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Meeting Report

The Eleventh Triticeae Meeting of Japan, 2016

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The Eleventh Triticeae Meeting of Japan was held at Institute of Plant Science and Resources, Okayama University, Kurashiki on December 10 and 11, 2016 as a joint program of the Chugoku branch meeting of Japanese Society of Breeding. A total of 156 attendee including researchers and students participated in the meeting (Fig. 1). This meeting includes a session of National BioResource Project (NBRP) - Barley and Wheat. The objectives of the meeting were to share the information about genetic and genomic resources in Triticeae and to discuss their efficient use in the research community. The meeting had 13 oral and 64 poster presentations as shown below. The next meeting will be held at Kyoto University next year.

ABSTRACTS & TITLES

Oral Presentation

O01.* The current challenges and future prospects of plant genome editing. – How to apply genome editing into crop breeding? –

Keishi Osakabe
Fac. Biosci. Bioind,, Tokushima Univ., Japan

O02.* Plant artificial chromosomes: Present and future

Minoru Murata
IPSR, Okayama U., Japan

O03.* Genetic study and improvement of capsaicinoid and its analogs with chili pepper bio-resource.

Yoshiyuki Tanaka
Okayama U. Japan

O04.* Morphological variations of starch grains in cereals

Ryo Matsushima
IPSR, Okayama U., Japan

O05. Barley genome information

Kazuhiro Sato
IPSR, Okayama University, Japan

A BAC physical map and sequences in gene space have been released in 2012 by the international consortium. The continuing efforts of BAC based analysis for individual chromosome have been done by contributing organizations and will be published after the end of 2016. The sequences are already available from the database at IPK, Germany under registration and acceptance of condition for uses. IPK has started sequencing 20,000 genebank accessions by GBS method and might finish most of them. The large exome capture based sequencing is also underway at JKI, UK. The present status of barely genome analysis and its future is discussed in the talk.

O06. Impact of wheat lines with related wild species on heat stress tolerance

Keiichi Mochdia[1, 2, 3]
[1]CSRS, RIKEN, Japan
[2]KIBR, Yokohama City U., Japan
[3]IPSR, Okayama U., Japan

In the family *Poaceae*, *Brachypodium* is a temperate grasses of the *Pooideae* subfamily that includes some major crops such as wheat, barley and rye. The close phylogenetic relation between *Brachypodium* and the *Triticeae* species suggests that the *Brachypodium* genome and associated

resources will be beneficial for gene discovery and structural genomic studies in grasses. Recently developed *Brachypodium* resources are compared to those of wheat and barley, to promote the mutual access to *Poaceae* resources.

O07. Current status of the reference genome sequencing of wheat

Hirokazu Handa
NARO Institute of Crop Science, Japan

The International Wheat Genome Deciphering Consortium (IWGSC) was established in 2005 to create the reference genome sequence of wheat. After more than 10 years' efforts of IWGSC, we are in the final step towards the creation of the wheat reference genome sequence. In this presentation, the author presented the current status of wheat genome sequencing by IWGSC, especially the recent change of IWGSC's strategy by the introduction of new assembly technique (DeNovo MAGIC ™, NRgene). And also the author introduced information about the research movement after completion of the reference genome sequence.

O08. Prospects of crop research in the genome editing technology era - utilization and development of resources and technologies of model plants and Pooideae

Masatomo Kobayashi
RIKEN BioResource Center, Japan

During recent years, life science is making remarkable progress by the emergence of novel technologies such as next generation sequencer and genome editing technology. However, utilization of genome editing technology in plant science is less significant than that in animal science. The reasons are as follows:

1) Embryo manipulation technology that is indispensable for efficient application of genome editing technology has not been established yet in plants.
2) Thus genome editing is carried out using transformation technology in plants.
3) However, transformation efficiency is relatively low in most of crops.
4) Also, transformation technology is under the strict control by the Cartagena Law.

In order to overcome these disadvantages, it is important to utilize experimental plants that are easy to handle in the laboratory. We introduce *Brachypodium distachyon* as an experimental plant of monocot that has short life cycle and is able to grow in the laboratory conditions. We are developing resources, technologies and information of Brachypodium in order to fully utilize this plant in the crop science, especially wheat and barley.

Fig. 1 The Eleventh Triticeae Meeting of Japan, 2016

O09. Barley mutants: powerful aids for gene identification

Shin Taketa
Institute of Plant Science and Resources, Okayama University, Japan

The history and current status of barley mutant researches in Kurashiki are briefly summarized. International research trends of barley mutants are briefly summarized, with particular emphases on their effective uses in validation of gene cloning and biological analysis of gene functions. My personal perspective is that molecular dissections of barley under the international standard of rice or maize, should drastically improve the quality of barley science.

O10. Enhancement of ABA receptor function confers water-saving drought tolerance in wheat

Ryosuke Mega[1] Fumitaka Abe[2] June-Sik Kim[3], Keisuke Tanaka[4], Hisato Kobayashi[4], Yoichi Sakata[5], Hisashi Tsujimoto[1], Kousuke Hanada[6] and Masanori Okamoto[1,7]
[1]ALRC, Tottori University, Japan
[2] Institute of Vegetable and Floriculture Science, NARO, Japan
[3]CSRS, RIKEN, Japan
[4]NODAI Genome Research Center, Japan
[5]Applied Bioscience, Tokyo University of Agriculture, Japan
[6]Frontier Research Academy for Young Researchers, Kyushu Institute of Technology, Japan
[7]PRESTO, JST, Japan

Global climate change has accelerated water scarcity followed by huge drought, which led to massive loss of crop production and may threaten food security in many countries. Therefore, a drought tolerant trait which can save water consumption (water-saving) is being demanded recently. Abscisic acid (ABA) synthesis is induced by drought stress. Consequently, stomatal closure is facilitated to suppress transpiration via ABA signaling pathway. This pathway is commonly found in terrestrial plants, modulating PYR/PYL can be a good option to improve crop drought tolerance. However, since wheat genome database has not been established yet, wheat ABA receptors (TaPYLs) were not completely identified. To improve wheat drought tolerance, we characterized TaPYLs from wheat genome and generated the transgenic wheat overexpressing wheat PYR/PYL (TaPYLox). In TaPYLox, biomass amount and seed yield produced from 1L of water is significantly increased compared with control cultivar. Our study indicates that the enhancement of ABA receptor expression contributes to not only drought tolerance but also the "water-saving drought tolerance" phenotype which can perform highly efficient seed production with limited water.

O11. Construction of genome sequence of wheat chromosome 6B and its application for wheat study

Fuminori Kobayashi, Hirokazu Handa
Institute of Crop Science, NARO, Japan

For better understanding the genome structure of wheat and accelerating the gene isolation and breeding for wheat, our research group, as a member of International Wheat Genome Sequencing Consortium (IWGSC), constructed the pseudomolecule of wheat chromosome 6B of 'Chinese Spring' (CS) by the BAC-by-BAC sequencing approach. Genome assemblies constituting the pseudomolecule were highly ordered along the chromosome 6B by conducting the scaffolding and radiation hybrid mapping. This genome sequence for chromosome 6B allowed us to study a genomic region for the leaf rust resistance gene, *LrRW12*. The *LrRW12* was genetically mapped on the long arm of chromosome 6B by the GBS approach. The SNP markers were developed along the pseudomolecule, and finally about 4 Mb region was identified to include *LrRW12*. Using the genome sequence for this region, we could predict gene loci and detect several SNPs in these loci between resistant and susceptible accessions by transcriptome data. In this way, application of genome sequence highly facilitates the estimation of target genomic region and its structural analysis, even in common wheat. This work was supported by grants from the Ministry of Agriculture, Forestry and Fisheries of Japan (NGB1003) and JSPS KAKENHI Grant Number JP24780008.

O12. Genome editing in plants and barley transformation

Hiroshi Hisano
Institute of Plant Science and Resources, Okayama University, Japan

Genome editing is a new technology to produce mutants by designer nucleases e.g. Transcription Activator-Like Effector Nucleases (TALEN) and Clustered Regularly Interspaced Short

Palindromic Repeats/ CRISPR-associated 9 (CRISPR/Cas9). In this presentation, the brief overview of genome editing was explained, and it included about particular formation of TALEN and CRISPR/Cas9, differences of procedure for genome editing between in animals and in plants, comparison between conventional transformation and genome editing, and mechanisms of knock-in and knock-out in target genes. Also published reports and current states of genome editing in plants was inducted.
On the other hand, author presented about a project for genome editing in barley. Then author introduced about identification of the genomic region responding to transformation amenability in barley. The efficiency of transformation is important for current genome editing in plants to introduce the genes encoding those nucleases. Author found several loci showing segregation distortion of SNPs markers in transgenic barley plants derived from a cross between cvs. Haruna Nijo as recalcitrant of transformation and Golden Promise as reliable for transformation. These loci could be necessary or advantageous for transformation in barley.

O13. Durum wheat breeding in WARC/NARO

Mikiko Yanaka
Western Region Agricultural Research Center, NARO, Japan

Durum wheat (*Triticum turgidum* L. *ssp*. *durum*) is mainly used for pasta production. It has not been cultivated in Japan because of its late maturity and its very weak resistances to Fusarium head blight (FHB) and pre-harvest sprouting (PHS), compared with bread wheat (*T. aestivum* L.). However, a demand for pasta made from domestic durum wheat is increasing in Japan. WARC/NARO thought that Setouchi area seems to be most preferable for durum wheat cultivation in Japan because it has less rainfall during the cultivation, and then started durum wheat breeding in the late 1990s. In 2015, WARC/NARO released a new durum wheat cultivar named 'Setodure', which is a first durum wheat cultivar in Japan, after the evaluation of its pasta quality by Nippon Flour Mills. 'Setodure' showed maturity similar to that of the bread wheat cultivar 'Norin61', weak resistances to FHB and PHS and pasta quality which is superior to bread wheat, but inferior to the imported durum wheat brand. WARC/NARO is trying to improve the resistances to PHS or FHB by the introduction of the reported resistance genes or QTLs from bread wheat and to improve the pasta quality by the introduction of the genes related to pasta quality from durum wheat.

Poster Presentation

P01.*
QTL analysis of α-amylase activity in barley
Matsumoto, S.[1], H. Hisano[1], M. Kihara[2], T. S. Zhou[2] and K. Sato[1] ([1]IPSR, Okayama U., Japan [2]BRDD, Sapporo Brew. Ltd., Japan)

P02.*
Barley albino lemma mutant: molecular genetic analysis and spike-photosynthesis measurement
Hattori, M., T. Takami, W. Sakamoto and S. Taketa (IPSR, Okayama U.)

P03.*
Genetic linkage analysis for identifying root-knot nematode *(Meloidogyne incognita*) resistance gene in sweetpotato
Kishimoto, K[1], K. Shirasawa[2], R. Sasai[1], A. Kuramoto[3], S. Isobe[2], M. Tahara[1], Y. Okada[4], H. Tabuchi[4], A. Kobayashi[4] and Y. Monden[1] ([1]Grad. Sch. Environ. Life Sci., Okayama U., [2]Kazusa DNA Res. Inst., [3]Grad. Sch. Agr., Kyoto U., [4]KONARC)

P04.*
16S metagenomics analysis of microbiome communities in root-knot nematode (*Meloidogyne incognita*) and *Streptomyces ipomoea* infected soils
Nakashima, H.[1], T. Ishige[2], T. Kuranouchi[3], Y. Momota[4], K. Yonemoto[5], M. Tahara[1] and Y. Monden[1] ([1]Grad. Sch. Environ. Life Sci., Okayama U., [2]NODAI Genome Research Center, [3]NICS, [4]CARC, [5]TAFFTSC)

P05.*
Identifying genomic regions associated with *Streptomyces ipomoea*e pathogen resistance by using SNP data
Aikawa, Y.[1], K. Shirasawa[2], A. Kuramoto[3], Y. Imai[4], S. Isobe[2], M. Tahara[1], Y. Okada[5], O. Jahana[6] and Y. Monden[1] ([1]Grad. Sch. Environ. Life Sci., Okayama U., [2]Kazusa DNA Res. Inst., [3]Grad. Sch. Agr., Kyoto U., [4]Tottori U. Technical dept., [5]KONARC, [6]OPARC)

P06.*
Experimental assessment of simplified cultivar identification method in azuki processed products using single tag hybridization (STH) chromatographic printed array strip (PAS).
Sasai, R.[1], M. Tahara[1], K. Takasaki[2] and Y. Monden[1] ([1]Grad. Sch. Environ Life. Sci.,

Okayama U., [2]FASMAC Co., Ltd.)

P07.*
Development of cultivar identification DNA markers for purple sweetpotato using retrotransposon insertion polymorphisms
Ono, N.[1], K. Kishimoto[2], M. Tahara[2] and Y. Monden[2] ([1]Fac. Agr., Okayama U., [2]Grad. Sch. Env. & Life Sci., Okayama U.)

P08.*
Morphological characteristics in F_1 populations derived from cultivated and wild sweetpotato strains
Kimura, T.[1], M. Tanaka[2], S. Isobe[3], M. Tahara[4] and Y. Monden[4] ([1]Fac. Agr., Okayama U., [2]KONARC, [3]Kazusa DNA Res. Inst., [4]Grad. Sch. Environ. Life Sci., Okayama U.)

P09.*
Introduction of chromosome arm 1EL partial region with high-molecular-weight glutenin subunit genes associated with strong dough into common wheat by homoeologous chromosome recombination
Hayashi, N. and H. Tanaka (Fac. Agr., Tottori U.)

P10.*
MSD population: New source of heat tolerance of wheat in high-temperature environments
Elbashir, A. A. E.[1,3], Y. S. A. Gorafi[2,3], I. S. A. Tahir[3], A. M. A. Elhashimi[3], M. G. A. Abdalla[3] and H. Tsujimoto[2]
([1]United Grad. Sch. Agr. Sci., Tottori U., Japan, [2]Arid Land Res. Center, Tottori U., Japan, [3]Agr. Res. Corp., Wad Medani, Sudan)

P11.*
Compensational application of *Leymus racemosus* markers to analyze genetic diversity in tribe Triticeae
Edet, O.[1,2,5], J.-S. Kim[3], K. Hanada[4], M. Okamoto[1] and H. Tsujimoto[1]
([1]Arid Land Res. Center, Tottori U., Japan, [2]United Grad. Sch. Agr. Sci., Tottori U., Japan, [3]RIKEN Center for Sustainable Res. Sci., Japan, [4]Dept. Biosci. Bioinformatics, Kyushu Inst. Tech., Japan, [5]Dept. Crop Sci, U. Calabar, Nigeria)

P12.*
Molecular phylogenetic analysis of some crops using 26S rRNA and ribulose1, 5-bisphosphate carboxylase/oxygenase (Rubisco large subunit genes)
Hassan, E. M., G. H. Badawi and M. H. Eltahir (Fac. Agr., U. Khartoum, Sudan)

P13.*
Molecular genetic analysis of the rice stay-green mutant *dcd1*
Yamatani, H.[1], K. Kohzuma[1,2], M. Nakano[1], Y. Hayashi[3], T. Takami[4], Y. Kato[4], Y. Monden[5], T. Kumamaru[6], Y. Okumoto[7], W. Sakamoto[2,4], T. Abe[3] and M. Kusaba[1,2]
([1]Grad. Sch. Sci., Hiroshima U., [2]CREST, [3]RIKEN, Nishina Cent, [4]Inst. Plant Sci. Res., Okayama U., [5]Grad. Sch. Environ. Life Sci., Okayama U., [6]Fac. Agr., Kyusyu U., [7]Grad. Agr., Kyusyu U.)

P14.*
Map-based cloning in the genus Chrysanthemum
Aruga, Y.[1], M. Nakano[1], T. Kozuka[1], S. Isobe[2], K. Taniguchi[1] and M. Kusaba[1] ([1]Lab. Plant Chromosome Gene Stock, Hiroshima U., [2] Kazusa DNA Res. Inst.)

P15.*
Molecular genetic analysis of leaf senescence regulated by blue light
Shimono, Y.[1], T. Kozuka[1], R. Inoue[1], M. Kusaba[1,2] ([1]Hiroshima U., [2]CREST)

P16.*
Mechanisms of functionalization in plant duplicate genes
Ezoe, A.[1], K. Shirai[1], K. Hanada[1] ([1]Kyushu Inst. Tech.)

P17.*
Search novel hormone like peptides in *Arabidopsis thaliana* by treatment assay
Torii, R.[1], Y. Kim[1], T. Takeda[1], M. Higuchi[2], I. Obayashi[1], M. Okamoto[3], M. Shimizu[2], T. Yoshizumi[2], K. Nakaminami[2], R. Nishi[2], K. Shinozaki[2], M. Seki[2], M. Matsui[2] and K. Hanada[1,2] ([1]Kyushu Inst. Tech., [2]RIKEN, [3]Tottori U.)

P18.*
Exhaustive search of alternative splicing changes under shade avoidance in *Arabidopsis thaliana* throughout next generation sequencing analysis
Nose, T.[1], K. Shirai[1], F. Christian[2], T. Matsushita[3] and K. Hanada[1] ([1]Kyushu Inst. Tech., [2]Lausanne U., [3]Kyushu U.)

P19.*
Transcriptome analysis of *Leymus racemosus* with Next-generation sequence
Takeda, T.[1], K. Tanaka[2], H. Kobayashi[2], H. Tsujimoto[3], M. Okamoto[3] and K. Hanada[1]
([1]Kyushu Inst. Tech., [2]Tokyo U. Agr, [3]Tottori U.)

P20.[*]
Search for novel hormone-like peptides involved in the regulations of initial growth and flowering time in *Arabidopsis thaliana*
Yano, T.[1], R. Torii[1], I. Obayashi[1], K. Shirai[1], A. Ezoe[1] and K. Hanada[1] ([1]Kyushu Inst. Tech.)

P21.[*]
Genetic analysis on heading time in RILs population derived from a cross of barley cultivars "Kashimamugi" and "Ishukushirazu"
Nishida, H.[1], S. Yokota[2], E. Aoki[3] and K. Kato[1] ([1]Grad. Sch. Environ. Life Sci., Okayama U., [2]Fac. Agr. Okayama U., [3]NICS)

P22.[*]
Field survey of *Cucumis* species in western part of Nepal
Thuy, D. T.[1], K. Yashiro[2], K. Shimomura[3] and K. Kato[1)] ([1]Grad. Sch. Environ. Life Sci., Okayama U., [2]Ibaraki Agr. Center, Plant-Biotech. Inst., [3]NIVFS)

P23.[*]
Effect of interaction between *LUX/PCL1* genotypes on heading time of wheat, revealed by the analysis of a wheat DH population derived from "Chogokuwase" and "Kinuiroha"
Haque G. K. M. N.[1], H. Nishida[1], H. Matsunaka[2], M. Seki[3], N. Mizuno[4], M. Fujita[5], S. Nasuda[4] and K. Kato[1] ([1]Grad. Sch. Environ. Life Sci., Okayama U., [2]KARC/NARO, [3]CARC/NARO, [4]Grad. Sch. Agr., Kyoto U., [5]NICS)

P24.[*]
Interspecific hybrids obtained by crossing cultivated melon and wild species of *Cucumis*
Pervin, M. N.[1], G. Shigita[1], T. Ishikawa[2], K. Sakamoto[1], T. P. Dung[1], K. Tanaka[3], H. Nishida[1] and K. Kato[1] ([1]Grad. Sch. Environ. Life Sci., Okayama U., [2]Ibaraki Agr. Center, Plant-Biotech. Inst., [3]Fac. Agr. Life Sci., Hirosaki U.)

P25.[*]
Expression analysis on flowering-related genes by RNAseq in a wheat breeding line "Chogokuwase" and its progenitor lines
Masuda, H.[1], H. Nishida[1], N. Mizuno[2], S. Nasuda[2], M. Fujita[3] and K. Kato[1] ([1]Grad. Sch. Environ. Life Sci., Okayama U., [2]Grad. Sch. Agr., Kyoto U., [3]NICS)

P26.[*]
A study directed to uncover the origin of a vernalization response gene *Vrn-D4* in wheat
Harada, H., H. Nishida and K. Kato (Grad. Sch. Environ. Life Sci., Okayama U.)

P27.[*]
Genetic diversity analysis of melon germplasm collection using GBS
Shigita, G.[1], M. N. Pervin[1], H. Nishida[1], Y. Monden[1], M. Sugiyama[2], K. Tanaka[3] and K. Kato[1] ([1]Grad. Sch. Environ. Life Sci., Okayama U., [2]NIVFS, [3]Fac. Agr. Life Sci., Hirosaki U.)

P28.[*]
Fine mapping of the 'Chogokuwase (extra-early flowering)' gene in wheat
Sato, H.[1], A. Ebara[1], G. K. M. N. Haque[2], H. Masuda[2], H. Yamashita[2], H. Nishida[2], N. Mizuno[3], M. Fujita[4], S. Nasuda[3] and K. Kato[2] ([1]Fac. Agr., Okayama U. [2]Grad. Sch. Environ. Life Sci., Okayama U., [3]Grad. Sch. Agr., Kyoto U., [4]NICS)

P29.[*]
Mapping of a novel flowering time QTL on 2HS chromosome derived from a barley cultivar Morex
Yokota, S.[1], M. Irisawa[1], R. Tanabe[2], H. Nishida[2], E. Aoki[3] and K. Kato[2] ([1]Fac. Agr., Okayama U., [2]Grad. Sch. Environ. Life Sci., Okayama U., [3] NICS)

P30.
Breeding of barley with new useful quality in KONARC.
Tonooka, T., M. Taira and T. Sugita (Kyushu Okinawa Agric. Res. Cent., NARO)

P31.
Reproductive isolation between two wild einkorn wheat species
Takumi, S. (Grad. Sch. Agr. Sci., Kobe U.)

P32.
Evaluation of efficiency of transient expression in the wheat leaf using Gene Gun System GDS-80
Mizoo, N. and K. Yoshida (Org. Adv. Sci. Tech., Kobe U.)

P33.
Application of RNA-seq-based BSA to fine mapping in synthetic hexaploid wheat
Nishijima, R.[1], K. Sakaguchi[1], K. Yoshida[2], K. Sato[3] and S. Takumi[1] ([1]Grad. Sch. Agr. Sci., Kobe U., [2]Org. Adv. Sci. Tech., Kobe U., [3]IPSR, Okayama U.)

P34.
Application of the genome-wide polymorphisms to gene mapping in *Aegilops umbellulata*
Okada, M.[1], K. Yoshida[2], K. Sato[3] and S. Takumi[1] ([1]Grad. Sch. Agr. Sci., Kobe U., [2]Org. Adv. Sci.

Tech., Kobe U., [3]IPSR, Okayama U.)

P35.
RNA-seq analysis of near-isogenic lines for chlorina mutations in tetraploid wheat
Nishigaki, K.[1], K. Yoshida[2], K. Sato[3], N. Watanabe[4] and S. Takumi[1] ([1]Grad. Sch. Agr. Sci., Kobe U., [2]Org. Adv. Sci. Tech., Kobe U., [3]IPSR, Okayama U., [4]Fac. Agr., Ibaraki U.)

P36.
Screening of NAC and MYB transcription factor genes related to cell death in common wheat
Hosokawa, S.[1], K. Yoshida[2] and S. Takumi[1] ([1]Grad. Sch. Agr. Sci., Kobe U., [2]Org. Adv. Sci. Tech., Kobe U.)

P37.
Genetic analysis of domestication related traits in emmer wheat: seed morphology and weight
Miyazaki, Y.[1], Pham Minh Ngoc[1], Liberatore Katie[2], Shahryar Kianian[2], N. Mori[1] ([1]Lab. Crop Evol., Grad. Sch. of Agric. Sci., Kobe U., [2]USDA-ARS Cereal Disease Lab., U. Minnesota)

P38.
Quantitative analysis of intra-molecular recombination of mitochondrial genome in wheat
Ohta, S.[1], M. Makita[1], M. Tsujimura[2], T. Terachi[2] and N. Mori[1] ([1]Lab. Crop Evol., Grad. Sch. Agric. Sci., Kobe U., [2]Fac. Life Sci., Kyoto Sangyo U.)

P39.
Genetic analysis of the domestication related traits using backcross derived lines in emmer wheat.
Shimada, S.[1], K. Gyu[1], C. Vladutu[1], T. Ishii[2], S. Kianian[3], N. Mori[1] ([1]Lab. of Crop Evol., Grad. Sch. Agr. Sci., Kobe U., [2]Lab. of Plant Breed., Grad. Sch. Agr. Sci., Kobe U., [3]USDA-ARS Cereal Disease Lab., U. Minnesota, U. S. A)

P40
Toward the QTL analysis of grain dimensions and dormancy in wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*)
Terada, N.[1], N. Mori[1] and S. Ohta[2] ([1]Lab. Crop Evol., Grad. Sch. Agr. Sci., Kobe U., [2]Dept. Biosci., Fukui Pref. U.)

P41
Molecule breeding of salt-tolerant wheat using RNAi
Ishihara, M., K. Kawaura and M. Isshiki (KIBR, Yokohama City U.)

P42
Selection of high-efficiency gRNA for genome editing of *Triticum aestivum* L. using CRISPR/Cas9 system
Inomata, M., Y. Kamiya, K. Kawaura and M. Isshiki (KIBR, Yokohama City U.)

P43
Study on traits showing heterosis in synthetic hexaploid wheat
Watanabe, R., Y. Jung, Y. Ogihara and K. Kawaura (KIBR, Yokohama City U.)

P44
Identification of genes for sham ramification in wheat
Mitsuhashi, Y.[1], S. Sakuma[2,3] and K. Kawaura[1] ([1]KIBR, Yokohama City U., [2]IPK, [3]Tottori U.)

P45
QTL analysis of salt-tolerance in Shirasagi-komugi using Rad-Seq method
Matsuda, S.[1], A. Tokunaga[1], S. Sakuma[1,2,3], Y. Ogihara[1], A. J. Nagano[4] and K. Kawaura[1] ([1]KIBR, Yokohama City U., [2]IPK, [3] Tottori U., [4]Ryukoku U.)

P46
Evaluation of salt tolerance in synthetic hexaploid wheat produced by CIMMYT
Tadokoro, M.[1], A. Tokunaga[1], S. Sakuma[1,2,3] and K. Kawaura[1] ([1]KIBR, Yokohama City U., [2]IPK, [3]Tottori U., [4]CIMMYT)

P47
Genetic analysis of putative suppressor of α-gliadins in bread wheat
Suzuki, S., Y. Kamei, M. Miura and K. Kawaura (KIBR, Yokohama City U.)

P48
KODA mediated changes in Japan wheat core collection harvest in the field with low fertilizers
Sekine, A.[1], E. Haque[1], S. Taniguchi[1], S. Ogawa[2], K. Takagi[2], M. Yokoyama[1] and T. Ban[1]
([1]KIBR.Yokohama City U., [2]Tech. Eng. Center, Shiseido Co., Ltd)

P49
Identification of florigen gene family in breed wheat and their expression profiling in the synthetic wheat
Mitsuhashi, A.[1], R. Shimizu[2], S. Takumi[3], K. Shimizu[2], H. Tsujimoto[4], T. Ban[1] and H. Tsuji[1] ([1]KIBR, Yokohama City U., [2]U. Zurich, [3]Grad. Sch. Agr. Sci., Kobe U., [4]Arid Land Res. Cent., Tottori U.)

P50
Identification of *FT* genes to reveal the mechanism for bulb formation of *Hordeum bulbosum*
Arai, Y., K. Taoka and T. Ban (KIBR, Yokohama City U.)

P51
Elucidation of epigenetic regulation mechanism of flowering promote gene *VRN1*
Umekita, K.[1], K. Nagaki[2], M. Murata[2] and K. Murai[1] ([1]Dep. Biosci., Fukui Pref. U., [2]IPSR, Okayama U.)

P52
Epigenetic regulation of floral MADS-box genes in polyploid wheat
Kuwabara, T.[1], K. Nagaki[2], M. Murata[2] and K. Murai[1] ([1]Dep. Biosci., Fukui Pref. U., [2]IPSR, Okayama U.)

P53
Analysis of amino acid sequence variation among VRN1 proteins and construction of VRN1 protein expression system using *E.coli*
Tanaka, C. and K. Murai (Dep. Biosci., Fukui Pref. U.)

P54
Influences of *Aegilops mutica* cytoplasm on the agronomic characters of Japanese wheat cultivars
Matsumura, M. and K. Murai (Dep. Biosci., Fukui Pref. U.)

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Genomic cross-talk mechanism among homoeologous genes for photoperiod pathway in bread wheat
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