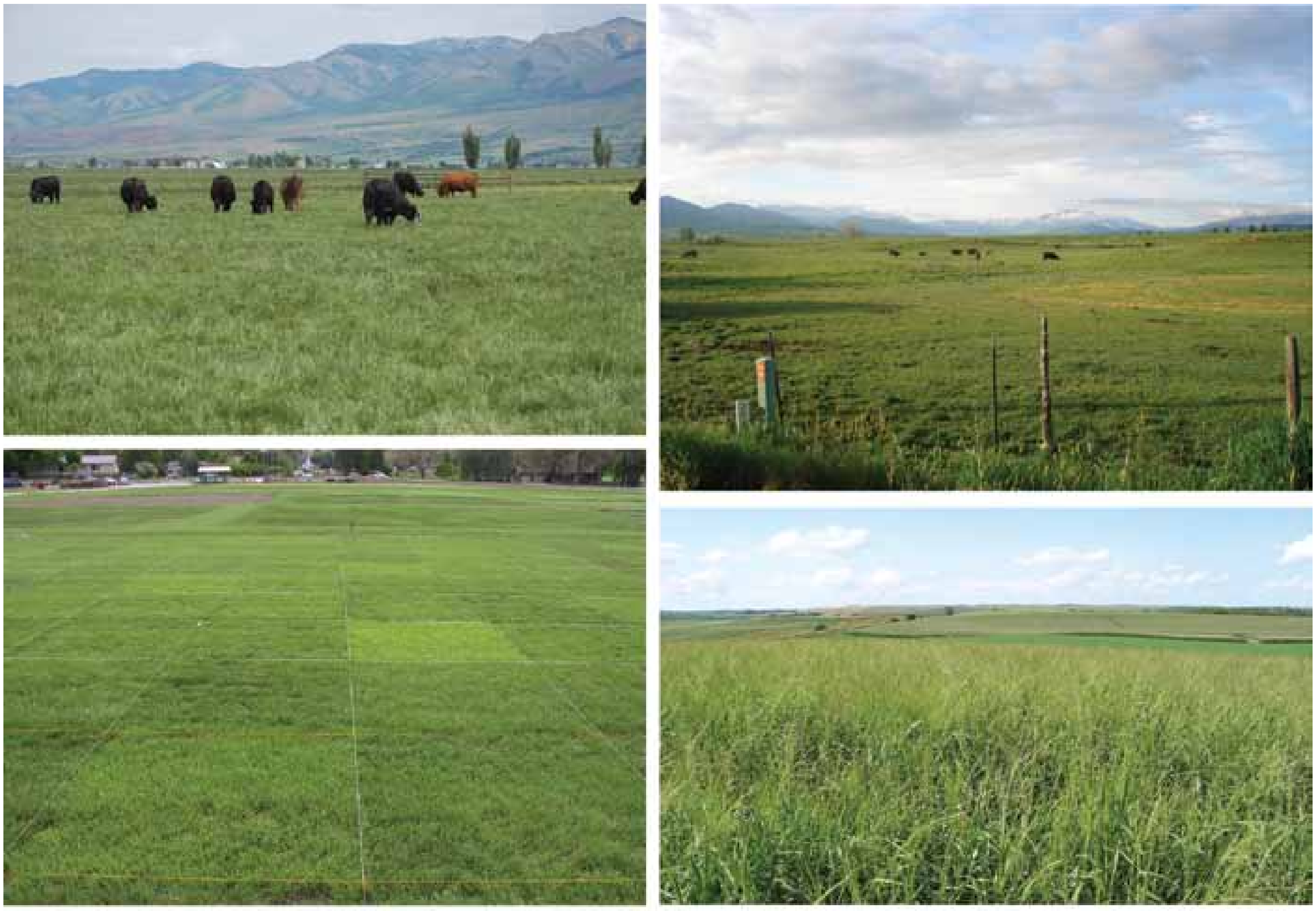
Proceedings of the 7th International Symposium on the Molecular Breeding of Forage and Turf

MBFT2012 – Salt Lake City, Utah, USA

June 4-7, 2012



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The seventh International Symposium on the Molecular Breeding of Forage and Turf, MBFT2012, was held in Salt Lake City, UT, USA, from June 4 – 7, 2012. One-hundred and fifteen researchers from around the world presented oral and poster formats relating to ten general topics: Genetic mechanisms and applications, comparative genomics, herbage quality, symbionts, bioenergy, germplasm/diversity/and its impact on breeding, abiotic and biotic stresses, genomic selection and plant improvement, functional genomics and gene discovery, and transgenic processes and procedures. A tour was included to forage research plots at Evan's farm, National Turfgrass Evaluation Program and other turf research plots at Greenville farm, and grazing research at Lewiston farm; all used by the USDA-ARS Forage and Range Research Laboratory and Utah State University. In this proceedings are selected manuscripts of invited speakers, and abstracts of oral and poster presentations. We thank the participants and organizing committee for the outstanding research and presentations at this symposium.

ISBN 978-1-4675-4762-8

Selection of *Paspalum* spp. accessions for use as turfgrass

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Paspalum spp. is a large genus with more than 400 identified species grouped into 20 taxonomic groups. In Brazil, there are around 220 native species. Embrapa Cattle-Southeast located in São Carlos, state of São Paulo, maintains a large germplasm bank of the genus with more than 320 accessions of 37 species collected in various regions of the country. Recently, a project coordinated by Embrapa Cattle-Southeast was initiated with the objectives of evaluating accessions for use as turf. An experiment was conducted in Campo Grande, MS, with 27 accessions belonging to ten species in plots 1.0 to 1.5 m2 in three replications. Plots were established with individual cuttings spaced 15 cm from each other on February 2011 and evaluated for plant survival and soil cover. In the beginning of the rainy season in November, plots were cut to a 5 cm height and growth above that was harvested every fortnight in a 1 m2 area. Data were analyzed by SAS. Of the 27 accessions, nine presented more than 80% survival 45 days after planting, and more than 80% soil cover 4 months after planting. These are: *P. modestum* 2 and 5, *P. lividum* 4, *P. rhodopedum* 8, *P. notatum* 13, 20 and 22 and *Paspalum* sp. 18. *Paspalum oteroi* 12 showed little plant survival but good soil cover. One year after planting soil cover varied from 3.4 m2 to 32 m2. Total dry matter in the rainy season varied from 0.3 to 1.0 kg/m2 in a maximum of 11 harvests. Accessions 2, 4 and 5 produced less than 400 g in 9 harvests. Considering highest soil cover and lower number of harvests, dry matter yields and flowering, accessions of *P. modestum*, *P. oteroi* and *P. lividum* showed great promise to be used as turf, emphasizing the great potential of this germplasm collection.

The National BioResource Project *Lotus japonicus* and *Glycine max / soja* in Japan

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The National BioResource Project (NBRP) aim is to collect, preserve and provide bioresources that are basic materials for life sciences research, and to upgrade the bioresources responding to the demands of the present age by adding higher values through developing preservation technology, genome analysis, and others systematically. In addition, reinforcement of the function of the information center, which provides information of whereabouts and others, is included. Japanese trefoil (*Lotus japonicus*) is a wild perennial plant with a small genome and a short life cycle. This plant is expected to play a role as the model organism of leguminous plants, which include important crop plants. Additionally, the soybean, *Glycine max* (L.) Merr., is the most important grain legume crop in terms of total production and international trade of agricultural products. Legume Base, a resource center for *L. japonicus* and *G. max*, was established in April 2004. The scope of Legume Base is the collection, development and conservation of the genetic resources of *L. japonicus* and *G. max* and the distribution for the utilization by the research community. DNA resources including genomic DNA clones will be also available through Legume Base web site (http://www.legumebase.brc.miyazaki-u.ac.jp). In here, we will introduce NBRP Japan and Legume Base.