

Dear International Brachypodium Community,

Below is the list of candidates in alphabetical order and by region for consideration on the IBSC. The candidates provided this information to help inform your decision.

North America

Kira Glover-Cutter (USA)

My research interest focuses on the intersection of oxidative stress and enhanced abiotic stress resistance for increased food security using *Brachypodium* as a model system. My current work at the USDA focuses on transcription factors from the proline catabolism pathway as an entry point for enhancing oxidative stress resistance. My degrees are in Chemical Engineering (BSE, Michigan State University) and Biophysics and Genetics (PhD, David Bentley Lab, University of Colorado) with postdoctoral fellowships in Genetics from Harvard Medical School (Keith Blackwell) and Plant Molecular Biology from the USDA Cereal and Forage Seed Research Unit (Ruth Martin). The Agronomic Traits Division at Dow AgroSciences recently closed its research division in Portland, so I am currently in transition from a Senior Scientist position at Dow AgroSciences to a second research position at the USDA in Corvallis, Oregon.

Samuel P. Hazen (USA)

Dr. Sam Hazen is an Associate Professor of Biology at the University of Massachusetts. His laboratory explores the mechanisms that regulate growth and cell wall thickening in grasses. Dr. Hazen was the Local Organizing Chair of the 2015 International Brachypodium Conference, is PI or Co-PI of several Community Science Program projects to synthesize genes and sequence genomes of *Brachypodium distachyon*. He is also the author of ten *B. distachyon* publications. <http://www.bio.umass.edu/biology/hazen/>

John Vogel (USA)

For over 12 years Dr. Vogel has been a leader in the development of resources for the *Brachypodium* community. These resources include T-DNA lines, genome sequences, germplasm and methods for high-efficiency transformation, crossing, and mutagenesis. A summary of these resources can be found on this website: <http://jgi.doe.gov/our-science/science-programs/plant-genomics/brachypodium/>. He has been an advocate for *Brachypodium* funding and has organized a *Brachypodium* community organizational meeting at the Plant and Animal Genome conference for many years. In his current position at the DOE Joint Genome Institute Dr. Vogel is leading a project to sequence thousands of chemical mutants and is developing resources to allow several *Brachypodium* spp. to be used as models for polyploidy and perenniality. Dr. Vogel has authored 27 *Brachypodium* research papers, 14 *Brachypodium* reviews/book chapters and edited the first book focused solely on *Brachypodium*, which is in press now.

Asia

Zhiyong Liu (China)

My lab is working on genetic control of cereal diseases including wheat rusts, powdery mildew, spot blight, and virus. We use *Brachypodium* as a model system to study the interaction between host resistance gene and Barley Stripe Mosaic Virus (BSMV). We have

mapped and cloned a BSMV resistance gene *Bsr1* from *Brachypodium distachyon* accession Bd3-1 and explored its allelic variations in *B. distachyon*, *B. stacei* and *B. hybridum*. We also use *Brachypodium* genome sequences to perform comparative genetics analysis in mapping wheat genes responsible for disease resistance and other agronomic traits. My lab is also responsible for coordinating the *Brachypodium* research committee in China.

Keiichi Mochida (Japan)

Our team at RIKEN aims to develop plants with improvements in the quantitative and qualitative productivity of cellulosic biomass. By using *Brachypodium*, we carry out gene discovery to improve biomass productivity and adaptation to environmental changes. Furthermore, we are promoting applied research for plants for biomass resources in collaboration with other universities and institutes. I am also the author of 7 *Brachypodium* related publications (Takei et al. 2015 (PMID: 26419335), Onda et al. 2015 (PMID: 26156770), Noda et al. 2015 (PMID: 25996877), Mochida and Shinozaki 2013 (Review) (PMID: 24204022), Mochida et al. 2013 (PMID: 24130698), Brkljacic et al. 2011 (PMID: 21771916), Mochida et al. 2011 (PMID: 21729923)). Cellulose Production Research Team Leader RIKEN Center for Sustainable Resource Science, Japan

http://www.riken.jp/en/research/labs/csrs/biomass_eng/cell_prod/

Organizer of 1st and 3rd Japanese *Brachypodium* workshop
Developer of RIKEN *Brachypodium* full-length cDNAs and RBFLDB

http://epd.brc.riken.jp/en/pdna/pdb_distachyon

<http://brachy.bmep.riken.jp/ver.1/index.pl>

Dr. Muhammad Nawaz (Pakistan)

Assistant Professor

Department of Botany

Deputy Director, QEC

Govt. College University Faisalabad, Pakistan

Europe

Pilar Catalan (Spain)

I am Professor in Botany at the Universities of Zaragoza (Spain) and Tomsk State University (Russia). I focus on plant evolutionary biology, speciation, hybridization, polyploidization, ecological adaptation, landscape genetics and comparative genomics of monocots, especially temperate grasses (Pooideae, *Brachypodium*, Loliinae). My lab has implemented new approaches in analysis of genomic inheritance in plant polyploids. I was one of the coauthors proposing *Brachypodium distachyon* as model plant for monocots and grasses in the early 90's. Since then, I have conducted phylogenetic, genetic and phenotypic analysis within the *B. distachyon* complex, describing the three currently accepted annual species (*B. distachyon*, *B. stacei*, *B. hybridum*), and of the whole genus, providing the first genus-wide phylogenetic framework for the 20 annual and perennial species of *Brachypodium*. I am part of the international *Brachypodium* research group that is conducting comparative genomics and phylogenomic analysis of the sequenced *Brachypodium* species and of the pangenomes of annual *B. distachyon* and perennial *B. sylvaticum*. My lab will organize the 2019 International *Brachypodium* Conference that will be held in Zaragoza-Huesca (Spain).

<http://bifi.es/bioflora/new-page.html>

Boulos Chaloub (France)

<http://www.versailles.inra.fr/urgv/chalhoub.htm>

Robert Hasterok (Poland)

Robert Hasterok is the Professor of Biology and the Head of the Department of Plant Anatomy and Cytology at the University of Silesia in Katowice, Poland. From the very beginning (2000), he was the proponent of establishing *Brachypodium distachyon* (Brachypodium) as the model system, useful in various areas of biology. His primary research interests are linked with molecular cytogenetics of various *Brachypodium* species and his expertise in this field is documented by +25 publications in high impact journals and books. He was also one of the founders of the International Brachypodium Initiative (2006) and participated in the Brachypodium whole genome sequencing project (completed in 2010), contributing to the integration of the physical map with the chromosomes of this species. Using various DNA sequences as molecular probes in FISH, he and his group have undertaken a complex study on the structure, evolution and dynamics of *Brachypodium* genomes at the cytomolecular level as well as provided necessary research foundations and infrastructure for further advanced cytomolecular study. In 2004, along with his collaborators from Aberystwyth University (UK), he was the first to articulate that the cytotypes of Brachypodium with 20 and 30 chromosomes can, in fact, represent two distinct species, one of them to be of the allotetraploid origin. Since 2012, these two species are known as *B. stacei* and *B. hybridum*. More recently, his group has extended this study to the perennial representatives of the genus, and have contributed to the deciphering of the evolutionary history of the *Brachypodium* genus. They were also the pioneers of applying BAC-FISH-based 'chromosome painting' and 'chromosome barcoding' to study monocot genomes. Using this powerful methodology, now they for example analyse the arrangement of chromosome territories at interphase and reconstruct the evolution of *Brachypodium* genomes at the level of chromosome. At present, Robert Hasterok is the PI of several large projects on *Brachypodium* species funded by the Polish Science Centre and has joint projects with many colleagues from the UK, USA, Spain, Turkey, France and Hungary. More detail can be found here: <http://www.wbios.us.edu.pl/hasterok/>

Nicola Pecchioni (Italy)

I present myself as candidate to IBSC for the region Europe; I would like therefore to be one of EU representatives to take to the world community of Brachypodium the same enthusiasm and spirit of service that animated the past years of my active participation to most Brachy initiatives. Scientifically and in perspective I would like to intensify the relationships of the Brachypodium community with the barley and wheat ones. Because of my new position, I am presently active in the International Wheat Initiative, and also member of the European barley genomics network (BGN), and these two relationships could help the above mentioned aim.

POSITION. Director, CRA-CER Cereal Research Centre, Foggia, Italy. Associate Professor, Department of Life Sciences of Università di Modena e Reggio Emilia.

EDUCATION. MSc in Agricultural Sciences, 1990; PhD in Plant Biotechnology, 1994

RESEARCH. At present, Director of the Cereal Research Centre of Foggia, Italy. With 12 researchers it is one of the biggest research groups mainly devoted to durum wheat research; the Centre is also studying genetic and technological factors limiting production in cereals, and recently started using the model grass Brachypodium to study proteins and protein interactions during salt stress. Formerly, N.P. established in 2005 the 'Crop Production' group

of UNIMORE, with a platform for plant genotyping and marker-assisted selection. He has a long experience in agricultural plant genetics and genomics. He used DNA polymorphism for studying plant genetic diversity, performed QTL mapping for tolerance to abiotic and biotic stresses in barley, and their fine mapping. Identification of *Vrn* vernalization genes in barley. Investigation of the role of candidate genes to explain biologically QTLs in plants, cloning the *Fr-H2* frost tolerance and the *eam6* early maturity QTLs in barley. Studies of determinants of grain yield under drought in barley. GWAS for drought adaptation and cold tolerance. He produced the first QTL map in the model species *Brachypodium distachyon*, finely mapped two QTLs, and performed a transcriptomic experiment of *P. brachypodii* rust infection. He is author or co-author (1991-october 2015) of 111 scientific publications on journals (Scopus H index = 20) and of 14 book chapters. Associate editor of Journal Euphytica since 2011. He has been referee for 25 International Journals; he is National and international project reviewer since 2006. As a service to *Brachypodium* community, he organized in Modena, Italy, in 2013, the 1st International *Brachypodium* Conference, and he participated to the scientific committee for the organization of the International *Brachypodium* Conference in Amherst, 2015.

Coordinator of National and Regional projects, responsible of private-funded projects, participant in EU project and responsible of bilateral projects.

Brachypodium-related papers:

- Barbieri M, TC. Marcel, R.E. Niks, E. Francia, M. Pasquariello, V. Mazzamurro, D.F. Garvin, and N. Pecchioni (2012). QTLs for resistance to the leaf rust *Puccinia brachypodii* in the model grass *Brachypodium distachyon* L. *Genome* 55: 152-163
- Catalan P., B. Chalhoub, V. Chochois, D.F. Garvin, R. Hasterok, A.J. Manzaneda, L.A.J. Mur, N. Pecchioni, S.K. Rasmussen, J.P. Vogel, A. Voxeur (2014). Update on the genomics and basic biology of *Brachypodium*. *Trends in Plant Science* 19(7): 414-418.
- Mur L.A.J., V. Mazzamurro and N. Pecchioni (2015) *Brachypodium* as a model for grass and cereal diseases (Vogel J. ed.) Springer, in preparation

Richard Sibout (France)

Richard Sibout works at the Institut National de la Recherche Agronomique (INRA) in Versailles, France. He currently focuses his research on the *Brachypodium* cell wall and lignification. He developed genetic resources both for *B. distachyon* and *B. stacei* (chemical mutants, natural accessions, RILs) and contributed to the organization of the international *Brachypodium* meeting in 2011 hosted at the INRA-Versailles

Australia & the south Pacific, Africa & the Middle East

Justin Borevitz (Australia)

We have sampled extensively in Australia and imported thousands of *Brachypodium* accessions from collaborators in the North. Via Genotyping By Sequencing we have assessed ploidy state, identified many divergent lineages suitable for Genome Wide Association Studies and clustered remaining accessions into close family groups where epigenomic variation is being explored. We are also developing 3D/4D multi spectral phenotyping approaches to assess climate adaptation in simulated chamber conditions. My group and I have presented at previous International *Brachypodium* conferences and will continue to collaborate broadly with this important cereal model.

<http://borevitzlab.anu.edu.au/>

Hikmet Budak (Turkey)

<http://myweb.sabanciuniv.edu/budak/>

Mhemmed Gandour (Tunisia)

Mhemmed Gandour is an Associate Professor of Genetics at the Faculty of Sciences and Technology of Sidi Bouzid from 2012 and senior researcher at the Center of Biotechnology of Borj-Cedria (CBBC) in Tunisia from 2008. He founded the first Tunisian Association of Genetic Resources (TAGR) and is currently the vice-president of this Association. He teaches courses of Genetics, Molecular Genetics, Population Genetics, Biogeography and Biostatistics. He received his MSc degree (DEA) in Biochemistry in 2004 from Tunis El Manar University. He then carried out his PhD at the same University and obtained in 2009 his PhD degree in Biology, specializing in Genetic and Molecular Biology. He has performed and directed several research projects related to plant genetic diversity and the evolution of adaptive traits under abiotic stresses. He published more than 30 papers in peer-reviewed journals. The long-term goal of his research is to understand both the molecular mechanisms and the evolution of adaptive traits. To this end, he is using both phenotype-first and genotype-first approaches to identify genetic variants with a potential role in local, regional or global adaptation. To date, his group has used several local systems (e.g. *Cakile*, *Sulla*, *Medicago*, *Brachypodium*), which were investigated through functional and comparative genomic studies. For the next stage of his research he plans to focus on a monocot model system *B. distachyon* and related species to develop knowledge that will ultimately be used to improve biomass production and yield of cultivated species like wheat and barley.