

## 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](#).



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Chemical and radiation mutants.

## Announcements (updated 1-2-2025)

## ***Let us know if you have an announcement***

The International Brachypodium Research Conference 2025 will be held in Monte Verità, Switzerland from June 6 - 10, 2025. Please visit the meeting website for more information [www.brachypodium2025.org](http://www.brachypodium2025.org)

## **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 1 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](#). 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 also been [collected from Spain](#).

### **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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Bragg, J. N., T. Ludmila and Vogel, J.P. 2012 *Brachypodium distachyon*, A Model for Bioenergy Grasses. Handbook of Bioenergy Crop Plants. Kole, C., Joshi, C.P. and Shonnard, D.R., Boca Rotan, Taylor & Francis Group. p 593-618

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Bevan, M.W., Garvin, D.F., Vogel, J.P. 2010 *Brachypodium distachyon* genomics for sustainable food and fuel production. Current Opinion in Biotechnology 21: 211-217

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Vogel, J. 2008 Unique aspects of the grass cell wall. Current Opinion in Plant Biology. 11: 301-307

Garvin, D., Gu, Y., Hasterok, R., Hazen, S., Jenkins, G., Mockler, T., Mur, L.J., and Vogel, J.P. 2008 Development of genetic and genomic research resources for *Brachypodium distachyon*, a new model for grass crop research. Crop Science 48: S69-S84

## 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)

Sancho, R., Cantalapiedra, C.P., López-Alvarez, D., Sean P. Gordon, S.G., Vogel, J.P., Catalán, P., Contreras-Moreira, B., 2017 Comparative plastome genomics and phylogenomics of *Brachypodium*: flowering time signatures, introgression

and recombination in recently diverged ecotypes. *New Phytologist* doi: 10.1111/nph.14926

O'Connor DL, Elton S, Ticchiarelli F, Hsia MM, Vogel JP, Leyser T. 2017 Cross-species functional diversity within the PIN auxin efflux protein family. *eLife* 6 Hsia, M.M., O'Malley, R., Cartwright, A., Nieu, R., Gordon, S.P., Sandra Kelly, K., Williams, T.G., Wood, D.F., Zhao, Y., Bragg, J., Jordan, M., Markus Pauly, M., Joseph R. Ecker, J.R., Yong Gu, Y., Vogel, J.P., 2017 Sequencing and functional validation of the JGI *Brachypodium distachyon* T-DNA collection. *Plant Journal* 91(3): p. 361-370.

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Woods, D.P., Bednarek, R., Bouché, F., Gordon, S.P., Vogel, J.P., Garvin, D.F., and Amasino, R.M. 2017 Genetic architecture of flowering-time variation in *Brachypodium distachyon*. *Plant Physiology* 173(1): 269-279

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Collier, R., Bragg, J., Hernandez, B.T., Vogel, J.P., Thilmony, T., 2016 Use of *Agrobacterium rhizogenes* strain 18r12v and paromomycin selection for transformation of *Brachypodium distachyon* and *Brachypodium sylvaticum*. *Frontiers in Plant Science* Volume 7, Article number 716

Petrikk, D.L., Cass, C.L., Karlen, S.D., Foster, C.E., Padmakshan, D., Vogel, J.P.,4 Ralph, J., 2,5, and Sedbrook, J.C., 2016 BdCESA7, BdCESA8, and BdPMT utility promoter constructs for targeting gene-of-interest expression to secondary cell wall forming cells of grasses. *Frontiers in Plant Science* Volume 7, Article number 55

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