

Brachypodium Resources

Brachypodium distachyon is a small annual grass that researchers use as a model for the grasses used to produce biomass, food, feed and forage. Unlike the grasses grown as crops, *B. distachyon* is well suited to experimental manipulation in the laboratory because of its small size, compact genome, diploid nature, self compatibility, rapid generation time and simple growth requirements. In addition, numerous resources and methods (e.g. complete genome sequence, high efficiency transformation, large collections of natural accessions, many sequenced accessions and several RIL populations) are available that allow researchers to apply a suite of modern research methods to understand the unique aspects of grass biology. [See here for a review of *B. distachyon* as a model system.](#)

In addition to *B. distachyon*, other species in the genus are being used to study polyploidy (*B. hybridum* and *B. stacei*) and perenniability (*B. sylvaticum*).

Below are links to announcements and experimental resources and background information. If you have suggestions, [please contact us](#).



Chemical and radiation mutants.

[Announcements \(updated 5-25-2023\)](#)

Let us know if you have an announcement

The 5th International Brachypodium Conference (IBC 2023) will be held on July 10-13, 2023 in Hammamet, Tunisia. More information can be found at the conference [website](#).

The 2022 virtual international Brachypodium meeting was held from June 14th-16th 2022.

Reference genomes for the polyploid *Brachypodium hybridum* and *Brachypodium stacei*, one of its diploid progenitors, have been published along with additional genomes that enabled a [pan-genomic analysis of polyploid genome evolution](#). All genomes are now freely available on Phytozome.

The 4th International Brachypodium Conference that was held in Huesca, Spain from June 25-28, 2019 was a resounding success. The program is still available on the meeting [website](#). In addition, a virtual special edition featuring 11 papers describing advances presented at the conference has been published in New Phytologist. An accompanying [commentary](#) provides an overview of the papers. Approximately 2 million SNP mutations are now searchable on Phytozome. Look in [jbrowse](#) on the Bd21-3 reference genome.

The pan-genome of *B. distachyon* has been published in Nature Communications and is available [online](#).

[BrachyPan](#), a pan-genome website is now available to download and interrogate 54 *de novo* assemblies that were used to create a *B. distachyon* pan-genome.

Resources and methods

T-DNA mutants

[A collection of 23,649 T-DNA mutants is available.](#)

Chemical and radiation mutants

A CSP project [“Creating a genome-wide sequence-indexed collection of grass mutants”](#) to sequence populations of EMS, fast neutron and sodium azide *B. distachyon* mutants was initiated in 2015. This project is a collaboration with researchers in France (Richard Sibout, INRA, IJPB) and the United States (Debbie Laudencia-Chingcuanco, USDA-ARS, WRRC). To date, **approximately 2 million mutations from 2,000 lines have been identified and are available as a [jbrowse track](#) on the Bd21-3 reference genome on Phytozome**. If you would like to be involved in the screening or characterizing of this collection, [please contact us](#).

Reference genomes

An extremely high quality reference genome for *B. distachyon* Bd21 is available on [Phytozome 12](#). Details of this highly [improved assembly](#) are available on Phytozome.

Additional reference genomes are available on Phytozome for [*B. distachyon* Bd21-3](#) (parent of mutant populations), [*B. distachyon* Bd1-1](#), [*B. distachyon* Bd30-1](#), [*B. stacei*](#), the allotetraploid [*B. hybridum*](#) and the perennial [*B. sylvaticum*](#).

Germplasm

A large collection of inbred lines from geographically diverse locations has been established. A large collection of lines from Turkey are described in “[Development of SSR markers and analysis of diversity in Turkish populations of *Brachypodium distachyon*](#)” and “[Molecular, Morphological, and Cytological analysis of diverse *B. distachyon* inbred lines](#)”. Most of the Turkish lines can be ordered from the [National Plant Germplasm System](#). Many lines have been also been [collected from Spain](#).

[Garvin lab stocks including RIL populations](#).

Pan-genome and resequenced lines

A *B. distachyon* pan-genome created from 54 *de novo* assemblies has been [published](#) and is available from the [BrachyPan](#) website. An additional 65 lines have been sequenced and assembled and will be available shortly. [Download this spreadsheet for a complete list of sequenced lines and their status](#).

Protocols

Transformation:

[Current Vogel lab *B. distachyon* transformation protocol](#)

Original transformation publications:

- [High-efficiency Agrobacterium-mediated transformation of *Brachypodium distachyon* inbred line Bd21-3](#)
- [Agrobacterium-mediated transformation and inbred line development in the model grass *Brachypodium distachyon*](#)

[The Vogel lab *B. sylvaticum* transformation protocol](#)

Crossing:

[Vogel lab crossing method](#)

[Garvin lab crossing method](#)

EMS mutagensis:

[Vogel lab EMS mutagenesis protocol](#)

Publications

Book

Genetics and Genomics of Brachypodium. 2016 Vogel, J.P. Ed., Springer, Switzerland. ISBN: 978-3-319-26942-9

Review

- Fitzgerald, T. L., J. J. Powell, K. Schneebeeli, M. M. Hsia, D. M. Gardiner, J. N. Bragg, C. L. McIntyre, J. M. Manners, M. Ayliffe, M. Watt, J. P. Vogel, R. J. Henry and K. Kazan (2015). "Brachypodium as an emerging model for cereal-pathogen interactions." *Annals of Botany* 115(5): 717-731.
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Research papers

- Gordon, S.P., Contreras-Moreira, B., Woods, D.P., Des Marais, D.L., Burgess, D., Shu, S., Stritt, C., Roulin, A.C., Schackwitz, W., Tyler, L., Martin, J., Lipzen, A., Dochy, N., Phillips, J., Barry, K., Geuten, K., Budak, H., Juenger, T.E., Amasino, R., Caicedo, A.L., Goodstein, D., Davidson, P., Mur, L.A.J., Figueroa, M., Freeling, M., Catalan, P., and Vogel, J.P., 2017 Extensive gene content variation in the *Brachypodium distachyon* pan-genome correlates with population structure. *Nat. Comm.* doi: [10.1038/s41467-017-02292-8](https://doi.org/10.1038/s41467-017-02292-8)
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