

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

To address these challenges, we encourage communities of researchers to undertake systematic pre-breeding efforts to generate recombinant populations of introgressed lines in adapted cultivated backgrounds, evaluate them in diverse environments, and share the lines and associated information with breeders, farmers, researchers, and policy makers. The long time horizon and uncertainties associated with "pre-breeding" often impede investment from private breeding programs. Therefore, we urge increased investment from foundations and the public sector to support such efforts across major crop families, expanding on recent efforts by the Global Crop Diversity Trust, CGIAR, and other organizations. As products of pre-competitive research, pre-bred lines could be deposited into genetic stock centers and made available to both public and private breeding programs with explicit procedures to fulfill access and benefit sharing obligations (see below).

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

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

Mission of DivSeek International Network

The DivSeek International Network is a global, community-driven organization that facilitates the generation, integration and sharing of information related to plant genetic resources, thereby empowering genebank managers, researchers, breeders, and farmers to more effectively utilize genetic variation for research, accelerated crop improvement, and sustainable production. DivSeek comprises ~65 members from >30 countries, and includes a broad array of academic and research institutions, government agencies, and inter-governmental organizations (https://divseekintl.org/members/). To help achieve its goals, DivSeek has established several Working Groups to engage members and assist them in addressing issues of importance to the DivSeek Community. The activities undertaken by DivSeek's three current Working Groups are summarized below.

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

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

International Policies: DivSeek aims to help members of the international plant community to understand the legal and policy framework for sharing information about plant genetic resources, lead discussions about the technological requirements for data-sharing across constituencies, and share perspectives on benefit sharing practices that are aligned with international treaties. All international agreements governing the utilization of plant genetic resources share the same basic objectives: conservation and sustainable use of resources, ease of access to them, and fair and equitable sharing of benefits derived from their use (https://www.cbd.int/; http://www.fao.org/plant-treaty/en/). However, rapid technological developments are changing the way scientists explore, utilize, and exchange information about plant genetic resources, creating new value for the information itself, and new opportunities for access and benefit-sharing, while at the same time challenging existing agreements (Marden 2018). In particular, new breeding techniques that can take advantage of genomic and phenotypic data without accessing physical germplasm have led to a debate about open access to sequence data and the best ways to implement benefit-sharing requirements (Laird et al., 2020).

Call for Global Participation

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

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

147

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.